Comprehensive analysis of early pregnancy loss based on cytogenetic findings from a tertiary referral center

Xiaoqing wu
Fujian Maternity and Child Health Hospital, Affiliated Hospital of Fujian Medical University
https://orcid.org/0000-0003-2605-2362
Linjuan Su
Fujian Maternity and Child Health Hospital, Affiliated Hospital of Fujian Medical University
Xiaorui Xie
Fujian Maternity and Child Health Hospital, Affiliated Hospital of Fujian Medical University
Deqin He
Fujian Maternity and Child Health Hospital, Affiliated Hospital of Fujian Medical University
Xuemei Chen
Fujian Maternity and Child Health Hospital, Affiliated Hospital of Fujian Medical University
Meiying Wang
Fujian Maternity and Child Health Hospital, Affiliated Hospital of Fujian Medical University
Linshuo Wang
Fujian Maternity and Child Health Hospital, Affiliated Hospital of Fujian Medical University
Liangpu Xu
Fujian Maternity and Child Health Hospital, Affiliated Hospital of Fujian Medical University
Lin Zheng (zlin1536@126.com)
Fujian Maternity and Child Health Hospital, Affiliated Hospital of Fujian Medical University

Research

Keywords: Products of conception, Chromosomal abnormalities, Maternal age, Live birth history, Previous miscarriage, Mode of conception

Posted Date: September 17th, 2021

DOI: https://doi.org/10.21203/rs.3.rs-889210/v1

Version of Record: A version of this preprint was published at Molecular Cytogenetics on December 1st, 2021. See the published version at https://doi.org/10.1186/s13039-021-00577-8.

Abstract

Background

Pregnancy loss is one of the most common complications during pregnancy. Clinical consultation and comprehensive understanding of the etiology are critical for reducing anxiety, distress, and depression. This study aimed to perform a comprehensive analysis for products of conception (POC) in miscarriage based on genetic etiology and clinical information.

Methods

Retrospective observation was performed on cytogenetic findings of 1252 POC form spontaneous pregnancy loss over an 11-year period. The frequencies and profiles of chromosomal abnormalities were discussed according to the classification of women with different maternal age, previous miscarriage history, normal live birth history, and different mode of conception.

Results

A total of 667 (53.2%) chromosomal abnormalities were observed, including 597 (47.7%) cases of numerical abnormalities, 33 (2.6%) cases of unbalanced structural abnormalities, 32 (2.6%) cases of mosaicism, and 5 (0.4%) cases of balanced rearrangement. In group of women above 40 years of age, the detection rates of chromosomal abnormalities and viable autosomal trisomy were significantly higher than those in groups of ≤ 29, 30 ~ 34, 35 ~ 39 years of age ($p < 0.05$). The detection rate of abnormal karyotype in women with normal live birth history was 61.1%, significantly higher than 52.5% in women without normal live birth history ($p < 0.05$). There was no significant difference among women without, with 1–2, and ≥ 3 previous miscarriages in the rate of abnormal karyotype ($p > 0.05$), and viable autosomal trisomy was less common in women with ≥ 3 previous miscarriages. The frequency of chromosomal abnormalities was 49.0% and 41.0% in women with assisted conception and natural conception ($p > 0.05$), respectively, and monosomy X was more frequently detected in women with natural conception.

Conclusion

The frequencies and profiles of chromosomal abnormalities in early miscarriages are strongly associated with clinical information including the maternal age, previous miscarriage, live birth history, and mode of conception. Even in women with a first miscarriage, or with a history of normal live births, chromosomal analysis of POC should be recommended for etiological assessment.

