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Chromosome 8p23.1 Deletions as a Cause of Complex Congenital Heart Defects and Diaphragmatic Hernia

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Abstract

Recurrent interstitial deletion of a region of 8p23.1 flanked by the low copy repeats 8p-OR-REPD and 8p-OR-REPP is associated with a spectrum of anomalies that can include congenital heart malformations and congenital diaphragmatic hernia (CDH). Haploinsufficiency of GATA4 is thought to play a critical role in the development of these birth defects. We describe two individuals and a monozygotic twin pair discordant for anterior CDH all of whom have complex congenital heart defects caused by this recurrent interstitial deletion as demonstrated by array comparative genome hybridization. To better define the genotype/phenotype relationships associated with alterations of genes on 8p23.1, we review the spectrum of congenital heart and diaphragmatic defects that have been reported in individuals with isolated GATA4 mutations and interstitial, terminal, and complex chromosomal rearrangements involving the 8p23.1 region. Our findings allow us to clearly define the CDH minimal deleted region on chromosome 8p23.1 and suggest that haploinsufficiency of other genes, in addition to GATA4, may play a role in the severe cardiac and diaphragmatic defects associated with 8p23.1 deletions. These findings also underscore the importance of conducting a careful cytogenetic/molecular analysis of the 8p23.1 region in all prenatal and postnatal cases involving congenital defects of the heart and/or diaphragm.

Keywords

Congenital heart defects; 8p23.1 deletion syndrome; Diaphragmatic hernia; Array comparative genomic hybridization; *GATA4*; Prenatal diagnosis

INTRODUCTION

Published deletions involving chromosome 8p23.1 range from large terminal deletions that are easily detectable by routine chromosome analysis to small interstitial deletions which are best identified using fluorescence in situ hybridization (FISH) or molecular techniques such as array comparative genomic hybridization (aCGH) [Paez et al., 2008; Reddy 1999; Devriendt et al., 1999]. Recurrent deletions of a region of 8p23.1 flanked by low copy repeats 8p-OR-REPD (distal) and 8p-OR-REPP (proximal) are associated with a spectrum of anomalies including congenital heart malformations, congenital diaphragmatic hernia

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(CDH), developmental delay, and neuropsychiatric findings [Digilio et al., 1998; Ciccone et al., 2001; Shimokawa et al., 2005; Ciccone et al., 2006; Zuffardi et al., 2006].

This region contains the transcription factor gene *GATA4* which is known to play a key role in heart development in humans [Garg et al., 2003; Okubo et al., 2004; Sarkozy et al., 2005]. Disruption of *Gata4* in mice has also been shown to cause heart defects and anterior CDH [Molkentin et al., 1997; Kuo et al., 1997; Jay et al., 2007]. Mice homozygous for a *Gata4* null allele failed to form a heart tube and died between E7.0 and E9.5 [Kuo et al., 1997; Molkentin et al., 1997]. More recently, Jay et al. reported that a significant fraction of C57BL/6 mice heterozygous for a *Gata4* deletion in exon 2—which removed the translation start site and the N-terminal activation domain—died within 1 day of birth, and that developmental defects in these heterozygotes included atrial septal defects (ASD), ventricular septal defects (VSD) and atrioventricular septal defects (AVSD) [Jay et al., 2007].

In this report, we describe two individuals and an identical twin pair discordant for anterior CDH all of whom were diagnosed prenatally with complex congenital heart defects and were subsequently shown to have interstitial 8p23.1 deletions. We review the spectrum of congenital heart and diaphragmatic defects that have been reported in individuals with isolated *GATA4* mutations and interstitial, terminal, and complex chromosomal rearrangements involving 8p23.1 and discuss the implications of this data on our understanding of the gene(s) within this region which may play a role in heart and diaphragm development.

CLINICAL REPORTS

Patient 1

Patient 1 is a male born at 39 3/7 weeks gestation to a 26-year-old G2P1→2 mother. Both parents were Hispanic and nonconsanguineous. Prenatal ultrasound revealed pulmonary and tricuspid atresia. No amniocentesis was performed. Birth weight was 2.82 kg (10th centile), length was 48.5 cm (50th centile) and frontooccipital circumference (OFC) was 31.5 cm (25th centile). In the neonatal period he was noted to have a two-vessel umbilical cord, a very large anterior fontanelle, downslanting palpebral fissures, mild micrognathia, a short neck, slender fingers, and proximally implanted thumbs. Head ultrasound revealed normal anatomy with possible thinning of the corpus callosum.

Shortly after birth he was admitted to the neonatal intensive care unit for respiratory distress and tachypnea. Postnatal cardiac evaluation revealed a complex single ventricle anatomy consisting of a double outlet right ventricle, unbalanced complete atrioventricular septal defect (AVSD) with left atrioventricular (AV) valve atresia and left ventricular hypoplasia, pulmonary atresia, and D-transposition of the great vessels. Despite stenting of his ductus ateriosus, he continued to have limited pulmonary outflow. During surgery to create a systemic-to-pulmonary artery (Blalock-Taussig) shunt and to ligate the stented patent ductus arteriosus (PDA), he was found to have bilateral superior vena cavae with absence of a bridging innominate vein.

Approximately 6 weeks after birth, he experienced a cardiopulmonary arrest requiring resuscitation and emergent use of extracorporeal membrane oxygenation (ECMO). While on ECMO he developed seizures. He was weaned, decannulated and maintained for a short period of time on high-dose inotropic support before dying at age one month.

Patient 2

Patient 2 is a female born via cesarean at 35 weeks to a G2P1→3 mother as part of a twin gestation. Prenatal ultrasound showed complex congenital heart disease and intra-uterine growth retardation. No anomalies were identified in the male twin. No amniocentesis was performed.

