A Large-scale Karyotype Analysis of Genetic Counselors and Fetuses Among Hakka Population in Southern China

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Research

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Abstract

Background: Karyotype analysis has been used in a clinical cytogenetic laboratory. A retrospective analysis of karyotype analysis in Meizhou area to provide valuable reference for clinical genetic counseling. A retrospective analysis of 5-year data of karyotype analysis from 5,289 peripheral blood samples and 2,882 fetuses between January 2015 and March 2020 in Meizhou area.

Results: Chromosomal abnormalities were detected in a total of 392 peripheral blood samples, and the abnormality detection rate (ADR) was 7.41% (392/5,289). The ADR for sex chromosome aneuploidies, autosomal aneuploidies, structural abnormalities and chromosome polymorphisms were 1.29% (68/5,289), 0.72% (38/5,289), 1.55% (82/5,289) and 3.86% (204/5,289). Among cases with chromosomal abnormalities, numerical abnormalities, chromosomal structural abnormalities and chromosome polymorphism accounted for 27.04% (106/392), 20.92% (82/392) and 52.04% (204/392), respectively. There were statistically significant differences in the chromosomal abnormalities rate different types of patients. In addition, chromosomal abnormalities were detected in a total of 307 fetus samples, and the ADR was 10.65% (307/2,882). The ADR for sex chromosome aneuploidies, autosomal aneuploidies, triploid/tetraploid, structural abnormalities and chromosome polymorphisms were 1.70% (49/2,882), 5.45% (157/2,882), 0.14% (4/2,882), 1.39% (40/2,882) and 1.94% (56/2,882). Among fetuses with chromosomal abnormalities, numerical abnormalities, chromosomal structural abnormalities and chromosome polymorphism accounted for 68.40% (210/307), 13.03% (40/307) and 18.24% (56/307), respectively. The chromosomal abnormalities rate was higher than that in non-elderly pregnant women. Abnormal chromosome karyotype detection rate is higher in genetic counselors in Meizhou area.

Conclusions: Karyotype analysis has great significance for clinical diagnosis, guide the healthy birth, and improve the quality of the population.

Background

Human cytogenetics was born in 1956 with the fundamental, but great significance, discovery that normal human cells contain 46 chromosomes[1, 2]. Cytogenetics is mainly from the perspective of cytology, especially from the structure and function of chromosomes, the relationship between chromosomes and other organelles to study the genetic phenomenon and clarify the mechanism of inheritance and variation[3]. Chromosome is the carrier of genetic material, chromosome abnormality leads to the dose effect and location effect of genetic material. Chromosomal numerical abnormality and structural abnormality can lead to the occurrence of chromosome diseases, which cannot be cured at present. It has a long-term impact on the growth and development of individuals and their fertility, including congenital malformation, growth retardation, mental retardation, abnormal development of reproductive system and low fertility.

Infertility is the inability to conceive without using any contraception and having a normal sex life. There are studies shown that the prevalence of infertility was 20–25% among couples of reproductive age in China[4, 5]. More and more researches shown that genetic material variation, including chromosomal abnormalities, as an important cause of infertility[6–8]. Adverse pregnancy is a common pregnancy pathological phenomenon, mainly including recurrent abortion, stillbirth, birth of mentally retarded and deformed children, and so on. Among them, embryo arrest and recurrent abortion are the main clinical manifestations[9, 10]. There are many causes of adverse pregnancy, including abnormal uterine structure, reproductive tract infection, abnormal endocrine metabolism, maternal systemic diseases, immune factors, environmental factors and chromosome abnormalities, among which chromosome abnormalities are one of the important causes[11]. Mental retardation (MR) is a common disease in the children's genetic counseling, is mainly due to cognitive skills and adapt ability of defects caused by damages of central nervous system, its prevalence in the population was 1 ~ 3%[12]. In addition, chromosomal abnormalities can be detected in the patients with growth retardation[13, 14].