Background

Pregnancy loss before 12 weeks of gestation is the most common complication of early pregnancy and has a substantial impact on couple's physical and psychological well-beings. The frequency was estimated to be 10% ~ 15% of all pregnancies[1]. Understanding the etiology of miscarriage is of great benefits to reduce anxiety, support clinical consultant as well as medical management for future reproductive planning. Abnormal embryonic karyotype are recognized as most important and detectable factors [2–5]. De novo numerical abnormalities, especially autosomal trisomies, may explain a vast proportion of recurrent spontaneous miscarriage [6]. Therefore, in our center, G-banding karyotyping is sometimes more acceptable because of it's detectability of numerical anomalies and lower cost than molecular methodology. Most genetic anomalies that lead to miscarriage are sporadic, probably led by random errors during gametogenesis, and seem to have no association w the future pregnancies. However, some abnormalities may indicate a potential recurrence risk of chromosomal abnormality, especially for viable autosomal trisomies including trisomy 13, trisomy 18 and trisomy 21. Viable autosomal trisomies are the most major components of abnormal karyotypes in prenatal screening and diagnosis, but their performance in early pregnancy loss was rarely discussed.

There is sufficient evidence for the necessity of genetic analysis of POC in patients with recurrent miscarriage [7–9], but in our clinical practice, for women who was experiencing the first pregnancy loss, or who already had normal child, the chromosomal analysis of POC was not routinely opted by them. In this study, we comprehensively investigated the associations between chromosomal abnormalities of POC and clinical information including the maternal age, history of miscarriage, normal live birth history, as well as the mode of conceptions, in order to revaluate the influence of these factors on the frequencies or profiles of genetic abnormalities in early pregnancy loss.

Results

None of the 50 samples underwent QF-PCR showed maternal cell contamination. Abnormal karyotypes were detected in 667 out of 1252 (53.2%) cases, including 592 (47.3%) numerical abnormalities, 38 (5.7%) cases of structural abnormalities, and 37(5.5%) cases of mosaic abnormalities. All chromosomes except chromosome 1 were involved chromosomal trisomies, with trisomy 16 as the most common finding (Fig. 1). The detection rate of viable autosomal trisomy including T21, T13, T18 were 3.0%, 1.9% and 1.0%, respectively. Monosomy X was the most frequently encountered sex chromosomal abnormalities and the detection rate was 5.8%. Parental inherited balanced rearrangement were detected in five cases, including 3 cases of Robert translocation, 1 case of balanced translocation, and 1 case of insertional abnormalities. The details are summarized in Table 1.

Table 1
The details of 667 cases of chromosomal abnormalities.

	Numbers (n)	Frequency in 667 cases with chromosomal abnormalities	Frequency in total cases
Numerical abnormalities			
Trisomy 21	37	5.5%	3.0%
Trisomy 13	24	3.6%	1.9%
Trisomy 18	12	1.8%	1.0%
Other Autosomal Aneuploidy	366	54.9%	29.2%
45,X	73	10.9%	5.8%
47,XXY	4	0.6%	0.3%
Triploidy	47	7.0%	3.8%
Hypotriploidy or hypertriploidy	8	1.2%	0.6%
Tetraploidy	19	2.8%	1.5%
Hypotetraploidy or hypertetraploidy	2	0.3%	0.2%
Total	592	88.8%	47.3%
Structural abnormalities			
Unbalanced structural abnormalities	33	4.9%	2.6%
Balanced rearrangement	5*	0.7%	0.4%
Total	38	5.7%	3.0%
Mosaic abnormalities	37	5.5%	3.0%
*, The karyotypes were: 46,XX,ins(11;13)(q23;q22q32) mat, 45,XX,rob(14;15)(q10;q10) pat, 45,XY,rob(13;14) (q10;q10) mat, 46,XX,t(1;15)(q44;q14) mat, 45,XY,rob(13;14)(q10;q10) mat			

The associations between abnormal karyotype and maternal age, previous miscarriages, live birth history and mode of conception are presented in Table 2. Similar incidence of chromosomal abnormalities were found among women aged ≤ 29, 30–34, and 35–39 years old ($p > 0.05$). The detection rate was significantly higher in women ≥ 40 years old ($p < 0.05$). The frequency of viable autosomal trisomy increased with the maternal age, while the incidence of monosomy X decreased with the maternal age. Similar frequencies of abnormal karyotype were observed in women without, with 1–2 and ≥ 3 previous miscarriage ($p > 0.05$). In women with ≥ 3 previous miscarriage, the detection rate of viable autosomal

trisomy was significantly lower than that in women with < 3 previous miscarriage ($p < 0.05$). Women with normal live birth history were more likely to have abnormal karyotype than women without normal live birth history. With regard to different modes of conception, women with assisted pregnancy has a higher incidence of monosomy X than women with natural pregnancy ($p < 0.05$).