The family history was significant for postaxial polydactyly in father, paternal half brother and maternal half sister. A paternal half brother had aortic insufficiency but this was felt to be secondary to rheumatic heart disease.

Birth weight was 1320 gm (<5th centile), length was 39 cm (<5th centile) and frontooccipital circumference (OFC) was 27 cm (<5th centile). His weight, length, and OFC were at approximately the 50th centile level for a 29-30 week gestation infant, consistent with symmetric intra-uterine growth retardation. Postaxial polydactyly of the left hand was noted along with prominent heels. No facial dysmorphic features were noted.

Shortly after birth, the patient developed respiratory distress requiring intubation and mechanical ventilation. Cardiac evaluation by ECHO and cardiac angiography revealed a complex cardiovascular malformation consisting of an unbalanced AVSD, left AV valve atresia, hypoplastic left ventricle, severe tricuspid regurgitation, absent intrahepatic inferior vena cava and hemiazygos continuation to a left superior vena cava. Head and abdominal ultrasounds were normal.

Considering the severity of the cardiac condition, life-support was withdrawn with parental consent and the patient died at 88 days of life.

Patient 3

Patient 3 is a male infant born at 34 5/7 weeks via cesarean to a 33-year-old G1P0→2 mother as part of a monozygotic twin gestation (see Patient 4). Prenatal ultrasound at 20-weeks gestation revealed an AVSD with a large inlet ventricular septal defect (VSD) extending to the perimembranous septum, aortic hypoplasia, a dominant pulmonary artery, and mild tricuspid regurgitation. An amniocentesis was performed and aCGH and chromosome analyses revealed a deletion on chromosome 8p.

Birth weight was 1835 grams (25th centile), length was 44.5 cm (50th centile), and frontooccipital circumference (OFC) was 29 cm (10th centile). At birth, examination revealed a holosystolic murmur, mild dysmorphic facial features, minor digital anomalies, and a sacral dimple. Spinal cord tethering was ruled out by spinal ultrasound.

Postnatal cardiac evaluation revealed a balanced type A complete AVSD with mild AV regurgitation, moderate atrial septal defect (ASD), hypoplastic aortic arch, a narrow left ventricular outflow tract, a large PDA, and good biventricular function. At surgery, he was found to have a right atrium with two appendages and absence of a bridging innominate vein.

Shortly after birth, the patient was transferred to the neonatal intensive care with tachypnea and desaturations. Further evaluation revealed evidence of a large anterior congenital diaphragmatic hernia with herniation of the liver, levoposition of the heart and a hypoplastic, posteriorly rotated left lung.

The patient remained hospitalized until approximately 12 weeks of age and is presently 5-months-old.

Patient 4

Patient 4 is the male monozygotic twin of patient 3. Prenatally, he was found to a balanced complete AVSD, a small aortic arch, and a large PDA. An amniocentesis was performed and aCGH and chromosome analyses revealed a deletion on chromosome 8p.

He was born at 2020 grams (25th centile), with a length of 44.8 cm (30th centile), and frontooccipital circumference (OFC) of 29.5 cm (10th centile). Additional findings on postnatal cardiac evaluation included a small aortic valve, bilateral peripheral pulmonary stenosis, and mild right ventricular dilatation. He was also found to have a small right choroid plexus cyst and a sacral dimple. Spinal cord tethering was ruled out by spinal ultrasound.

He was discharged home on day of life 38, with a discharge weight of 2960 g, a length of 48.5 cm and an OFC of 33 cm.

MATERIALS AND METHODS

Patients

All four patients were referred for clinical cytogenetic testing. Institutional review board approved informed consent was obtained for high-resolution studies.

Clinical Cytogenetic Tests

Standard laboratory procedures were used for metaphase preparations. G-banded chromosome analysis and FISH analysis were performed in either Medical Genetics Laboratories at Baylor College of Medicine or by the referring center. DNA was extracted from peripheral blood [Ou et al., 2008] and amniotic fluid samples [Bi et al., 2008] as previously described. Patients 1 and 2 were examined in the neonatal period and Patients 3 and 4 in the prenatal period. In the case of Patients 1, 3, and 4, aCGH testing and chromosome analysis were performed concurrently at the Medical Genetics Laboratories at Baylor College of Medicine. For Patient 2, aCGH analysis was performed following normal chromosome analysis results. All clinical aCGH analyses were performed using Baylor College of Medicine (BCM) Chromosomal Microarray version 6 (CMA V6) manufactured by Agilent Technologies (Santa Clara, CA) according to the manufacturer's instructions with modifications [Ou et al., 2008].

High-Resolution aCGH Analysis

DNA from Patients 1 and 4 was further evaluated by high resolution genome-wide aCGH using Human Genome CGH 244K Oligo Microarray Kits G4411B (Agilent Technologies, Santa Clara, CA) according to the manufacturer's protocol version 2.0. Arrays were scanned using an Agilent DNA Microarray Scanner (Agilent Technologies, Santa Clara, CA). Data extracted using Feature Extraction Software Version 9.1.3 (Agilent Technologies, Santa Clara, CA) was analyzed using CGH Analytics 3.4.40 Software (Agilent Technologies, Santa Clara, CA) with copy number changes identified with the assistance of the Aberration Detection Method 2 algorithm (threshold 6.0). Control DNA consisted of DNA from a healthy gender-matched reference individual with no personal or family history of heart or diaphragm defects.

