Association of consanguinity with congenital heart diseases in a teaching hospital in Western Iraq

Zaid R. Al-Ani, *CABP, DCH.*

ABSTRACT

الأهداف: دراسة العلاقة بين زواج الأقارب وظهور تشوهات القلب الولاديه (CHDs).

الطريقة: أُجريت هذه الدراسة في مستشفى الرمادي للولادة والأطفال، محافظة الأنبار، العراق وذلك خلال الفترة من يناير 2009م إلى يناير 2010م. شملت الدراسة كافه المرضى الذين يعانون من علامات مرض تشوه القلب الولادي، حيث أُجريت لهم بعض الفحوصات التشخيصية للكشف عن هذا المرض. تضمنت المعلومات التي جُمعت حول المرضى كلاً من: اسم الطفل، وعمره، وجنسه وسبب دخوله إلى المستشفى، فيما تضمنت المعلومات الخاصة بالوالدين كلاً من: العمر، والسكن، ودرجه القرابة بين الزوجين، بالإضافة إلى تاريخ تكرر هذا المرض في العائلة. تم اختيار 3 أطفال غير مصابين بهذا المرض (مجموعة التحكم) مقابل كل مريض مُصاب بتشوهات القلب الولادية لعمل مقارنة فيما بينهما اعتماداً على معدل صله القرابة بين الأبوين. وجرى استخدام النسبة الترجيحية (OR) لحساب تأثير معدل زواج الأقارب والمتغيرات المتعلقة الأخرى على ظهور تشوهات القلب الولادية.

النتائج: وصل عدد الحالات المصابة بتشوهات القلب الولادية إلى 86 حالة وكان عدد الحالات الغير المصابة من مجموعة التحكم 258 حالة. لقد كانت أكثر التشوهات التي سُجلت تحت مُسمى هذا المرض هي الفتحه بين البطينين الولاديه، والفتحه بين الأذينين الولاديه، ورباعيه فالوت. وكانت صلة القرابة موجودة في 78% من الحالات المصابة، وفي 43.3% من الحالات الغير مصابة، فيما شملت صلة القرابة من الدرجة الأولى 66.2% من الحالات المصابة، و35.6% من الحالات الغير مصابة وذلك من المجموع الكلي للزيجات. يشكل زواج الأقارب عامل خطر يزيد من احتمالية الإصابة بتشوهات القلب الولاديه وخصوصاً فتحه القلب بين البطينين وفتحة القلب بين الأذينين وذلك أكثر من رباعية فالوت، بينما لم يكن لعمر الأبوين أو جنس الطفل تأثيراً يزيد من خطر الإصابة بتشوهات القلب الولادية.

خاتمة: أثبتت الدراسة علاقة زواج الأقارب بزيادة خطر الإصابة بحالات تشوه القلب الولاديه لذلك علينا الاهتمام بتثقيف الناس حول خطورة زواج الأقارب وخصوصا في هذه المدينة العشائرية حتى نقلل من عدد هذه التشوهات المميتة.

Objectives: To study the association of consanguinity as a risk factor for congenital heart diseases (CHDs).

Methods: Patients with suggestive signs of CHD admitted to the Al-Ramadi Maternity and Children Hospital, Al-Anbar Governorate, Iraq from January 2009 to January 2010 were subject to diagnostic investigations. Case data includes: name, age, gender, and cause of admission. Parents' data includes: age, residence, degree of consanguinity, and history of family recurrent CHDs. Three controls to one case (3:1) were selected to compare their consanguinity with the CHD cases. Odds ratio was used for the measurement of consanguinity and other variable risks on CHD occurrence.

Results: The CHD cases were 86. Selected controls were 258 non-CHD cases. The most recorded subtypes were ventricular septal defect (VSD), atrial septal defect (ASD), and tetralogy of fallot (ToF). Consanguinity was found in 78% of cases and 43.3% in controls. First cousin consanguinity comprised 66.2% in cases and 35.6% in controls from all their marriages. Consanguinity was found a significant risk factor, more affecting the VSD and ASD than ToF subtypes, while parental age and infant gender were not found as risk factors.