Table 2
Association between clinical information and the frequency of chromosomal abnormalities

	Abnormal karyotype (n, %)	**Viable autosomal trisomy (n, %)**	**Monosomy X (n, %)**
Maternal age (years) (N = 1252)			
≤ 29 (n = 537)	279, 52.0%,	24, 4.5%	35, 6.5%
30–34 (n = 452)	230, 50.9%	24, 5.3%	28, 6.2%
35–39 (n = 201)	115, 57.2%,	14, 7.0%	11, 5.5%
≥ 40 (n = 62)	43, 69.4%,	12, 19.4%	3, 4.8%
p	< 0.05	< 0.05	> 0.05
Normal live birth history (N = 895)			
No (n = 185)	113, 61.1%	12, 6.5%	11, 5.9%
Yes (n = 710)	373, 52.5%	50, 7.0%	41, 5.8%
p	< 0.05	> 0.05	> 0.05
Previous miscarriage (N = 895)			
0 (n = 273)	146, 53.5%	20, 7.3%	11, 4.0%
1–2 (n = 504)	271, 53.8%	39, 7.7%	32, 6.3%
≥ 3 (n = 117)	117, 59.0%	2, 1.7%	8, 6.8%
p	> 0.05	< 0.05	> 0.05
Mode of conception (N = 895)			
Assisted conception (n = 115)	57, 49.0%	8, 7.0%	1, 0.9%
Natural conception (n = 780)	320, 41.0%	52, 6.7%	38, 4.9%
p	> 0.05	> 0.05	*< 0.05*

Discussion

Although various molecular methodology have been applied in the genetic analysis of POC, we focused on the cytogenetic results due to the following reasons: first, in clinical practice, conventional karyotyping was still opted by many women due to lower cost compared to molecular testing; second, large fragmental abnormalities are lethal, and contribute to miscarriage [10], while submicroscopic aberrations could be viable and contribute to prenatal ultrasound anomalies or neurodevelopmental disorders [11].

Consistent with previous reports, nearly half of the pregnancy loss were attributed to fetal chromosomal anomalies, with vast majority of them being numerical anomalies. Autosomal trisomies were highly prevalent, with trisomy 16 being the most frequent finding. Chromosome 1 and 19 were rarely involved, in line with previous reports [1, 12, 13]. The phenomenon could be explained by the mechanism of gamete meiosis, but the exact mechanism is still unclear. Unbalanced structural abnormalities were detected in 33 cases, and 6 of them were confirmed to be resulted from a parent with balanced translocation. Balanced rearrangement, involving Robert translocation, balanced translocation, and insertional abnormalities were observed in five cases, which were finally confirmed to be parental inheritance. Balanced rearrangement may not be the explanation of pregnancy loss, but a parent with balanced structural rearrangement are at a greater risk of recurrent miscarriage than those without it.

Advanced maternal age (≥ 35) is a well-known independent factor associated with the frequencies of cytogenetic abnormalities in early miscarriages [1, 12, 14]. In this study, the frequencies of abnormal karyotype in women aged up to 30 years, between 30 and 34 years, as well as between 35 and 39 were comparable, while the frequency was significantly higher in women ≥ 40 years old. The tendency was in line with that of viable autosomal trisomy, which confirmed the close association between maternal age and viable autosomal trisomy. Monosomy X was the most commonly encountered viable sex chromosomal abnormalities. Unlike viable autosomal trisomy, the frequency of monosomy X did not change with the maternal age, in agreement with a previous report [15]. This might be attributed to the speculation that monosomy X is more likely derived from a meiotic error in the father than in the mother [16, 17]. These results may suggest that maternal age has different effects on meiosis of different chromosomes.