Sequencing Analysis

PCR amplification of genomic fragments was performed using previously described primer pairs [Okubo et al., 2004]. PCR-fragments were cleaned and sequenced commercially (Agencourt Bioscience, Beverly, MA) and DNA changes were identified by comparing the

published *GATA4* sequence to sequence data obtained from patient samples using Sequencher 4.5 software (GeneCodes, Ann Arbor, MI).

RESULTS

Visible deletions of 8p were identified on the chromosome analysis for Patients 1, 3 and 4 (Fig 1). Chromosome analysis and FISH for 22q11.2 deletions performed on a peripheral blood sample from Patient 2 at an outside facility were reported as normal.

Clinical aCGH detected an identical 8p23.1 deletion in all four patients with a minimal deletion size of 2.945 Mb (8,850,913 to 11,796,333) and a maximal deletion size of 6.352 Mb (6,436,314 to 12,788,647) (Fig 1). Parental studies confirmed that all of the deletions were de novo.

High resolution aCGH analyses confirmed the deletions previously seen in the clinical studies. In each case the deletion was flanked by the low copy repeats 8p-OR-REPD and 8p-OR-REPP with differences in apparent deletion size between Patients 1 and 4 being attributable to known copy number variant regions within and/or directly adjacent to the low copy repeats. The minimal deleted interval encompassed twenty-two known genes/open reading frames including *GATA4* (Fig 2).

To determine whether disruption of both *GATA4* alleles could explain the severe cardiac defects and CDH seen in our patients, we screened the entire *GATA4* coding sequence and intron/exon boundaries of the remaining GATA4 allele in Patients 1 and 4. No variations from the published *GATA4* reference sequence were identified in the coding sequence or the intron/exon boundaries of these DNA samples.

DISCUSSION

We have described the phenotype associated with the recurrent deletion of 8p23.1 in four patients with prenatally diagnosed complex congenital heart defects. The *GATA4* gene resides within this recurrently deleted interval and has been implicated as the gene responsible for heart defects associated with 8p23.1 deletions. The role of *GATA4* in heart development is supported by mouse models [Kuo et al., 1997; Molkentin et al., 1997; Jay et al., 2007] and studies of patients with *GATA4* gene mutations.

Some of the most compelling evidence that mutations in *GATA4* are associated with heart defects in humans come from studies of seven families in which ASD was found to segregate with heterozygous *GATA4* mutations with varying levels of penetrance (Table I) [Garg et al., 2003;Hirayama-Yamada et al., 2005;Sarkozy et al., 2005;Okubo et al., 2004]. The *GATA4* gene has also been screened in individual patients with ASD, VSD, AVSD, and tetralogy of Fallot (TOF). Although a number of non-synonymous changes were identified in these studies, it was often difficult to conclude whether these changes were causal due to a lack of parental/population controls and/or functional studies. This is particularly true of changes that are inherited from a non-affected parent. The most convincing of these changes include a de novo E216D missense mutations in two individuals with TOF that was shown to have reduced transcriptional activity in a reporter assay, and a frameshift mutation (Pro226fs) and a premature stop codon mutation (Arg266Ter)—which severely truncate the protein—each found in a patient with atrioventricular septal defects (AVSD) (Table II) [Nemer et al., 2006;Reamon-Buettner et al., 2007].

The complex cardiac phenotypes seen in our patients led us to question whether the spectrum of heart defects associated with 8p23.1 deletions was more severe than that seen in patients with *GATA4* mutations. With this in mind we reviewed previous reports of

interstitial, terminal and complex deletions of 8p23.1 (Table III) to determine the spectrum of cardiac phenotypes associated with these deletions. Previously reported patients with interstitial deletions were found to have a spectrum of cardiac defects that included ASD, VSD, AVSD, pulmonary stenosis, pulmonary valve stenosis, tetralogy of Fallot, and/or combinations of these defects. Cardiac defects in patients with terminal deletions extending to at least 8p23.1 included AVSD, hypoplastic left heart, hypoplastic right ventricle, pulmonary atresia/stenosis, pulmonary valve stenosis, partial anomalous pulmonary venous return, subaortic stenosis, transposition of the great arteries, double inlet/double outlet right ventricle, double inlet left ventricle and tetralogy of Fallot.

When combined with data from the four patients described in this report, it would appear that the spectrum of heart defects is more severe in interstitial and terminal deletions involving 8p23.1 when compared to defects seen in patients with heterozygous *GATA4* mutations. Although this increase in severity could be due to deleterious mutations in the remaining *GATA4* allele, we did not detect such mutations in Patients 1 and 4. A similar evaluation carried out by Paez et al. also failed to identify mutations in the remaining *GATA4* allele in two patients with 8p23.1 deletions involving *GATA4* who also presented with heart defects [Paez et al., 2008].

An alternative explanation for the increase in severity would be the existence of another gene(s) in the recurrent 8p23.1 deletion region that impact heart development. Of the genes deleted along with *GATA4*, *SOX7* is one of the most likely candidate genes. *SOX7* is expressed in mouse and human adult heart, and in the early cardiogenic region of *Xenopus* embryos [Takash et al., 2001; Taniguchi et al., 1999; Zhang et al., 2005]. *SOX7* mRNA injection induced cardiogenic marker expression in *Xenopus* animal cap explants whereas knockdown of *SOX7* using morpholinos decreased the expression of cardiogenic markers *MHCα* and *Nkx2.5*; and marker expression was rescued by injection of RNA encoding a *SOX7* transcript [Zhang et al., 2005]. Interestingly, silencing of *Sox7* in mouse F9 embryonal carcinoma cells blunts the increase in *Gata4* mRNA levels seen after treatment with all trans-retinoic acid/dibuterol cAMP [Futaki et al., 2004]. In contrast, silencing of *Gata4* did not result in decreased *Sox7* expression in the same system. This suggests that *Sox7* lies upstream of *Gata4*, and that haploinsufficiency of *SOX7* may exacerbate the cardiac phenotype of individuals with *GATA4* deletions.