The detection of abnormal chromosomes has important guiding significance for the treatment of children in genetic counseling, eugenics of adults with childbearing age. This report, a retrospective analysis of 5-year data of chromosome karyotypes of genetic counselors, pediatrics and prenatal diagnosis in Meizhou area, has revealed the difference chromosome abnormalities spectrum of different populations. The results of this study provide valuable reference for clinical genetic counseling.

Results

Population characteristics

A total of 5289 patients (4871 adults (> 14 years) and 418 children (≤ 14 years)) performed karyotype analysis were recruited in the study, and the age ranges from 1 day to 67 years old. In addition, karyotype analysis was performed on 2882 fetuses, including 382 villi samples, 2372 amniotic fluid samples and 128 umbilical cord blood samples.

Chromosomal abnormalities of peripheral blood samples

Chromosomal abnormalities were detected in a total of 392 peripheral blood samples, and the abnormality detection rate (ADR) was 7.41% (392/5,289), which 6.73% (328/4,871) in adults and 15.31% (64/418) in children. The ADR for sex chromosome aneuploidies, autosomal aneuploidies, structural abnormalities and chromosome polymorphisms were 1.29% (68/5,289), 0.72% (38/5,289), 1.55% (82/5,289) and 3.86% (204/5,289) for all peripheral blood samples, which 1.21% (59/5,289), 0.12% (6/5,289), 1.50% (73/5,289), 3.90% (190/5,289) for adults and 2.15% (9/418), 7.65% (32/418), 2.15% (9/418), 3.35% (14/418) for children. The ADR of chromosome numerical abnormalities in children cases was significantly higher than those in adults (10.05% vs. 1.33%, $P < 0.05$) (Table 1).

Table 1

Chromosomal abnormalities detected in adults and children.

Chromosomal abnormalities	Adults (n=4871)			Children (n=418)			Total (n=5289)		
	No. Abn Cases	ADR (%)	RF (%)	No. Abn Cases	ADR (%)	RF (%)	No. Abn Cases	ADR (%)	RF (%)
Numerical abnormality									
Sex Chromosome Aneuploidy									
Males									
47,XXY	46	0.94	14.07	1	0.24	1.56	47	0.89	11.99
45,X[22]/46,X,Yqh-[28]	1	0.02	0.30	0	0.00	0.00	1	0.02	0.26
45,XO[37]/46,XY[13]	1	0.02	0.30	0	0.00	0.00	1	0.02	0.26
46,XY[36]/47,XXY[64]	1	0.02	0.30	0	0.00	0.00	1	0.02	0.26
47,XYY	0	0.00	0.00	0	0.00	0.00	0	0.00	0.00
48,XXYY	0	0.00	0.00	1	0.24	1.56	1	0.02	0.26
48,XXXY	0	0.00	0.00	0	0.00	0.00	0	0.00	0.00
Females									
45,XO	6	0.14	1.83	6	1.44	9.38	12	0.23	3.06
47,XXX	2	0.04	0.61	0	0.00	0.00	2	0.04	0.51
45,X[10]/46,XX[40]	1	0.02	0.30	0	0.00	0.00	1	0.02	0.26
46,XX[45]/47,XXX[5]	1	0.02	0.30	0	0.00	0.00	1	0.02	0.26
45,X[62]/46,X,der(X)(p11.2)[38]	0	0.00	0.00	1	0.24	1.56	1	0.02	0.26
Subtotal	**59**	**1.21**	**17.99**	**9**	**2.15**	**14.06**	**68**	**1.29**	**17.35**
Autosomal Aneuploidy									
Trisomy 21	6	0.12	1.83	32	7.65	50.00	38	0.72	9.69
Trisomy 18	0	0.00	0.00	0	0.00	0.00	0	0.00	0.00
Trisomy 13	0	0.00	0.00	0	0.00	0.00	0	0.00	0.00
Subtotal	**6**	**0.12**	**1.83**	**32**	**7.65**	**50.00**	**38**	**0.72**	**9.69**
Total	**65**	**1.33**	**19.82**	**41**	**9.81**	**64.06**	**106**	**2.00**	**27.04**
Structural abnormality	**73**	**1.50**	**22.26**	**9**	**2.15**	**14.06**	**82**	**1.55**	**20.92**
Chromosome polymorphism	**190**	**3.90**	**57.93**	**14**	**3.35**	**21.88**	**204**	**3.86**	**52.04**
All chromosomal abnormalities	**328**	**6.73**	**100.00**	**64**	**15.31**	**100.00**	**392**	**7.41**	**100.00**

ADR, abnormality detection rate (%); RF, relative frequency by (%); *Statistically different from ADR in prenatal setting ($P < 0.05$).