To the best of our knowledge, the association between the normal live birth history and chromosomal abnormalities in POC is rarely discussed. In our clinical practice, patients having a normal child always believed that they were less likely to have chromosomal abnormalities in the next pregnancy and decline the detection of POC. However, in our study, the rate of abnormal karyotype in women with a history of normal live birth was significantly higher than that in women without it. This might be attributed to the maternal age, because women with a history of normal birth tend to be older, especially under the two-child policy in China, which resulted in an increasing proportion of women with advanced maternal age [18, 19]. Therefore, genetic testing is also meaningful for women with a history of normal live births. The relationship between the number of previous miscarriages and abnormal karyotype is controversial. In certain studies, there was a lower frequency of chromosomal abnormalities in recurrent miscarriages

than that in sporadic miscarriages [20–23], whereas some reports concluded that the frequency of chromosomal abnormalities did not change with the miscarriage history [24–26]. In present study, high detection rate for abnormal chromosome were observed in different miscarriage history, and no correlation was found between the frequency of abnormal karyotype and miscarriage history. So cytogenetic tests might be offered if the couples would like to find out the cause for the first miscarriage. For the viable autosomal trisomy, the frequency was remarkably decreased in women with ≥ 2 miscarriage. We concluded that viable autosomal trisomy less likely occurred in pregnancy loss after 3 miscarriage history.

Assisted reproductive technology (ART) enables infertile couples achieve pregnancy. However, miscarriage is still inevitable. The prevalence of early miscarriage following ART ranges from 22%-63% and one of the major causes is embryonic chromosomal abnormality [27, 28]. Whether assisted conception increase or decrease the risk of chromosomal abnormalities in early spontaneous abortion is controversial. Our study showed no significantly differences in the frequencies of abnormal karyotypes, or viable autosomal trisomy between assisted conception and natural conception. But the detection rate of monosomy X was significantly lower in the assisted conception group. It may be explained by different ART treatments. Previous studies demonstrated that the incidence of monosomy X was significantly higher in abortus following intracytoplasmic sperm injection (ICSI) treatment, compared to that following in vitro fertilization (IVF) [29, 30]. The mechanism is unclear. It is possible that the damage to the cytoskeleton caused by injection leads to mitotic errors [31] or that the preferential location of X chromosome in the subacrosomal region of the sperm nucleus is related to reduced DNA decondensation and its propensity for inactivation [32]. Therefore, we believe that the reason for the low frequency of detection of monosomy X could be attributed to the low proportion of ICSI patients in the assisted reproduction group; but it could not be confirmed owing to the lack of information on the ART used in our study.

There are limitations that might lead to biased results of the study. First, clinical information were not available for all cases. Second, maternal cell contamination was not evaluated for all samples.

Conclusions

The frequencies and profiles of chromosomal abnormalities in early miscarriages are strongly associated with clinical factors including the maternal age, previous miscarriage, live birth history, and mode of conception. Chromosomal analysis of POC should be recommended even in women with first miscarriage, or women with normal live birth history if the patients wondering the cause of miscarriage.

Materials And Methods

Data resources

This is a retrospective study of chromosomal analysis from 1430 patients with early pregnancy loss who underwent curettage procedure between April 2009 and September 2020. Excluding 178 cases of cultural failure, a total of 1252 POC including 1250 chorionic villi and 2 foetal tissues were enrolled. The mean age of the patients was 35.5 years old, ranged from 19 to 47 years, and the mean gestational age was 10.1 weeks, ranged from 7 to 14 weeks.

Because clinical information including early miscarriage history, normal live birth history, and mode of conception were not correctly recorded in 357 cases, they were available in only 895 cases. Maternal age was classified into the following four groups: ≤ 29, 30 ~ 34, 35 ~ 39, and ≥ 40 years of age. The numbers of previous early miscarriages was classified into the three groups: 0, 1 ~ 2, and ≥ 3. The normal live birth history was categorized as “0” and “≥ 1” groups. The mode of conception was categorized as groups of assisted conception and natural conception.

The present study was approved by the Protection of Human Ethics Committee of Fujian Provincial Maternity and Children’s Hospital, affiliated Hospital of Fujian Medical University. Written informed consent was obtained from individual or guardian participants.