Genes outside the GATA4 region may also be involved in abnormal cardiac development based on reports of patients with inverted duplication deletion events involving 8p. The mechanism involved in creation of the most common inverted duplication deletion events of 8p has been well described [Ciccone et al., 2006]. These events typically result in loss of copy number (deletion) of 8p distal to 8p-OR-REPD, normal copy number of the GATA4 region between 8p-OR-REPD and 8p-OR-REPP, and a variable region of increased copy number (duplication) proximal to 8p-OR-REPP. The number of cardiac malformations associated with patients carrying the inverted duplication deletion 8p was 11/39 (28.2%), a much lower proportion than 17/18 (94.4%) and 45/60 (75%) associated with interstitial and terminal deletions, respectively (Table III). In general, the spectrum of cardiac malformations in these cases is also milder but still includes ASD, VSD, right aortic arch, and pulmonary stenosis (Table III). If we assume normal expression of GATA4 and other genes between 8p-OR-REPD and 8p-OR-REPP, we are left to conclude that decreased expression of one or more genes distal to 8p-OR-REPD and/or over expression of one or more genes proximal to 8p-OR-REPP can also contribute to the development of some heart defects.

Congenital diaphragmatic hernia is also common in patients with a deletion encompassing 8p23.1 with, at least, nine previously reported cases [Holder et al 2007]. CDH is associated

with 4/18 (22.2%) of reported interstitial deletions and 5/60 (8.3%) of terminal deletions but has not been described in patients with inverted duplication deletions. This is, presumably, due to the fact that terminal deletions may not always include the CDH minimal deleted interval and that this interval has a normal copy number in individuals with inverted duplication deletions.

The majority of CDH patients with 8p23.1 deletions have been described as having left sided (assumedly-posterior) CDH. Indeed, Patient 3 is the only individual described to date with an anterior CDH associated with an 8p23.1 deletion. This is surprising since the heterozygous *Gata4* mice described by Jay et al. have anterior CDH similar to that seen in our patient [Jay et al., 2007]. Using array data presented here and previously reported molecularly-defined deletions associated with CDH, the minimal deleted region for CDH on 8p can be defined as the region bounded by 8p-OR-REPD distally and 8p-OR-REPP proximally (Fig 3) [Faivre et al., 1998; Slavotinek et al., 2004; Shimokawa et al., 2005].

Although the use of array comparative genome hybridization can aid in the identification of 8p23.1 deletions in patients with heart and/or diaphragm defects, caution must be used in the interpretation of these findings. Chromosome 8p contains many copy number variant regions whose potential contribution to the development of birth defects has not been adequately studied. Recently Chen et al. [2007] described a patient with a Fryns-like phenotype including congenital diaphragmatic hernia, macrocephaly, brachytelephalangy, nail hypoplasia, short webbed neck with redundant posterior nuchal skin, coarse face, flat and broad nasal bridge, hypertelorism, macrostomia, microretrognathia, and low-set ears. The patient's phenotype was attributed to a de novo 0.7 MB deletion within 8p23.1 [Chen et al., 2007]. However, this deletion lies entirely within a known copy number variant region making it difficult to determine if this deletion is causal. Without careful evaluation, physicians may erroneously quote sibling and offspring recurrence risks that are either too low or too high based on an incorrect assumption of causality.

When used properly, aCGH detects detrimental submicroscopic changes that can be easily missed on routine chromosomal analysis especially in prenatal samples where the band resolution may be compromised [Pecile et al., 1990; Wu et al., 1996; Faivre et al., 1998]. This is illustrated well in Patient 2 where chromosome analysis failed to identify an 8p deletion which was easily detected by aCGH. This, and the high frequency of cardiac and diaphragmatic defects associated with 8p23.1 interstitial deletions, leads us to recommend that aCGH be performed on all prenatal and postnatal cases with congenital cardiac and/or diaphragm defects. At the present time we do not recommend that the GATA4 gene be sequenced in patients with cardiac defects since the percentage of cases with protein-altering changes in GATA4 is likely to be small— approximately 1% based on the articles reviewed—and the clinical significance of the majority of GATA4 changes remains unclear.

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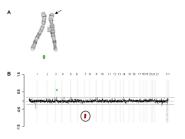


Figure 1.Partial karyotype and clinically based array comparative genomic hybridization results for Patient 4. A) Chromosome 8 partial karyotype showing an interstitial deletion of 8p23.1. B) Prenatal clinical array (BCM CMA V6) confirming deletion of chromosome 8p23.1 with the oligonucleotide probes detecting the copy number loss marked in red. This array also detected a gain in copy number of four genes (*SLC2A9*, *WDR1*, *ZNF518B*, *MIST*) on chromosome 4 (marked in green) all of which are lie partially or completely within known copy number variants.

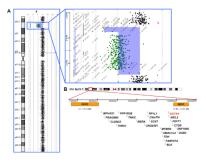


Figure 2.

A) High resolution array comparative genomic hybridization analysis of Patient 4 showing an interstitial deletion of chromosome 8p23.1. B) Graphical representation of unique genes (RefSeq reviewed or validated) located between segmental duplications 8p-OR-REPD and 8p-OR-REPP which are deleted in all of the patients reported in this study. Defensin genes, which are present in multiple copies within segmental duplications, are not shown.

