The Study Of Karyotypes In Patients With Congenital Heart Diseases Of Gujarat State

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Abstracts: Introduction: Congenital heart disease (CHD) is the most common of all the birth defects and is a leading cause of mortality in the 1st year of life. Congenital heart disease can be related to chromosomal aberrations and mutation of single gene. Material and Method: In this study a total of 24 confirmed cases of CHD were considered of age ranging from Day 1 to 15 years. A prior Written consent was taken from the parents of these patients. The relevant clinical data, important investigations and blood samples where collected. A conventional cytogenetic study was performed on the 24 selected patients. Results: Out of 24 patients 1 patient showed a chromosomal abnormality in the form of trisomy 21. Conclusion: Hence the present study was carried out as a Continued research on the genetic cause of congenital heart diseases and to augment our understanding of the mechanisms underlying the normal and abnormal development of the cardiac structures. [Modasia U et al NJIRM 2012; 3(3) : 33-35]

Key words: Congenital heart disease, Karyotype.

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Introduction: Congenital heart disease is defined as "A gross structural abnormality of the heart or intra-thoracic great vessels that is actually or potentially of functional significance."[1] Congenital heart disease is the most common of all birth defects and is the leading cause of mortality in the 1st year of life with a prevalence of 1% in live births & 10% in spontaneously aborted fetus[2].

Malformations are due to complex multifactorial genetic and environmental causes. Multifactorial disorders account for 90% of all cardiac malformations, recognized chromosomal aberrations and mutations of single genes account for < 10% of all cardiac malformations, environmental teratogens affecting disorder account for 2 % of all cardiac malformation[3]. Continued research on the genetic cause of congenital heart diseases promises to augment our understanding of the mechanisms underlying the normal and abnormal development of the cardiac structures.[4,,5]Confirmation of chromosomal anomalies as a cause of congenital heart disease diagnosed by karyotyping can help in proper management after knowing right etiology.[5]

Hence, in the present study clinical and karyotypic (cytogenetic) profile of congenital heart disease has been studied to confirm the diagnosis, predict severity of the condition, determine the risk, status of patient's relatives and establish the basis to augment our ability to counsel families on the recurrence risk with greater accuracy.

Material and Method: This study includes 24 cases clinically diagnosed having Congenital Heart Diseases, who were outdoor and indoor Patients in paediatric department in civil hospital, Ahmadabad. In all cases, relevant history, clinical findings and necessary investigations were noted and assessed. Blood samples were obtained in Heparinized container with prior written consent from the parents of these patients.

The collected samples were processed for culture setting on the same day followed by harvesting and slide preparation 72 hours later. After the aging process of 7 days slides with good metaphase plates were selected and the banding procedure was carried out using freshly prepared EDTA-Trypsin solution and Giemsa stain.[6] About 25 metaphase plates were observed and a photograph was obtained from a good quality metaphase slide with the help of digital camera attached with a photomicroscope .The chromosomal findings were described according to International

System of Human Cytogenetic Nomenclature and finally, Karyotype was prepared using conventional cut and paste technique. In four cases the metaphase plates were not found. Correlation of chromosomal findings was done with other Clinical parameters.

Result: The study group included 14 male and 10 female patients with following age groups. Out of total 24 patients 10 were below 3 years, 9 patients were between 3 to 10 years and 5 patients above 10 years.

Table-I: Age distribution in CHD patients studied.

Age (in years)	0-3	4-6	7-9	10-12	13-15	Total
Number	10	6	3	3	2	24

As per the birth weight was concern We observed that maximum patients (62.5%) of cases were in the birth weight of less than 2500 grams. Only one patient was below 1500 grams and 9 cases were above 2500 gms

Table-II: Birth weight distribution in CHD patients studied

Birth weight (in grams)	<1500	1500-2500	>2500	Total
Number of cases	1	14	9	24

Out of all the cases 2 cases also had a positive family history and in 1 case parents had a consanguineous marriage.