Conventional Karyotyping And Maternal Cell Contamination Evaluation

The specimens were carefully rinsed with sterile physiological saline and dissected from blood, clot and maternal decidua base on operation experience. Cell culture and G-banded karyotyping was performed according to the standard protocols in our laboratory. The specimens were cultivated for about 9 to 14 days, then arrested in metaphase and finally Wright's stain was used for G-banding at a resolution of 320–400 banding. Karyograms were prepared using CytoVision, a computer-assisted karyotyping system (Leica Biosystems, Newcastle, UK). Before 2019, maternal cell contamination evaluation were conducted by selecting typical villi through morphological identification to prevent contamination of decidual tissue. Thus maternal peripheral blood was obtained in only 100 cases for the quantitative fluorescent-polymerase chain reaction (QF-PCR) to exclude maternal cell contamination after 2019.

Statistical Analysis

We evaluated the overall chromosomal abnormalities, viable autosomal trisomies and monosomy X to identify the frequencies and profiles of abnormal karyotypes among different categories. All data were entered into a Microsoft Excel 2016 (Microsoft Corp., Redmond, WA) spreadsheet, and SPSS software version 26.0 (SPSS, Inc., Chicago, IL) was used for statistical analysis. Statistical comparisons were performed using c2 test, and $p < 0.05$ was considered statistically significant.

Declarations

Ethics approval and Consent to participate

The present study was approved by the Protection of Human Ethics Committee of Fujian Provincial Maternity and Children's Hospital, affiliated Hospital of Fujian Medical University. Written informed consent was obtained from individual or guardian participants.

Consent for publication

All patients have provided written informed consent prior to participating in the present study.

Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Competing interests

There is no conflict of interests regarding the publication of this paper.

Acknowledgements

We would like to thank Danhua Guo, Meiying Cai for the collection of primary data.

Authors' contributions

Xiaoqing Wu, Lin Zhen, Liangpu Xu prepared the main manuscript; Xiaorui Xie, Meiying Cai, Linjuan Su, prepared the experiment. Xuemei Chen and Denqin He were responsible for data collection. All authors have read and approved the final article.

References

1. Menasha J, Levy B, Hirschhorn Kand Kardon NB. Incidence and spectrum of chromosome abnormalities in spontaneous abortions: new insights from a 12-year study. Genet Med. 2005;7(4):251–63.
2. Reddy UM, Page G, Pand Saade GR. The role of DNA microarrays in the evaluation of fetal death. Prenat Diagn. 2012;32(4):371–5.
3. Sahoo T, Dzidic N, Strecker MN, Commander S, Travis MK, Doherty C, et al. Comprehensive genetic analysis of pregnancy loss by chromosomal microarrays: outcomes, benefits, and challenges. Genet Med. 2017;19(1):83–9.
4. Du Y, Chen L, Lin J, Zhu J, Zhang N, Qiu X, et al. Chromosomal karyotype in chorionic villi of recurrent spontaneous abortion patients. Biosci Trends. 2018;12(1):32–9.
5. van den Berg MM, van Maarle MC, van. Wely Mand Goddijn M. Genetics of early miscarriage. Biochim Biophys Acta. 2012;1822(12):1951–9.
6. Stephenson MD, Awartani K, Aand Robinson WP. Cytogenetic analysis of miscarriages from couples with recurrent miscarriage: a case-control study. Hum Reprod. 2002;17(2):446–51.