Conclusion: Consanguinity proved to be a risk factor for CHD. Further social education of the risks of consanguineous marriages in this tribal population is needed to reduce the prevalence of these morbid and mortal anomalies.

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From the Department of Pediatrics, Medical College, Al-Anbar University, Al-Ramadi, Iraq.

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Address correspondence and reprint request to: Dr. Zaid R. Al-Ani, Department of Pediatrics, Medical College, Al-Anbar University, Al-Ramadi, Iraq. Tel. +964 7807442775. E-mail: zaidrasheedalani@yahoo.com

Consanguinity is a common pattern of marriage in the Iraqi population. The Central Organization of Statistics and Information Technology (COSIT) recorded in 2004 that the first cousin consanguinity prevalence in Iraq was 33%.[1] Consanguinity prevalence is different from one country to another. In Jordan, it was 51%,[2] Kuwait - 54%,[3] Saudi Arabia - 56%,[4] Qatar - 54%,[5] Yemen - 40%,[6] Egypt - 29%,[7] Lebanon - 34.7%,[8] and India - 40%.[9] Consanguinity was seen 1.8 times more in Muslims than in the Christian populations,[10] and Arabic populations substantially were found having a high rate of autosomal recessive diseases due to high rate of consanguinity that ranges between 20-60% of all their marrieges.[11,12] Children born from consanguineous parents had significantly a higher incidence of congenital abnormalities than those of non-consanguineous families.[12-14] Several studies showed that the incidence of congenital heart diseases (CHD) increased in consanguineous than non-consanguineous families.[8,15-17] The incidence of CHD ranges between 0.5-0.8% of live births, and it is higher in stillborns, abortions, and premature deliveries, and will increase from 2-6% in a second pregnancy after the birth of a child with CHD, or if one of the parents is also affected by one of these CHD anomalies.[18] In India, CHD is the most common congenital anomalies, and represents 30% of their total anomalies.[19] Congenital heart disease is one of the most common recorded birth defects.[8,18,20] Most of these malformations are multifactorial in origin resulting from combined genetic, teratogens, monogenic diseases, and environmental factors, and in small percentage are due to chromosomal abnormalities.[8,14,21] Consanguinity increases the incidence of congenital malformations due to the expression of the deleterious recessive genes causing such anomalies.[7,10] In spite of the advance of cardiac surgery in the last 20 years, and the increase of survivals to adulthood, still CHDs are the leading cause of death in children with congenital malformations.[18] The aim of this study is to find out the association of consanguinity as a risk factor with the incidence of CHD in Al-Ramadi populations admitted to Al-Ramadi Maternity and Children's Teaching Hospital, and to study the types of these morbid and mortal anomalies.

Methods. This is a hospital-based case control study to find out the relation of parental consanguinity as a risk factor for CHD in patients from Al-Ramadi City admitted to the Al-Ramadi Maternity and Children Teaching Hospital, Al-Anbar Governorate, Iraq, during a one-year study period from January 2009 to January 2010. This hospital covers all the Ramadi City population, and serves as a referral hospital for other districts of the Governorate. All admitted patients to the neonatal intensive care unit and the post neonatal admission wards were examined, and any child with signs and symptoms suggesting CHD as cyanosis, tachypnea, dyspnea, cardiac murmur, chest deformities, abnormal parasternal pulsation, abnormal cardiac size on chest x ray, and signs of heart failure (poor feeding, dyspnea, sweating, hepatomegaly, failure to thrive) were subjected for chest x-ray, electrocardiography, and echocardiography to confirm the diagnosis and the type of the CHDs.