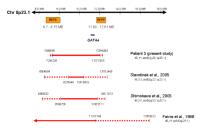


Figure 3. Molecularly defined deletions of 8p23.1 associated with CDH. Solid and dashed red lines indicate the minimally and maximally deleted regions, respectively, for each patient. The approximate location of the segmental duplications 8p-OR-REPD and 8p-OR-REPP are represented by green bars. *GATA4*, represented by the blue bar, is located within the minimal deleted region for CDH.

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Table I

GATA4 Alterations in Familial Heart Defects

Reference	Alteration (AA change) Phenotype	Phenotype	Penetrance	Families	Control chromosomes	Functional studies
Garg et al., 2003	Gly296Ser	Non-syndromic ASD (+/- VSD, PVS, cardiac valve insufficiency, AVSD)	100% of clinically evaluated affected individuals	1 Family	0/6000 (and 0/10 evaluated unaffected family members)	Disrupted interaction with TBX5, decreased DNA binding affinity, hypomorphic transactivation ability
	Glu359fs	Non-syndromic ASD	100% of evaluated affected individuals	1 family	0/6000 (and 0/2 evaluated unaffected family members)	Transcriptionally inactive
Okubo et al., 2004	Ser358fs	ASD +/- PS	100% of clinically evaluated affected individuals	1 family	0/200 (and 0/13 evaluated unaffected family members)	Frameshift & premature STOP codon at amino acid 403, likely results in haploinsufficiency, similar to 1075delG described by Garg et al., 2003
Sarkozy et al., 2005b	Gly296Ser	ASD, PVS, no conduction abnormalities	2/2 Affected individuals (family 1), 3/3 clinically evaluated affected individuals (family 2)	2/16 Families total	NR T	See Garg et al., 2003
Hirayama- Yamada et al., 2005	Glu359fs	ASD (5 individuals) dextrocardia (1 individual)	6/7 Affected individuals (family 1)	1 Family/16 families	NR	
	Ser52Phe	ASD (3 individuals)	3/3 Affected individuals (family 2)	1 Family/16 families	0/202 Control chromosomes from healthy Japanese individuals	Decreased transcriptional activity (Schluterman et al., 2007), normal subcellular localization & DNA binding activity, Ser52 located in transactivation domain 1 (TAD1)

ASD, atrial septal defect; AVSD, atrioventricular septal defect; NR, not reported; PS, pulmonary stenosis; PVS, pulmonary valve stenosis; VSD, ventricular septal defect.

Table II

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GATA4 Alterations in Sporadic Heart Defects

Reference	Nucleotide Change¥	AA Change	Phenotype	Frequency	Inheritance pattern	Control Chromosomes	Functional studies
Poirier et al., 2003	NR	Ala411Val§	Cardiac hypertrophy	Unclear (95 individuals screened)	NR	NR	NR
Poirier et al., 2003	NR	Ser377Gly	Cardiac hypertrophy	Unclear (95 individuals screened)	NR	NR	NR
Reamon- Buettner et al., 2005	874T>C	Cys292Arg	VSD, ASD, AVSD		NR	0/40	NR
	T <dz< td=""><td>Arg229Ser</td><td>VSD, ASD, AVSD</td><td></td><td>NR</td><td>0/130</td><td>NR</td></dz<>	Arg229Ser	VSD, ASD, AVSD		NR	0/130	NR
	631T>C	Phe211Leu	VSD, AVSD		NR	0/130	NR
	731A>G	Tyr244Cys	VSD, AVSD		NR	0/130	NR
	743A>G	Asn248Ser	ASD, AVSD		NR	0/2	NR
	782T>C	Leu261Pro	VSD, ASD		NR	NR	NR
	677delC	Pro226fs	AVSD		NR	0/2	NR
	700G>A	Gly234Ser	AVSD		NR	0/4	NR
	755G>C	Arg252Pro	AVSD		NR	0/4	NR
	796C>T	Arg266Ter	AVSD		NR	0/2	NR
	818A>G	Asn273Ser	AVSD		NR	0/2	NR
	830C>T	Thr277Ile	AVSD		NR	NR	NR
	848G>A	Arg283His	AVSD, overriding aorta, ASD		NR	0/2	NR
	855T>G	Asn285Lys	AVSD		NR	NR	NR
	905A>G	His302Arg	AVSD		NR	NR	NR
	622T>C	Phe208Leu	VSD		NR	0/2	NR
	640G>A	Gly214Ser	VSD		NR	NR	NR
	CST>C	Met223Thr	VSD		NR	0/2	NR
	715A>G	Asn239Asp	VSD		NR	NR	NR
	716A>G	Asn239Ser	VSD		NR	NR	NR
	779G>A	Arg260Gln	VSD		NR	NR	NR
	779G>A	Ile255Thr	ASD		NR	NR	NR
	881C>T	Ala294Val	ASD		NR	NR	NR