Among cases with chromosomal abnormalities, numerical abnormalities, chromosomal structural abnormalities and chromosome polymorphism accounted for 27.04% (106/392), 20.92% (82/392) and 52.04% (204/392), respectively. The most frequently seen numerical chromosomal abnormalities by relative frequency (RF) were 47,XXY, trisomy 21, and 45,XO at 11.99%, 9.69%, and 3.06%. In adults, the most frequently seen numerical chromosomal abnormalities by RF were 47,XXY, trisomy 21, and 45,XO at 14.07%, 1.83%, and 1.83%. In children, the most frequently seen numerical chromosomal abnormalities by RF were trisomy 21, and 45,XO at 50.0%, and 9.38% (Table 1).

The most common structural chromosomal abnormalities were 46,XN,dup(1)(q11q12) (n = 11; RF = 13.41%), followed by 46,X,inv(Y)(p11.2q11.23) (n = 10; RF = 12.20%), and 45,XY,der(13;14)(q10;q10) (n = 5; RF = 6.10%) (Table S1). The most common chromosome polymorphisms were 46,XN,inv(9)(p13q13) (n = 65; RF = 31.86%), followed by 46,X,Yqh+ (n = 36; RF = 17.65%), and 46,X,Y(Y < G) (n = 21; RF = 10.29%) (Table S1).

Main clinical manifestations and chromosomal abnormalities

Based on the clinical information of the patients, we divided them into infertile group (n = 1994), adverse pregnancy and parturition history group (n = 1520), growth and developmental abnormalities group (n = 322), congenital diseases and mental retardation group (n = 113) and other (n = 1340). There were statistically significant differences in the chromosomal abnormalities rate in infertile group (χ^2 = 47.621, P< 0.001) and adverse pregnancy and parturition history group (χ^2 = 47.353, P< 0.001), growth and developmental abnormalities group (χ^2 = 10.740, P = 0.014), congenital diseases and mental retardation group (χ^2 = 242.107, P< 0.001). The main types of chromosomal abnormalities were chromosome polymorphism (n = 79; ADR = 3.96%) and sex chromosome aneuploidy (n = 40; ADR = 2.01%) in infertile group, which chromosome polymorphism (n = 68; ADR = 4.47%) and structural abnormality (n = 36; ADR = 2.37%) in adverse pregnancy and parturition history group, chromosome polymorphism (n = 12; ADR = 3.73%) and sex chromosome aneuploidy (n = 12; ADR = 3.73%) in growth and developmental abnormalities group, and autosomal aneuploidy (n = 33; ADR = 29.20%) in congenital diseases and mental retardation group (Table 2).

Table 2
Main clinical manifestations and chromosomal abnormalities.

Group	Numerical abnormality		Structural abnormality	Chromosome polymorphism	Total (n, %)	*P* value
	Autosomal Aneuploidy	Sex Chromosome Aneuploidy				
Infertile (n = 1994)	0(0)	40(2.01)	16(0.80)	79(3.96)	135(6.77)	< 0.001(χ^2 = 47.621)
Abnormal gestation and birth (n = 1520)	0(0)	3(0.20)	36(2.37)	68(4.47)	107(7.04)	< 0.001(χ^2 = 47.353)
Growth and developmental abnormalities (n = 322)	2(0.62)	12(3.73)	5(1.55)	12(3.73)	31(9.63)	0.014 (χ^2 = 10.740)
Congenital diseases and mental retardation (n = 113)	33(29.20)	3(2.65)	4(3.54)	4(3.54)	44(38.94)	< 0.001(χ^2 = 242.107)
Other (n = 1340)	3(0.22)	10(0.75)	21(1.57)	41(3.06)	75(5.60)	0.098(χ^2 = 6.309)