Cases due to chromosomal abnormalities as trisomy 21, 18 and 13, familial syndromic CHDs, patent ductus arteriosus in a premature infant, functional murmurs, and those residing outside Al-Ramadi city were excluded from the study. Cases that are previously diagnosed were double-checked clinically, and completed their missing diagnostic investigations to confirm the diagnosis. Confirmed cases were grouped into cyanotic and acyanotic CHD types according to the Nelson Textbook Classification System of CHD,[22] following their typing by echocardiography results. Cases with more than one anomaly were assigned as one principal CHD according to the Baltimore-Washington Infant Study (1981-1989) (BWIS),[23] which depends on the timing of the embryological development of the cardiac anomaly that divide the anomalies into early and late anomalies. Mothers of patients were interviewed for data collection.

Patient's data includes the child's name, age, gender, cause of admission, and the type of the CHD. Parental data includes the father's and mother's age during the patient's birth, their residence, their type of consanguinity, and any family history of another recurrent CHD cases. Parental relation is divided into 3 types: first cousin (including the 4 types), second cousins (including the second cousin and above), and no relation. Care was taken not to double list any patient with frequent admissions.

For every CHD cases, a 3 age-matched patients admitted at the same period in the same hospital were selected randomly as controls to compare their rate of consanguinity with that of our CHD cases, and for other certain variables. Selected controls must be without CHD or chromosomal abnormalities or genetic conditions, not related to the compared case, and from Al-Ramadi city residence only. Al-Anbar is the largest Governorate in Iraq and occupies approximately 1/3 of its total area. Al-Ramadi City (the center of the Governorate, 450000 populations) is the main center for diagnosis and management of CHD cases in the Governorate. The proportion of the CHD cases in the referred cases is more than the other types of conditions, and to avoid the disproportionate distribution of CHD cases with their controls in the study, both the cases and controls were selected from patients of Al-Ramadi city

residence only. Mothers of controls were interviewed for their name, age, gender, residence, cause of admission, degree of consanguinity with her husband, and for any family history of other CHDs. Care was taken not to double list any control with frequent admissions.

Statistical analysis was performed using the Statistical Package for Social Sciences version 17 (SPSS Inc, Chicago, IL, USA). Data presented as frequency and percentages, with test of significance between different proportions (qualitative data) was performed using the Pearson chi-squared test at 0.05 level of significance. Odd's ratio (OR) was calculated for the measurement of the risk of consanguinity, and other different variables with its 95% confidence interval (95% CI) was used for assessing the significance of the risk measurements.

Patient's family consent was not required and the Scientific Research Committee of the Medical College approved the research.

Results. During the study period, there were 9653 patients admitted to the hospital with different types of diseases from which, 98 cases (1%) proved to be CHD, giving a prevalence of 10.1/1000 of the total hospital admissions during the study. Twelve of the cases (12.2%) were excluded from the study, 7 had chromosomal abnormalities (6 Down syndrome, one Edward syndrome), and 5 from outside Al-Ramadi residence. The remaining 86 cases were the studied sample from Al-Ramadi residence; all were isolated non-syndromic CHD cases. Their age range was 11 days-14 years, and their gender composed of 50 males (58.1%) and 36 females (41.9%), with a male to female ratio of 1.4:1. The studied sample was composed of 18 (20.9%) cyanotic, and 68 (79.1%) acyanotic CHD types. Seventy cases (81.4%) were previously diagnosed as CHD cases and the remaining 16 (18.6 %) were undiagnosed CHD, but admitted for another cause, and were diagnosed in the hospital. These are composed of 9 (56.3%) ventricular septal defects (VSD), 3 (18.8%) atrial septal defects (ASD), 1 (6.25%) pulmonary stenosis (PS), 1 (6.25%) dextrocardia +ASD, 1 (6.25%) tetralogy of fallot (ToF) and 1 (6.25%) patent ductus arteriosus (PDA), all were acyanotic CHD types except the ToF case which was admitted for gastroenteritis and had mild unnoticed cyanosis by the family. Nineteen (22.1%) of CHD cases found associated with family recurrence of another CHD. These were: 6 (33.3%) ASD, 8 (19%) VSD, and 1 with each of ToF, PDA, PS, common AV canal and dextrocardia + ASD anomalies. The recurrent cases were of different CHD subtypes. Consanguinity was found in 67 (77.9%) of the studied CHD cases, 57 (66.2% of the total marriages) were of first cousins, and 10 (11.6%) were second cousin types.