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Reference	Nucleotide Change¥	AA Change	Phenotype	Frequency	Inheritance pattern	Control Chromosomes	Functional studies
Nemer et al., 2006	648C>G	Glu216Asp	TOF	2/26 Patients with TOF	De novo in both patients	0/446	Reduced transcriptional activity in reporter assay
Reamon-Buettner et al., 2007	1288C>G	Leu430Val	AVSD		NR	NR	NR
	1081A>G	Met361Val	VSD		NR	NR	NR
	1130G>A	Ser377Asn	VSD		NR	NR	NR
	1324G>A	Ala442Thr	VSD		NR	NR	NR
	1295T>C	Leu432Ser	ASD		NR	NR	NR
	1288C>G	Leu430Val	ASD		NR	NR	NR
Rajagopal et al., 2007	487C>T	Pro163Ser	ECD	1/43 Patients with ECD	Paternal, unaffected father	009/0	NR
	1037C>T	Ala346Val	ECD	1/43 Patients with ECD	Maternal, unaffected mother	009/0	NR
	T <d988< td=""><td>Gly296Cys</td><td>Secundum ASD, PVS</td><td>1/8 Patients with septal defects</td><td>Paternal, affected father (persistent left superior vena cava)</td><td>0/200</td><td>NR</td></d988<>	Gly296Cys	Secundum ASD, PVS	1/8 Patients with septal defects	Paternal, affected father (persistent left superior vena cava)	0/200	NR
	1207C>A	Leu403Met	Hypoplastic RV, sinus venosus ASD	1/9 Patients with RV hypoplasia	Unknown, no parental DNA available	0/200	NR
Tomita- Mitchell et al., 2007	278G>C§	Gly93Ala§	Secundum ASD	1/222 ASD patients	Mother carrier, father unknown	0/318	NR
	946C>G§	Gln316Glu§	ASD, small muscular VSDs, mild PVS	1/137 VSD patients	Both parents unknown	0/318	NR
	1232C>T\$	Ala411Val§	VSD	1/137 VSD patients	Both parents unknown	0/318	NR
	1273G>A§	$Asp425Asn^{\$}$	ASD	1/222 ASD patients	Mother carrier, father not carrier	0/528	NR
	1273G>A§	$Asp425Asn^{\$}$	TOF	1/201 TOF patients	Both parents unknown	0/528	NR
Posch et al., 2008	1232C>T [§]	Ala411Val§	Cribriform ASD and PAPVR	1/205 patients with congenital septal defects	unknown	009/0	NR

ASD, atrial septal defect; AVSD, atrioventricular septal defect; ECD, endocardial cushion defect; NR, not reported; PAPVR, partial anomalous pulmonary venous return; PVS, pulmonary valve stenosis; RV, right ventricle; TOF, tetralogy of Fallot; VSD, ventricular septal defect.

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TABLE III

Summary of Reported Cases Involving Deletion of 8p23.1

Other		Possible thinning of corpus callosum, large anterior fontanelle, dysmorphic features, 2-vessel umbilical cord	Symmetrical intrauterine growth retardation, familial postaxial polydactyly of the left hand	ith left Small sacral dimple but no evidence of spinal abnormalities	Small sacral dimple but no evidence of spinal abnormalities	MR, slow growth, dysmorphic features, broad chest, puffy hands and feet	Partial agenesis of corpus callosum	Slow growth, microcephaly, MR, dysmorphic features, broad chest, hypospadias		Slow growth, microcephaly, MR, dysmorphic features, broad chest, hypospadias, cryptorchidism	Basal ganglia calcification, arched palate, hypothyroidism, atrophic pancreas, lordosis, renal artery stenosis	Language delay, MR, dysmorphic features, esotropia, scoliosis	Hepatosplenomegaly, feet deformity	Developmental delay, behavioral disorder	ion nto Bilateral cryptorchidism	Ascites, polyhydramnios
Diaphragm/Lungs				Large anterior CDH with left lobe of liver in anterior mediastinum, left lung hypoplasia											Left CDH with herniation of abdominal organs into left thorax, left pulmonary hypoplasia	Left CDH, pulmonary hypoplasia, pleural effusions
Heart	INTERSTITIAL DELETIONS	Complete AVSD (unbalanced), complex single ventricle, double outlet right ventricle, pulmonary aresia, left arrioventricular valve arresia, hypoplastic LV, D-transposition of the great vessels	AVSD (unbalanced), left atrioventricular valve atresia, hypoplastic LV, severe tricuspid regurgitation, absent intrahepatic inferior vena cava, hemiazygos continuation to left SVC	Complete AVC (balanced type A), mild AV regurgitation, hypoplastic aortic arch, narrow left ventricular outflow tract	Complete AVSD (balanced), small aortic valve, bilateral peripheral pulmonary stenosis, mild right ventricular dilatation		PS, PFO	AVSD, subaortic stenosis, persistent left SVC	Complete AVSD, PS, persistent left SVC	AVSD, PS, dextrocardia, persistent left SVC, hypoplastic RV	Secundum ASD, PVS, 1eft SVC, cardiomyopathy	AVSD, TOF	ASD, VSD, PS	ASD	ASD	Large ASD, VSD
Cytogenetic findings		46,XY,del(8)(p23.1p23.1)	46,XY,del(8)(p23.1p23.1)	46,XY,del(8)(p23.1p23.1)	46,XY,del(8)(p23.1p23.1)	$46,XY,del(8)(pter\rightarrow p23::p21\rightarrow qter)^*$	$46,XY,del(8)(pter \rightarrow p23.2::p22 \rightarrow qter)$	del(8)(p21p23)	del(8)(p21p23)	del(8)(p21p23)	46,XX,del(8)(p23.1p23.2)	46,XX,del(8)(p23.1p23.2)	46,XY,del(8)(p23.1p23.1) or add(8)(p23.1)[20]	46,XY,del(8)(p23.1p23.1). ish del(8)(p23.1p23.1)(wcp8+, 8ptel+)	$46.{ m XY,del}(8)({ m p23.1p23.1})$	46,XY,del(8)(p23.1p23.1)
Reference		Present study, Patient 1	Present study, Patient 2	Present study, Patient 3	Present study, Patient 4	Orye and Craen, 1976	Hutchinson et al., 1992; Giglio et al., 2000	Digilio et al., 1998	Digilio et al., 1998	Digilio et al., 1998, 1999	Pehlivan et al., 1999	Pehlivan et al., 1999	Reddy, 1999	Reddy, 1999	Shimokawa et al., 2005	Slavotinek et al., 2005; 2006

Lopez et al., 2006

Reference

Paez et al., 2008

Paez et al., 2008

Patil and Hanson, 1980

Fraer et al., 1992

Wat et al.