7. Asgari A, Ghahremani S, Saeedi Sand Kamrani E. The study of chromosomal abnormalities and heteromorphism in couples with 2 or 3 recurrent abortions in Shahid Beheshti Hospital of Hamedan. Iran J Reprod Med. 2013;11(3):201–8.
8. Page JM, Silver RM. Genetic Causes of Recurrent Pregnancy Loss. Clin Obstet Gynecol. 2016;59(3):498–508.
9. Sato T, Migita O, Hata H, Okamoto Aand Hata K. Analysis of chromosome microstructures in products of conception associated with recurrent miscarriage. Reprod Biomed Online. 2019;38(5):787–95.
10. Wang Y, Li Y, Chen Y, Zhou R, Sang Z, Meng L, et al. Systematic analysis of copy-number variations associated with early pregnancy loss. Ultrasound Obstet Gynecol. 2020;55(1):96–104.
11. Cheng SSW, Chan KYK, Leung K K P, Au PKC, Tam WK, Li SKM, et al. Experience of chromosomal microarray applied in prenatal and postnatal settings in Hong Kong. Am J Med Genet C Semin Med Genet. 2019;181(2):196–207.
12. Tamura Y, Santo M, Araki Y, Matsubayashi H, Takaya Y, Kitaya K, et al. Chromosomal copy number analysis of products of conception by conventional karyotyping and next-generation sequencing. Reprod Med Biol. 2021;20(1):71–5.
13. Gu C, Li K, Li R, Li L, Li X, Dai X, et al. Chromosomal Aneuploidy Associated With Clinical Characteristics of Pregnancy Loss. Front Genet. 2021;12:667697.
14. Gomez R, Hafezi N, Amrani M, Schweiger S, Dewenter MK, Thomas P, et al. Genetic findings in miscarriages and their relation to the number of previous miscarriages. Arch Gynecol Obstet, 2020: 1–8.
15. Nybo Andersen AM, Wohlfahrt J, Christens P, Olsen Jand Melbye M. Maternal age and fetal loss: population based register linkage study. BMJ. 2000;320(7251):1708–12.
16. Terry Hassold F, B a ML. Cytogenetic and Molecular Analysis of Sex-Chromosome Monosomy. Am J Hum Genet. 1988;42(4):534–41.
17. Donnelly SL, Wolpert CM, Menold MM, Bass MP, Gilbert JR, Cuccaro ML, et al. Female with autistic disorder and monosomy X (Turner syndrome): parent-of-origin effect of the X chromosome. Am J Med Genet. 2000;96(3):312–6.
18. Zhang X, Chen L, Wang X, Wang X, Jia M, Ni S, et al. Changes in maternal age and prevalence of congenital anomalies during the enactment of China's universal two-child policy (2013–2017) in Zhejiang Province, China: An observational study. PLoS Med. 2020;17(2):e1003047–7.
19. Li HT, Xue M, Hellerstein S, Cai Y, Gao Y, Zhang Y, et al. Association of China's universal two child policy with changes in births and birth related health factors: national, descriptive comparative study. BMJ. 2019;366:4680.
20. Nikitina TV, Sazhenova EA, Tolmacheva EN, Sukhanova NN, Kashevarova AA, Skryabin NA, et al. Comparative Cytogenetic Analysis of Spontaneous Abortions in Recurrent and Sporadic Pregnancy Losses. Biomed Hub. 2016;1(1):1–11.