Chromosomal abnormalities of fetuses

Chromosomal abnormalities were detected in a total of 307 fetus samples, and the ADR was 10.65% (307/2,882), which 12.30% (47/382) in chorionic villus samples, 10.71% (254/2,372) in amniocentesis samples and 4.69% (6/128) in cord blood samples. The ADR for sex chromosome aneuploidies, autosomal aneuploidies, triploid/tetraploid, structural abnormalities and chromosome polymorphisms were 1.70% (49/2,882), 5.45% (157/2,882), 0.14% (4/2,882), 1.39% (40/2,882) and 1.94% (56/2,882), which 3.14% (12/382), 6.81% (26/382), 0.26% (1/382), 0.52% (2/382), 1.57% (6/382) for chorionic villus samples, 1.52% (36/2,372), 5.40% (128/2,372), 0.13% (3/2,372), 1.56% (37/2,372), 2.07% (49/2,372) for amniocentesis samples and 0.78% (1/128), 2.34% (3/128), 0.78% (1/128), 0.78% (1/128) for cord blood samples.

Among fetuses with chromosomal abnormalities, numerical abnormalities, chromosomal structural abnormalities and chromosome polymorphism accounted for 68.40% (210/307), 13.03% (40/307) and 18.24% (56/307), respectively. The most frequently seen numerical

chromosomal abnormalities by RF were trisomy 21, trisomy 18, 45,XO, and 47,XXY at 36.16%, 11.07%, 5.86%, and 4.89%. The most frequently seen numerical chromosomal abnormalities were trisomy 21, trisomy 18, and 45,XO at 25.53%, 19.15%, and 19.15% in chorionic villus samples, which trisomy 21, trisomy 18, and 47,XXY at 38.19%, 9.45%, and 5.51% in amniocentesis samples (Table 3).

Table 3

Chromosomal abnormalities detected in prenatal diagnosis.

Chromosomal abnormalities	Chorionic villus samples (CVS) (n=382)			Amniocentesis (AC) (n=2372)			Cord blood (CB) (n=128)			Total (n=2882)		
	No. Abn Cases	ADR (%)	RF (%)	No. Abn Cases	ADR (%)	RF (%)	No. Abn Cases	ADR (%)	RF (%)	No. Abn Cases	ADR (%)	RF (%)
Numerical abnormality												
Sex Chromosome Aneuploidy												
45,XO	9	2.36	19.15	8	0.34	3.15	1	0.78	16.67	18	0.62	5.86
45,X[26]/46,XY[4]	0	0.00	0.00	1	0.04	0.39	0	0.00	0.00	1	0.03	0.33
47,XXX	1	0.26	2.13	5	0.21	1.97	0	0.00	0.00	6	0.21	1.95
47,XXY	1	0.26	2.13	14	0.59	5.51	0	0.00	0.00	15	0.52	4.89
47,XXY[13]/46,XX[87]	1	0.26	2.13	0	0.00	0.00	0	0.00	0.00	1	0.03	0.33
47,XXY[16]/46,XY[34]	0	0.00	0.00	1	0.04	0.39	0	0.00	0.00	1	0.03	0.33
47,XYY	0	0.00	0.00	5	0.21	1.97	0	0.00	0.00	5	0.17	1.63
48,XXXY	0	0.00	0.00	1	0.04	0.39	0	0.00	0.00	1	0.03	0.33
48,XXYY	0	0.00	0.00	1	0.04	0.39	0	0.00	0.00	1	0.03	0.33
Subtotal	**12**	**3.14**	**25.53**	**36**	**1.52**	**14.17**	**1**	**0.78**	**16.67**	**49**	**1.70**	**15.96**
Autosomal Aneuploidy												
Trisomy 21	12	3.14	25.53	97	4.09	38.19	2	1.56	33.33	111	3.85	36.16
Trisomy 18	9	2.36	19.15	24	1.01	9.45	1	0.78	16.67	34	1.18	11.07
Trisomy 13	2	0.52	4.26	6	0.25	2.36	0	0.00	0.00	8	0.28	2.61
Other aneuploidy	3	0.79	6.38	1	0.04	0.39	0	0.00	0.00	4	0.14	1.30
Subtotal	**26**	**6.81**	**55.32**	**128**	**5.40**	**50.39**	**3**	**2.34**	**50.00**	**157**	**5.45**	**51.14**
Triploid & tetraploid	**1**	**0.26**	**2.13**	**3**	**0.13**	**1.18**	**0**	**0.00**	**0.00**	**4**	**0.14**	**1.30**
Total	**39**	**10.21**	**82.98**	**167**	**7.04**	**65.75**	**4**	**3.13**	**66.67**	**210**	**7.29**	**68.40**
Structural abnormality	**2**	**0.52**	**4.26**	**37**	**1.56**	**14.57**	**1**	**0.78**	**16.67**	**40**	**1.39**	**13.03**
Chromosome polymorphism	**6**	**1.57**	**12.77**	**49**	**2.07**	**19.29**	**1**	**0.78**	**16.67**	**56**	**1.94**	**18.24**
mos46,XX[28]/46,XY[22]	**0**	**0.00**	**0.00**	**1**	**0.04**	**0.39**	**0**	**0.00**	**0.00**	**1**	**0.03**	**0.33**
All chromosomal abnormalities	**47**	**12.30**	**100.00**	**254**	**10.71**	**100.00**	**6**	**4.69**	**100.00**	**307**	**10.65**	**100.00**