Cornelia de Lange-like features, CNS abnormalities, dysmorphic features, chylothorax, reduced muscle bulk, cryptorchidism CNS abnormalities, lacrimal sac fistula, dysmorphic features Hypotonia, slow growth, corpus callosum agenesis, dysmorphic features		ASD Heart Defects: 45/60 (75%) INVERTED DUPLICATION DELETION	$46,XY,del(8p23.1)$ Totals for this subgroup $inv\ dup\ del(8)(p11.2\rightarrow 23.1::p23.1\rightarrow qter)$ $inv\ dup\ del\ (8)(p11.2\rightarrow 23.2::p23.2\rightarrow qter)$
	CDH: 5/60 (8.3%)	Heart Defects: 45/60 (75%)	Totals for this subgroup
Cornelia de Lange-like features, CNS abnormalities, dysmorphic feat chylothorax, reduced muscle bulk, cryptorchidism	Left sided CDH and pulmonary hypoplasia, persistent pulmonary hypertension	ASD	46,XY,del(8p23.1)
Accessory spleen	Left CDH, pulmonary hypoplasia	ASD	46,XX,del(8)(p23.1)
Gross motor development delay, moderate delays in language and social skills until 6 years old			del(8)(p23)
Hypotonia, cerebral palsy, microcephaly, developmental delay, craniofacial abnormalities, eye abnormalities, pectus excavatum			46,XX,del(8)(p23.1)[20]
			(123:1)(13 do)(1:62d)

Devriendt et al., 1999 Devriendt et al., 1999

Reddy, 1999 Reddy, 1999 Reddy, 1999

Bhatia et al., 1999

Pehlivan et al., 1999 Pehlivan et al., 1999 Pehlivan et al., 1999

Faivre et al., 1998

Digilio et al., 1998

Digilio et al., 1998 Digilio et al., 1998 Digilio et al., 1998

Digilio et al., 1998 Digilio et al., 1998

		Wat	et al.																						
NIH-PA Author Manuscript	Other	Cerebral atrophy, dysmorphic features, asymmetric chest, restricted articular function in all major joints, thoracolumbar scoliosis	Spastic paraparesis, epilepsy, abnormal EEG, dysmorphic features, coloboma, umbilical hernia, supernumerary finger	Profound MR, hypotonia, dysmorphic features, scoliosis, long & hyperextensible fingers and toes, partial 2-3 syndactyly of toes	Severe MR	Hypotonia, brain anomalies, MR, dysmorphic facies	Hypotonia	Hypotonia, brain anomalies, dysmorphic facies	Hypotonia, brain anomalies, MR, dysmorphic facies	Hypotonia, brain anomalies, MR, dysmorphic facies	MR, short stature, dysmorphic facies	Hypotonia, MR, dysmorphic facies	Hypotonia, brain anomalies, MR, short stature, dysmorphic facies	Brain anomalies, MR, dysmorphic features	Hypotonia, brain anomalies, MR, dysmorphic facies	Hypotonia, psychomotor retardation, facial dysmorphic features	Severe psychomotor retardation, dysmorphic facies, left kidney hypoplasia	Severe MR, dysmorphic facies, contractures of extremities, severe scoliosis, left cryptorchidism	Profound MR, dysmorphic features, severe scoliosis, contractures of lower extremities	CNS abnormalities, MR, dysmorphic features, bilateral clinodactyly of fifth fingers	CNS abnormalities, dysmorphic features, hearing loss	Agenesis of corpus callosum, psychomotor delay, dysmorphic features	Hypotonia, severe MR, developmental delay, facial dysmorphic features	MR, hypotonia, agenesis of corpus callosum, facial dysmorphic features, umbilical hernia, hydronephrosis	MR, hypotonia, developmental delay, partial agenesis of corpus callosum, dysmorphic facies
NIH-PA Author Manuscript	Diaphragm/Lungs																								
NIH-F	Heart						Heart malformation										Dextrocardia					ASD		ASD, VSD	
NIH-PA Author Manuscript	Cytogenetic findings	46,XY,inv dup del(8)(p21.2→p23.1::p23.1→qter)	$46,XX,inv dup(8)(p21.1\rightarrow 23.3::p23.3\rightarrow qter)$	$46,XX,inv dup del(8)(p12\rightarrow p23.1::p23.1\rightarrow qter)$	46,XX,inv dup del(8)(p12 \rightarrow p23.1::p23.1 \rightarrow qter)	inv dup del(8)(p12 \rightarrow p22::p22 \rightarrow qter)	inv dup del(8)(p12 \rightarrow p22::p22 \rightarrow qter)	inv dup del(8)(p21.1 \rightarrow p22.1::p22.1 \rightarrow qter)	inv dup del(8)(p12 \rightarrow p22::p22 \rightarrow qter)	inv dup del (8)(p12 \rightarrow p22::p22 \rightarrow qter)	inv dup del (8)(p12 \rightarrow p22::p22 \rightarrow qter)	inv dup del (8)(p12 \rightarrow p22::p22 \rightarrow qter)	inv dup del(8)(p12 \rightarrow p23.1::p23.1 \rightarrow qter)	inv dup del(8)(p21.1 \rightarrow p22::p22 \rightarrow qter)	inv dup $del(8)(p12\rightarrow p23.1::p23.1\rightarrow qter)$	inv dup del(8)(p12→p23.1::p23.1→qter)	$46,XY,inv dup del(8)(p12\rightarrow p23.1::p23.1\rightarrow qter)$	inv dup del(8)(p21.1 \rightarrow p22::p22 \rightarrow qter)	inv dup del(8)(p11.2 \rightarrow p23.1 \rightarrow pt23.1 \rightarrow qter)	inv dup del(8)(p12 \rightarrow p23.1::p23.1 \rightarrow qter)	inv dup del(8)(p11.2→p23.1::p23.1→qter)	inv dup del(8)(p11.2→p23.1::p23.1→qter)			
	Reference	Jensen et al., 1982	Jensen et al., 1982	Dill et al., 1987	Henderson et al., 1992	Minelli et al., 1993	Minelli et al., 1993	Minelli et al., 1993	Minelli et al., 1993	Minelli et al., 1993	Minelli et al., 1993	Minelli et al., 1993	Minelli et al., 1993	Minelli et al., 1993	Minelli et al., 1993	Engelen et al., 1994; de Die-Smulders et al., 1995	Engelen et al., 1994; de Die-Smulders et al., 1995	Engelen et al., 1994; de Die-Smulders et al., 1995	Engelen et al., 1994; de Die-Smulders et al., 1995	Mitchell et al., 1994	de Die-Smulders et al., 1995	de Die-Smulders et al., 1995	de Die-Smulders et al., 1995	Guo et al., 1995	Guo et al., 1995