The total randomly selected controls were 258, 148 (57.4%) males and 110 (42.7%) females with a male to female ratio of 1.3:1. All were age matched cases without CHDs or chromosomal abnormalities admitted for different but non-genetic diseases (gastroenteritis - 133, different chest infections - 116, urinary tract infection and glomerulonephritis - 7, kerosene poisoning - 1, and neonatal sepsis - 1 case). Consanguinity was found in 112 (43.4% of the total marriages) of their parents, mostly of first cousins type, and occurs in 92 (35.6%) of the total marriages, and 20 (7.7%) were second cousins, while 146 (56.6%) were non-related parents.

Figure 1 shows the percentage of each recorded CHD subtypes. Ventricular septal defect was the most common recorded subtype followed by ASD, ToF, and then other CHD anomalies. Fourteen (16.8%) of these cases presented with more than one cardiac anomalies, each classified as one principal anomaly depending on the BWIS classification.[23]

Table 1 shows the number of the studied CHD subtypes and their distribution of consanguinity. The studied sample were grouped into a major group that include VSD, ASD, and ToF, which are the subtypes of high recorded numbers, and includes 70 (81%) of the cases, and the minor group of the small recorded numbers, and occupy 19% of cases and includes the rest of the recorded CHD subtypes. Consanguinity was found mostly related with ASD (94.5%) and VSD (90.3%) of the major group and all the minor group CHD subtypes, except one PDA case. First cousins was the principal consanguinity type found related with all cases except the ToF, PDA, and TGA malformations.

Table 2 shows the causes of admission of all studied CHD samples. The most common cause was recurrent

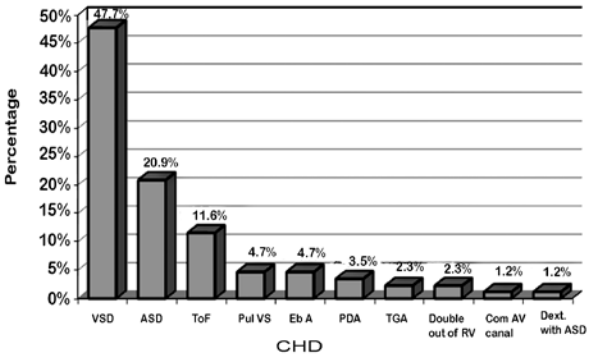

Figure 1 - The percentage of the studied congenital heart disease (CHD) subtypes. Fourteen patients presented with more than one CHD anomalies. VSD - ventricular septal defect, ASD - atrial septal defect, ToF - tetralogy of fallot, Pul VS - pulmonary valve stenosis, Eb A - Ebstien anomaly, PDA - patent ductus arteriosus, TGA - transposition of great arteries, double out RV - double outlet right ventricle, comm AV canal - common atrio ventricular canal, dext with ASD - dextrocardia with atrial septal defect.

Table 1 - The distribution of consanguinity in the studied congenital heart disease subtypes (N=86).

CHD subtypes	Number	Degree of consanguinity		
		First cousins	Second cousins	No relation
		n (%)		
Ventricular septal defect	41	27 (65.8)	10 (24.4)	4 (9.7)
Atrial septal defect	18	12 (66.6)	5 (27.8)	1 (5.5)
Tetralogy of Fallot	10	5 (50.0)	2 (20.0)	3 (30.0)
Pulmonary valve stenosis	4	3 (75.0)	1 (25.0)	-
Ebstien anomaly	4	4 (100)	- -	-
Patent ductus arteriosus	3	1 (33.3)	1 (33.3)	1 (33.3)
Transposition of great arteries	2	1 (50.0)	1 (50.0)	-
Double outlet right ventricle	2	2 (100)	-	-
Common atrioventricular canal	1	1 (100)	-	-
Dextrocardia+ atrial septal defect	1	1 (100)	-	-

Table 2 - The causes of admission of the studied congenital heart disease (CHD) subtypes (N=86).