21. Sullivan AE, Silver RM, LaCoursiere DY, Porter T, Fand Branch DW. Recurrent fetal aneuploidy and recurrent miscarriage. Obstet Gynecol. 2004;104(4):784–8.
22. Liu Y, Liu Y, Chen H, Du T, Tan Jand Zhang J. The frequencies of the presence of embryonic pole and cardiac activity in early miscarriages with abnormal karyotypes. Clin Exp Obstet Gynecol. 2015;42(4):490–4.
23. Ozawa N, Ogawa K, Sasaki A, Mitsui M, Wada Sand Sago H. Maternal age, history of miscarriage, and embryonic/fetal size are associated with cytogenetic results of spontaneous early miscarriages. J Assist Reprod Genet. 2019;36(4):749–57.
24. Grande M, Borrell A, Garcia-Posada R, Borobio V, Munoz M, Creus M, et al. The effect of maternal age on chromosomal anomaly rate and spectrum in recurrent miscarriage. Hum Reprod. 2012;27(10):3109–17.
25. Segawa T, Kuroda T, Kato K, Kuroda M, Omi K, Miyauchi O, et al. Cytogenetic analysis of the retained products of conception after missed abortion following blastocyst transfer: a retrospective, large-scale, single-centre study. Reprod Biomed Online. 2017;34(2):203–10.
26. Yang L, Tao T, Zhao X, Tao H, Su J, Shen Y, et al. Association between fetal chromosomal abnormalities and the frequency of spontaneous abortions. Exp Ther Med. 2020;19(4):2505–10.
27. Farr SL, Schieve L, Aand Jamieson DJ. Pregnancy loss among pregnancies conceived through assisted reproductive technology, United States, 1999–2002. Am J Epidemiol. 2007;165(12):1380–8.
28. Qin JZ, Pang LH, Li MQ, Xu Jand Zhou X. Risk of chromosomal abnormalities in early spontaneous abortion after assisted reproductive technology: a meta-analysis. PLoS One. 2013;8(10):e75953.
29. Zhang X, Wang Y, Zhao N, Liu Pand Huang J. Variations in chromosomal aneuploidy rates in IVF blastocysts and early spontaneous abortion chorionic villi. J Assist Reprod Genet. 2020;37(3):527–37.
30. Li G, Jin H, Niu W, Xu J, Guo Y, Su Y, et al. Effect of assisted reproductive technology on the molecular karyotype of missed abortion tissues. Biosci Rep. 2018;38(5):1–8.
31. Causio F, Fischetto R, Sarcina E, Geusa Sand Tartagni M. Chromosome analysis of spontaneous abortions after in vitro fertilization (IVF) and intracytoplasmic sperm injection (ICSI). Eur J Obstet Gynecol Reprod Biol. 2002;105(1):44–8.
32. Sbracia M, Baldi M, Cao D, Sandrelli A, Chiandetti A, Poverini R, et al. Preferential location of sex chromosomes, their aneuploidy in human sperm, and their role in determining sex chromosome aneuploidy in embryos after ICSI. Hum Reprod. 2002;17(2):320–4.

Figures

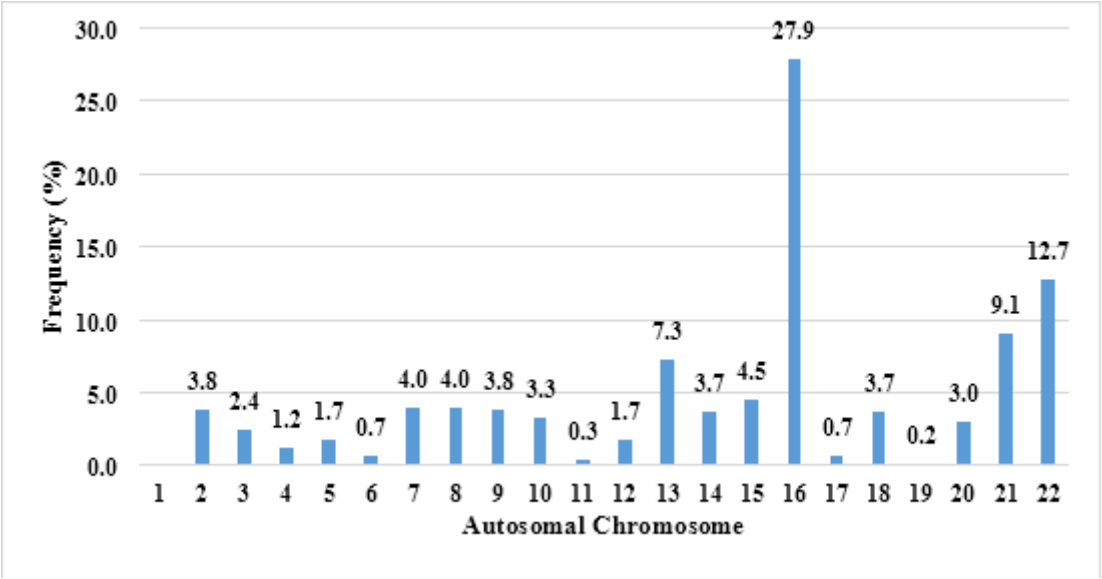

Figure 1

Distribution and frequency of autosomal chromosome involved in trisomy. All chromosomes except chromosome 1 were involved chromosomal trisomies, with trisomy 16 as the most common finding, followed by trisomy 22 and trisomy 21.