MR, developmental delay, hypotonia, agenesis of corpus callosum, cranial asymmetry, dysmorphic facies

Guo et al., 1995

inv dup del(8)(p11.2 \rightarrow p23.1::p23.1 \rightarrow qter)

Wat et al.

Floridia et al., 1996; Giglio et al., 2000 Floridia et al., 1996; Giglio et al., 2000 Yenamandra et al., 1999

Hypotonia, global developmental delay, CNS abnormalities, cerebral palsy etatarsal CDH: 0/39 (0%) COMPLEX CHROMOSOMAL REARRANGEMENTS Heart Defects: 11/39 (28.2%) 46,XX, der(8)del(8)(p23.1)dup(8)(p23.1p12) Totals for this subgroup

MR, craniofacial, ocular, skeletal anomalies MR, craniofacial, ocular, skeletal anomalies

cardiac anomalies cardiac anomalies

inv dup $del(8)(p12\rightarrow 23.1::p23.1\rightarrow qter)$

Shimokawa et al., 2004

Macmillin et al., 2000

Macmillin et al., 2000

Giglio et al., 2000

Shimokawa et al., 2004 Shimokawa et al., 2004

Shimokawa et al., 2004 Shimokawa et al., 2004

Sherr et al., 2005

Mattei et al., 1980	t(8;14)(8pter→8p11→8p23.1::8p23.1→8p11::14q13→14qter)	it)	Hypotonia, CNS abnormalities, dysmorphic features, phalangeal abnormalities
Brocker-Vriends et al., 1985	46, XY, der(8), t(8;13)(p21;q22), t(2;19)(q21;q13)		Mild dysmorphic features, laryngomalacia (infant)
Brocker-Vriends et al., 1985	46,XX,der(8),t(8;13)(p21;q22)		Pyloric stenosis, elbow hyperextensibility
van Balkom et al., 1992	46,XX,del(8)(p21)/46,XX,dup(8)(p21pter)		Agenesis of corpus callosum, short first metacarpals, short first metatars
Scarbrough et al., 1987	46,XX,der(8),t(3;8)(p21;p23)	2/6 systolic murmur	Hypotonia, dysmorphic features, long trunk, camptodactyly
Sujansky et al., 1993; Giglio et al., 2000	$46,XX,rec(8)(qter\rightarrow q22::p23.1\rightarrow qter)$	PS, PDA, ASD, VSD	MR
Digilio et al., 1994; Ciccone et al., 2006	mos 46,XX,psu dic(8)(p23.2)/46,XX,del(8)(p23.1)		Severe MR, dysmorphic features, kyphoscoliosis, globous abdomen, premature grey hair (at 14 years old)
Zahed et al., 1998	46,XX,rec(8)t(8;9)(p23.1;q34)mat		Hypotonia, developmental delay, hyperactivity, dysmorphic features
Giglio et al., 2000	46,XY,der(8)t(1;8)(q42;p23.1)pat	PS, PFO	MR, seizures, pyloric stenosis
Giglio et al., 2000	46,XY,der(8)t(8;16)(p21.3;q24)	PS, VSD, right aortic arch	Slight MR
Giglio et al., 2000	46,XY,der(8)t(8;16)(p21.3;q24)	PS	Slight MR
de Vries et al., 2001	46,XY.ish der(8)t(8;20)(p23;p13) (D8S2333-)	Murmur but no structural abnormalities	Delayed speech & language, dysmorphic features, blocked tear ducts, cryptorchidism

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ASD, atrial septal defect; AVC, atrioventricular canal; AVSD, atrioventricular septal defect; CDH, congenital diaphragmatic hernia; CNS, central nervous system; EEG, electroencephalogram.; HLHS, hypoplastic left heart syndrome; HTN, hypertension; IUGR, intrauterine growth retardation; LV, left ventricle; L-R, left-right; MR, mental retardation; PFO, patent foramen ovale; PDA, patent ductus arteriosus; PS, pulmonary stenosis; RV, right ventricle; SVC, superior vena cava; TOF, tetralogy of Fallot; VSD, ventricular septal defect.

* interstitial deletion, but insufficient resolution to determine if it deletes region of interest.

** karyotype nomenclature not provided.