ADR, abnormality detection rate (%); RF, relative frequency by (%); *Statistically different from ADR in prenatal setting (P< 0.05)

The most common structural chromosomal abnormalities were 46,X,inv(Y)(p11.2q11.23) (n = 4; RF = 10.0%), followed by 46,XN,dup(1)(q11q12) (n = 3; RF = 7.5%), and 46,XN,dup(1)(q11q21) (n = 2; RF = 5.0%) (Table S2). The most common chromosome polymorphisms were 46,XN,inv(9)(p13q13) (n = 28; RF = 50.0%), followed by 46,XN,inv(9)(p11q13) (n = 2; RF = 3.57%), and 46,XN,inv(9)(p13q13) (n = 2; RF = 3.57%) (Table S2).

The relationship of maternal age, gestational age and chromosomal abnormalities

Based on the age of the pregnant women, the cases included in this study were divided into less than 35 years old group and greater than or equal to 35 years old group. There were statistically significant differences in the chromosomal abnormalities rate between this two groups (χ^2 = 51.041, P< 0.001). The main types of chromosomal abnormalities were autosomal aneuploidy (n = 88; ADR = 3.89%) and chromosome polymorphism (n = 49; ADR = 2.16%) in less than 35 years old group, which autosomal aneuploidy (n = 69; ADR = 11.18%) and sex chromosome aneuploidy (n = 16; ADR = 2.59%) in greater than or equal to 35 years old group. Grouped according to gestational age, there were no significant differences in the chromosomal abnormalities rate in < 13 weeks group, 13–28 weeks group and > 28 weeks group (Table 4).

Table 4
Comparison of karyotype abnormalities at different maternal ages and gestational weeks.

Group	Numerical abnormality			Structural abnormality	Chromosome polymorphism	Total (n, %)	*P* value
	Autosomal Aneuploidy	Sex Chromosome Aneuploidy	Triploid & tetraploid				
Maternal age							
< 35 years (n = 2264)	88(3.89)	33(1.46)	4(0.18)	29(1.28)	49(2.16)	203(8.97)	< 0.001(χ^2 = 51.041)
≥ 35 years (n = 617)	69(11.18)	16(2.59)	0(0)	11(1.78)	7(1.13)	103(16.69)	
Gestational age							
< 13 weeks (n = 268)	16(5.97)	7(2.61)	1(0.37)	2(0.75)	6(2.24)	32(11.94)	0.428(χ^2 = 4.579)
13–28 weeks (n = 2462)	140(5.69)	40(1.62)	3(0.12)	36(1.46)	47(1.91)	266(10.80)	0.515(χ^2 = 4.023)
> 28 weeks (n = 151)	1(0.66)	2(1.32)	0(0)	2(1.32)	3(1.99)	8(5.30)	0.069(χ^2 = 9.645)