Causes for admission	CHD	
	n	(%)
Chest infection	51	(59.3)
Gastroenteritis	9	(10.5)
Cyanotic spells	5	(5.8)
Other infections	3	(3.5)
Failure to thrive	3	(3.5)
Pyrexia of unknown origin	2	(2.3)
Polycythemia	2	(2.3)
For follow up	2	(2.3)
Respiratory distress syndrome	2	(2.3)
Convulsion	2	(2.3)
Jaundice	2	(2.3)
Hemoptysis	1	(1.2)
Right sided hemiparesis	1	(1.2)
Supraventricular tachycardia	1	(1.2)

chest infections (59.3%) followed by gastroenteritis (10.5%), and then other causes.

Table 3 compares the distribution of the CHD sample gender, parental age, and consanguinity variables with that of the controls, to study the risk of these variables on the occurrence of the CHD malformations. No significant risk was found for the occurrence of CHDs with regard to gender. Parental age was found not increasing the incidence of the CHDs, while on the contrary, the father's age >40 were significantly decreases the incidence of CHDs when compared with the 20-39 years productive age group parents (OR= 0.38; 95% CI [0.20-0.72]). Regarding the effect of consanguinity as a risk factor for causing CHDs, parental consanguinity was found significantly increasing the CHDs in the overall consanguinity, first and second cousin parents when compared with consanguinity of controls, which indicates that consanguinity is a risk factor for the development of CHDs in related than non-related parents.

Table 4 shows the risk of consanguinity on the major group CHD malformations. Consanguinity was found significantly increasing the incidence, and regarded as a risk factor for the development of VSD, ASD, but not the ToF malformations.

Table 5 shows the relation of consanguinity with cyanotic and acyanotic CHDs. No significant difference was found in relation to consanguinity between the 2 groups of CHDs (p=0.754).

Table 6 shows the risk of family recurrence of another CHD cases in the studied sample compared with controls. Developing another CHD in the studied CHD families was found significantly higher than the non-CHD control families (p=0.0001), and developing CHD case in the family will increase their possibility to have another recurrent CHD cases.

Discussion. During the study, the most recorded CHD subtypes was VSD (47.7%), ASD (20.9%), and ToF (11.6%) malformations. Different patterns in different studies with lower rates for VSD (24.9%), ASD (14.4%) were recorded by Subramanyan study in Oman (2000),[24] while in Lebanon, Mansour et al[25] recorded higher rates for VSD and ASD (62%), and ToF (39%), and Yunis et al[26] recorded the same of our high rate for VSD (26.6%), followed by ASD (13.3%), but TGA (10.4%) not ToF CHD subtypes.

Sixteen (18.6%) of our studied cases were admitted for other causes, and were diagnosed incidentally in the hospital. All were acyanotic CHD types, except the (ToF) anomaly, which presented with unnoticed mild cyanosis and was diagnosed during the neonatal period. Cyanosis is a terrifying sign for families, and its absence

may be the cause of failure of the parents to suspect the disease, causing the delay of diagnosis. El-Hag study in Sudan[27] recorded 6% of his cases diagnosed in the hospital, and was of the same type pattern of this study, with all types were acyanotic, except one ToF cyanotic anomaly. A different result was noticed regarding the risk of parental age in causing the CHD malformations. Becker et al[15] in Saudi Arabia showed advancing maternal age as a risk factor, and both Nabulsi et al[8] and Yunis et al[26] in Lebanon showed no relation of maternal age for causing CHDs, while Ramegowda and Ramachandra[28] in India showed no relation of both the paternal and maternal age in causing these CHDs. These data were consistent with our result in which no relation was found with paternal and maternal ages, and on the contrary, we noticed advancing paternal age significantly decreases the incidence of these malformations. Such diverse paternal result, in spite of the age matching used during the selection of controls as long as the cases and controls belong to a different generations, could be due to the high control per case ratio (3:1) used in this study, which fits for the consanguinity assessment, but not for the other variables, and also due to many of the fathers are old and married with more than one wife, since polygamy is common in this tribal population city.