Following observations were made after noting down the maternal and paternal age of the cases.

Table-III:Maternal age distribution at pregnancy in CHD patients studied.

Maternal Age group (in year)	18-21	21-24	25-29	30-34	35-39	Total
Number of cases(%)	3 (12.5)	11 (45.83)	5 (20.83)	3 (12.5)	2 (8.33)	24

The findings of maternal age group at the time of pregnancy gave us the idea that about 67% of the mother was from 20-30 years. Only 8% mothers belong to age group above 35 years. The youngest age group of the mother was between 18 – 21 years.

Table-IV: Paternal age distribution in CHD patients studied:

Paternal Age (in years)	21-25	25-29	30-34	35-39	40 or more	Total
Number of cases (%)	4 (16.66)	12 (50)	5 (20.83)	2 (8.33)	1 (4.16)	24

As per the paternal age group, 50% of the fathers belong to 25-29 age group during the conception of the CHD patient. In our karyotypic analysis we found that only one patient was having the abnormal karyotype in the form of trisomy 21. That finding was noted in male patient who was of age 6 year.

Table-V: Cytogenetic findings by conventional Karyotyping

Metaphase finding	Trisomy 21		Translocation	Mosaicism	Normal		Metaphase not found		Total
	M	F			M	F	M	F	
patients	1	-	-	-	11	8	2	2	24

Discussion: M Ashok and G. Thangavel [7] found that the mean maternal age in study groups were 25 years (range, 17-41 yrs). M. Kava[8] found that the mean maternal age in study groups were 26 years (range, 16-45 yrs).Salvotore Caputo and Giovanbattista Capozzi[9] found that the mean maternal age in cases study groups were 29.6 years and in control study groups were 29 years. In the present study of 24 cases of CHD, increased incidence of CHD was found in maternal age group of 21-24 yrs (45.83%) with mean maternal age in study group were 25.2 years (range, 18-39). In the maximum cases (45.83%) maternal age was ranging from 25 -29 years.

As per the Paternal age is concern Tomaka Une[10] in japan found that the paternal age was more than 30 yrs in 2 cases and less than 30 yrs

in 4 cases. This study found the incidence of CHD in paternal age group of 25-29 years was greater than 50%. Increase in paternal age also plays a great role in development of Congenital heart disease. Birth weight is an important criterion in any congenital heart disease. In present study of 24 cases, 15 (62.5%) cases were less than 2500 gram birth weight and 9 (37.5%) cases were more than 2500 gram birth weight. Similar results by Miyague et al[11] found that patients with CHD had significantly low birth weight. Ingrid Emerit M.D.[12] studied 275 cases to determine the frequency of classical chromosomal syndrome as cause of CHD. Out of these, 119 had a known syndrome, trisomy 21. A sex chromosomal aneuploidy, complex mosaic was found in 39 cases, 1 cases of Fanconi anaemia showed abnormal karyotypes. Even Khalil[13] studied 43 cases of CHD; out of these 4 cases (9.3%) had Down syndrom. Osman Baspinar[1] studied 1693 cases of CHD. Chromosomal anomalies and syndromes were diagnosed in 106 patients (6.26%). In present study Karyotype analysis revealed that one case show trisomy 21 (4.16%) and 19 cases (79.16%) show normal karyotypes and 4 cases came out inconclusive.

Conclusion: In the present study Clinical & Karyotypic (Cytogenetic) profile of CHD has been studied to confirm the diagnosis, to establish presymptomatic diagnosis, to predict severity of the condition, to determine the risk of occurrence of disease and to establish the basis to augment our ability to counsel families on the recurrence risk with greater accurancy. However the cases that are declared normal karyotypes by conventional cytogenetics, require to be confirmed by more specific molecular genetic studies like Fluorescence in Situ Hybridization (FISH) technique, to excluded any molecular level anomaly.

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