Discussion

Chromosomal karyotype abnormality is one of the important causes of infertility, mental retardation, adverse pregnancy, asthenia and unexplained recurrent abortion, and karyotype analysis is an important detection method for chromosomal genetic diseases. The chromosome karyotype analysis of peripheral blood lymphocytes can provide scientific basis for the diagnosis and treatment of clinical chromosome diseases[15].

The most common reasons of genetic counseling patients are infertility, adverse pregnancy and parturition history, growth and developmental abnormalities and congenital diseases and mental retardation. The onset of these is mainly related to genetic, environmental, immune, among which chromosome abnormalities are one of the important causes of adverse pregnancy history. The results of this study showed that the chromosome karyotype abnormality rate of genetic counseling patients in Meizhou was 7.41%. That was lower than the 10.65% reported in previous study in Guangdong province[16], 9.89% in Shenzhen[17], 8.97% in Zaozhuang area[18], higher than the 6.65% reported in Wuhan in Hubei province[19], 5.12% in Lianyungang area[20], 4.39% in Yangzhou area[21].

Infertile men and women have a significantly increased risk of carrying chromosomal abnormalities. The results of this study showed that the chromosome karyotype abnormality rate of infertile male and female was 6.77% and the main types of chromosomal abnormalities were chromosome polymorphism and sex chromosome aneuploidy in these patients. Our results are consistent with some studies[22]. The rate of chromosomal anomaly in male infertile patients was 4.15% reported by M. Gao *et al* from Shenyang Women's and Children's Hospital[23]. The rate of chromosomal anomaly in the 14965 infertile couples was 3.84%, which 6.84% in the men and in 0.84% the women in Central China reported by Yan Liu *et al*[24]. The prevalence of chromosomal abnormalities was 10.55% among patients receiving genetic counseling in Jilin Province of China[25].

The chromosome abnormality rate in Chinese population is 0.5%-1.0%, while the chromosome abnormality rate in patients with adverse pregnancy and parturition history is 2%-10%[26]. The results of this study showed that chromosome abnormality rate in patients with adverse pregnancy and parturition history was 7.04%, which chromosome polymorphism was 4.47% and structural abnormality was 2.37%. It is consistent with those reported in other studies. The main types of chromosomal structure variation are balanced translocation of chromosome, Robertson translocation and inversion. Study has found that karyotype analysis of 1657 patients with abnormal reproductive history in Shenzhen showed that chromosome abnormality rate was 3.26% and polymorphism rate was 3.80%[27].

Mental retardation (MR) is a common disease in genetics counseling children, mainly due to central nerve damage caused by the cognitive ability of defects, such as in the crowd prevalence was 1%-3%[28]. Chromosomal abnormalities can be detected in 10% of patients with delayed growth or mental retardation[29]. Trisomy 21 is the most common type of chromosome abnormality in children genetic counseling. The Down syndrome critical region (DSCR) is located in 21q22, with a fragment size of about 5.4 Mb[30]. The duplication of this region can lead to a typical clinical phenotype of Down syndrome in an individual. These clinical manifestations include special facial features, short stature, muscle hypotonia, atlantoaxial instability, reduced neuronal density, cerebellar hypoplasia, intellectual disability and congenital heart defects[30, 31]. In this study, the number of children with trisomy 21 syndrome accounted for 50% (32/64) of the total number of abnormal karyotypes, followed by chromosome polymorphism 21.88% (14/64). Studies have shown that 17%-41% of children with mental retardation and developmental delay are caused by genetic factors, such as chromosome abnormality, single-gene disease and other genetic abnormalities[32]. If karyotype analysis is not easy to detect chromosomal abnormalities, 5%-20% of patients can be diagnosed with minor abnormalities by further fluorescence in situ hybridization, MLPA, and comparative genomic hybridization[33]. Studies have shown that 1q21.1, 15q13.3 and 16p11.2 are chromosome recombination hotspots for mental retardation, autism, epilepsy, schizophrenia and other diseases[34]. Therefore, the application of different testing techniques can provide stronger diagnostic evidence for genetic counseling and prenatal diagnosis.