The recent general population consanguinity rate in Al-Ramadi city is not known since the last population census was in 1997, and the wars, sanctions, emigration and urbanization during the last 13 years caused dramatic changes in the social habits of this population. The control sample of this study showed a consanguinity rate of 43.4%. This rate is the recent available report of consanguinity in Al-Ramadi city, and bio-statistically for comparison with cases to evaluate the risk of consanguinity, it is a representative consanguinity parameter in such hospital-based consanguinity study for the general population rate. Yunis et al's[26] hospital-based study in Great Beirut, Lebanon used a control to case ratio of 5:1, and showed a control consanguinity rate of 13.4%, which was near to the 15% general population rate of the same area recorded by the Lebanon Central Administration Center of Statistics

Table 3 - Distribution of gender, parental age, and consanguinity between cases and controls.

Variables	CHD cases (n=86) n (%)	Controls (n=258) n (%)	Odds ratio (95% Confidence intervals)
Gender			1.03 (0.61 - 1.75)
Male	50 (58.1)	148 (57.4)	
Female	36 (41.9)	110 (42.6)	
Father's age (years)			
<20	2 (2.3)	9 (0.4)	0.5 (0.07 - 2.59)
20-29	32 (37.2)	68 (14.7)	
30-39	36 (41.9)	86 (39.1)	
≥40	16 (18.6)	95 (45.7)	0.38* (0.20 - 0.72)
Mother's age (years)			
<20	12 (14.0)	46 (2.7)	0.37 (0.34 - 1.52)
20-29	40 (46.5)	119 (20.9)	
30-39	31 (36.0)	79 (40.7)	
≥40	3 (3.5)	14 (35.7)	0.6 (0.13 - 2.31)
Parental consanguinity			
Positive	67 (77.9)	112 (43.4)	4.60* (2.53 - 8.43)
First degree cousin	57 (66.2)	92 (35.6)	4.76* (2.57 - 8.89)
Second cousins	10 (11.6)	20 (7.7)	3.48* (1.43 - 10.28)
Negative	19 (22.1)	146 (56.6)	

CHD - congenital heart disease, *significant

Table 4 - The risk of consanguinity on the studied main congenital heart disease (CHD) subtypes.

CHD subtypes	n	First cousins n (%)	Second cousins n (%)	No relation	*P*-value compared with control
VSD	41	27 (65.8)	10 (24.4)	4 (9.8)	0.000
ASD	18	12 (66.6)	5 (27.8)	1 (5.6)	0.000
ToF	10	5 (50.0)	2 (20.0)	3 (30.0)	0.359
Control	258	92 (35.5)	20 (7.75)	146 (56.5)	-

CHD - congenital heart disease, VSD - ventricular septal defects, ASD - atrial septal defects, ToF - tetralogy of fallot,

Table 5 - Relation of consanguinity with cyanotic and acyanotic CHD types.

Consanguinity	Acyanotic CHD (n=68) n (%)	Cyanotic CHD (n=18) n (%)	OR (95% CI) compared to negative
Positive	53 (77.9)	14 (77.8)	1.01 (0.24-4.0)
First cousin	46 (86.8)	11 (78.6)	1.12 (0.25-4.64)
Second cousins	7 (13.2)	3 (21.4)	0.62 (0.08-4.87)
Negative	15 (22.1)	4 (22.2)	

CHD - congenital heart disease, OR - odds ratio, CI - confidence interval. p=0.745 (not significant)

Table 6 - Recurrence of CHDs in the studied sample compared with controls.