Chromosome polymorphism mainly occurs in the structural heterochromatin region, including heterochromatin region and satellite. Generally, it has no obvious phenotypic effect or pathological significance, and whether it causes clinical effect has been controversial[35]. In this study, there were 204 cases of chromosome polymorphism, with a detection rate of 3.86%, including qh+, pstk+, ps+, cenh+, inv(9), inv(Y), Y < G.

In this study, among the 2882 fetus samples, 307 cases of chromosomal abnormal karyotypes were detected, with an abnormal rate of 10.65%. Among the abnormal karyotypes, 210 fetus samples with numerical abnormality. And the trisomy syndrome was detected in 153 cases, accounting for 72.86% (153/210), which was the most common abnormal type. Advanced age is a high risk factor for chromosomal abnormalities, especially for aneuploidy. In this study, there were 617 pregnant women with advanced age (≥ 35 years), accounting for 21.41%. And the chromosomal abnormalities rate was higher than that in non-elderly pregnant women. In recent years, based on high-throughput sequencing technology to analyze fetal free DNA in maternal plasma, the noninvasive prenatal testing (NIPT) technology to detect fetal chromosome aneuploidy has been widely accepted by pregnant women due to its high sensitivity and specificity and no risk of miscarriage. NIPT mainly detects trisomy 21, 18 and 13, with an accuracy rate of more than 99%[36]. Its limitation is that the screening only detect numerical abnormalities, and cannot detect structural abnormalities such as chromosome deletion, duplication, translocation and inversion.

Conclusions

In conclusion, abnormal chromosome karyotype detection rate is higher in genetic counselors in Meizhou area. Abnormal chromosome karyotype can cause infertility, abnormal gestation and birth, growth and developmental abnormalities, congenital diseases and mental retardation, and other diseases. Therefore, karyotype analysis has great significance for clinical diagnosis, guide the healthy birth, and improve the quality of the population.

Methods

Patients

This retrospective clinical study included 5,289 adults and children cases, 2,882 fetuses performed chromosome karyotype in Meizhou *People'sHospital (Huangtang Hospital),* Meizhou Academy of Medical Sciences, *Meizhou* Hospital Affiliated to Sun Yat-sen University between January 2015 and March 2020. This study was conducted on the basis of the Declaration of Helsinki and was supported by the Ethics Committee of the Meizhou *People'sHospital*.

Karyotyping

Karyotyping was performed on G-band metaphases prepared from cultured cells of specimens obtained from peripheral blood (PB), chorionic villus sampling (CVS), amniocentesis (AC) and cord blood (CB), and following the laboratory's standardized procedures. The detected chromosomes were named according to the International System for Human Cytogenetic Nomenclature (ISCN).

Categorization of the chromosomal abnormalities

There are two main types of chromosomal abnormalities: (1) numerical abnormalities, including sex chromosome aneuploidies (47,XXY, 47,XYY, other X or Y aneuploidies for males and 45,X, 47,XXX, other X aneuploidies for females), autosomal aneuploidies (trisomy 21, trisomy 18, trisomy 13, and other autosomal aneuploidies), triploidy and tetraploidy; (2) structural abnormalities, including balanced rearrangements (reciprocal translocations, Robertsonian translocations, inversions, etc.) and unbalanced structural rearrangements (deletions, duplications,

etc.). The workflow of genetic counselors and prenatal diagnosis cases processing with detected chromosomal abnormalities and their categories is depicted in Figure 1.

Statistical analysis

SPSS statistical software version 21.0 was used for data analysis. Values are expressed as n (%). Fisher's exact tests were used to compare the positive ratios between groups. A value of $P<0.05$ was considered as statistically significant.