Recurrence of CHD	CHD cases (n=86) n %	Controls (n=258) n %	OR (95% CI) compared to negative
Positive	19 (22.1)	17 (6.6)	4.02* (1.87-8.65)
Negative	67 (77.9)	241 (93.4)	

CHD - congenital heart disease, OR - odds ratio, CI - confidence interval. *p=0.0001 (highly significant)

in 2000.[26] Beirut is one of the most modernized cities in the Middle East Region[26] and consanguinity rate in such modernized cities is expected to be less than that of the tribal population type. Using a lower control to case ratio (3:1) in this study will underestimate the general consanguinity population rate, and the rate in this tribal pattern area is expected to be more if a representative sample was taken randomly, and proportionate with the populations selected from the different localities of the city. The studied control consanguinity rate was higher than both the control and general population rates of Yunis et al's[26] study in Lebanon, and also it is higher than the general population rate in Egypt,[7] and lower than the rates from neighboring countries such as Jordan, Kuwait, and Saudi Arabia.[2-4]

Since several decades and until now, many studies proved that consanguinity marriages is one of the risk factors causing CHDs. The significant consanguinity risk on CHD occurrence noticed in this study (p=0.0001) was consistent with the findings of other studies in different countries.[2,7,8,13-16]

Other studies[8,14,15,26,28] showed that the risk of consanguinity that cause CHDs was higher in the first cousins than the second cousins related parents. In India,[27] the uncle-niece type of marriage was the most common type followed by the first cousin consanguinity. Uncle-niece type of marriage is not present in Arabs, and religiously it is forbidden in Islam and Muslim's populations. First cousin marriages as the most common type was consistent with our study, in which we found 66.2% of the studied sample were of this consanguinity type, and the risk of developing CHD in babies born from first cousin parents were 4 times higher and 3 times higher on babies born by second cousin parents compared to non-related parents (first cousins [OR=4.76; 95% CI=2.57-8.89], second cousins [OR=3.48; 95% CI=1.43-10.28]). The risk was also higher in Yunis et al's[26] study that recorded the first cousin consanguinity risk for having CHD affected babies is 2.3 times, and distant relatives 1.8 times when compared with the non-related parents.

The risk of consanguinity on the studied CHDs was shown differently in the major groups of VSD, ASD, and ToF malformations. We noticed the risk of consanguinity affecting VSD and ASD, but not the ToF subtypes. This was consistent with the result of Becker's[15] report in Saudi Arabia, but different than the Nabulsi[8] result in Lebanon that reported a significant association of consanguinity with all of these 3 CHD subtypes.

Studies suggested that congenital malformations had different models of inheritance, and ASD and PDA are caused by a recessive mode of inheritance.[29] Salvotore et al[30] recorded that familial recurrence of CHDs was found in 23% of isolated, and 13.6% in non-isolated ostium secundum ASD cases. Archana and Ramesh[31] recorded in India a ToF cases in both monozygotic twins. Twins have a special place in human genetics because they are useful in comparing the effect of the genes and environment.[31] In the present study, 33.3% of the ASD cases were found associated with recurrent CHDs and the highest rate of CHD recurrences compared to other CHD malformations, followed by VSD (19%), and ToF (10%) anomalies.

Significant consanguinity risks in the production of CHDs, specially the VSD and ASD, and the recorded high significant recurrence of another CHD cases in the studied cases specially ASD, VSD, and ToF indicates a high possibility of the presence of a deleterious recessive mode of inheritance in some of these CHD cases. Thus, every related couple will have a higher possibility for producing CHD affected babies, and when this happens, especially in those with ASD and VSD, they have a higher rate of a recurrence of another CHD affected babies than those of non-related families.

Few known CHD patients were not seen now in this hospital, and it is either they died or became old enough to visit another hospital, and their absence will reduces the prevalence and underestimates the CHD risk factors. The real incidence of a recurrent CHD may be underestimated because some of these cases are unnoticed by the family and not diagnosed and enrolled during the data collection. Maternal education, smoking, and CHD associated congenital anomalies risk factors were neglected because parts of their control data were missed after the data collection.

A more expanded multicenter study involving the whole Governorate Hospitals is recommended, which will give a large representative sample to assess the prevalence of these CHD malformations, and to study the major risk factors causing these morbid and mortal anomalies.

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Related topics

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