Declarations

Ethics approval and consent to participate

The study was approved by the Ethics Committee of Medicine, Meizhou People's Hospital (Huangtang Hospital), Meizhou Academy of Medical Sciences, Meizhou Hospital Affiliated to Sun Yat-sen University.

Consent for publication

Not applicable.

Availability of data and materials

The data used to support the findings of this study are available from the corresponding author upon request.

Competing interests

The authors declare that they have no competing interests.

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Authors' contributions

Heming Wu designed the study. Hua Zhong performed the experiments. Heming Wu and Hua Zhong collected clinical data. Hua Zhong, Zhikang Yu and Qingyan Huang analyzed the data. Heming Wu prepared the manuscript. All authors were responsible for critical revisions, and all authors read and approved the final version of this work.

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Figures

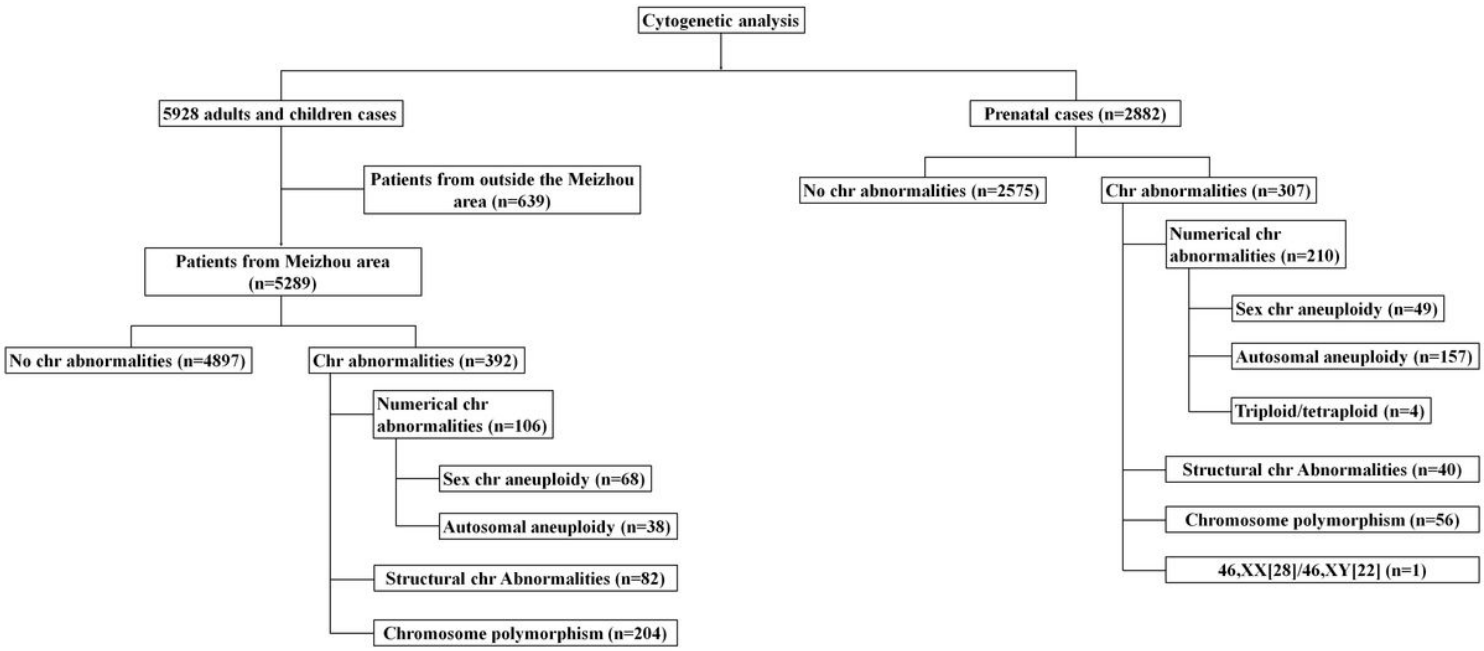

Figure 1

Flow-diagram for detection and categorization of chromosomal abnormalities in these cases.

Supplementary Files

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