The parental origin of chromosome aneuploidies

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INTRODUCTION

Aneuploidy is the most common chromosome abnormality in humans and is the leading genetic cause of miscarriage and congenital birth defects. It is estimated that approximately 5% of all clinically recognized pregnancies are trisomic or monosomic. Maternal age, abberent recombination and the occurrence of a previous trisomy are the only three factors that are incontrovertibly linked to human aneuploidy. The determination of the origin of the chromosome aneuploidy is of importance in understanding the underlying molecular basis of non-disjunction and for the development of therapies to reduce or eliminate it.

AIM OF THE STUDY

The aim of this study was to determine the parental origin of chromosomal aneuploidies in patients from the Republic of Macedonia.

MATERIALS AND METHODS

Parental origin was studied in 38 chromosomal aneuploidies detected in 33 prenatal cases and 5 spontaneously aborted fetuses.

The methodology included quantitative fluorescent polymerase chain reaction (QF-PCR) using 10 small tandem repeat (STR) markers on chromosome 21, six markers on chromosome 18, six markers on chromosome 13 and seven markers on chromosome X (Figure 1).

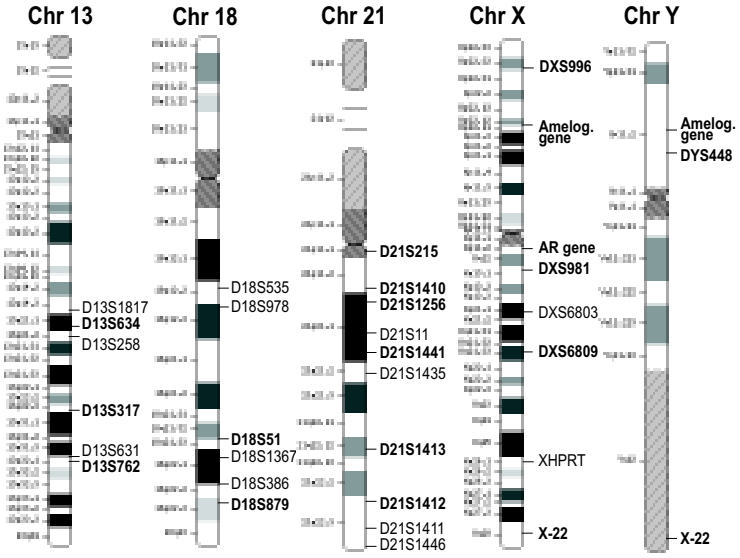

Figure 1. Chromosome location of the STR markers used for the detection of chromosome 13, 18, 21, X and Y aneuploidies.

RESULTS

In this study we determined the parental origin of 38 different chromosome aneuploidies detected in prenatal cases (n=33) and in material from spontaneous abortions (n=5). Sixteen of them were trisomies 21, eight trisomies 18 (one partial), three trisomies 13, five XO, three XXY syndromes and three triploidies. The parental origin of the chromosomal aneuploidies was determined by comparison of the STR alleles in the fetuses and their parents. Representative electrophoreograms from a fetuses with trisomy 21 and 18 and their parents are presented in Figure 2 and Figure 3, respectively.

The origin was maternal in all complete chromosome 13, 18 and 21 trisomies and paternal in the partial trisomy 18 in the 3 XXY cases, and in the majority of XO cases and triploidies (Figure 4).

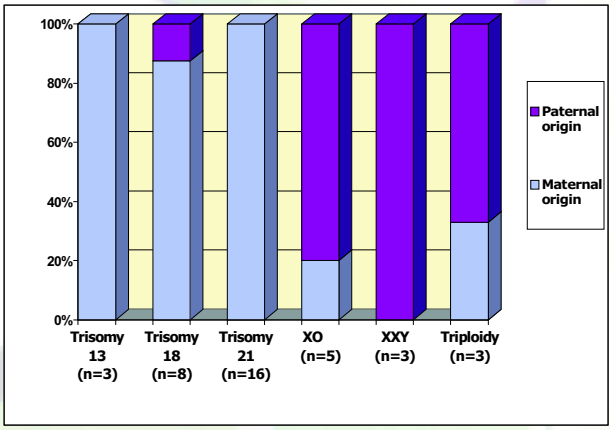

Figure 4. Parental origin of chromosomal aneuploidies

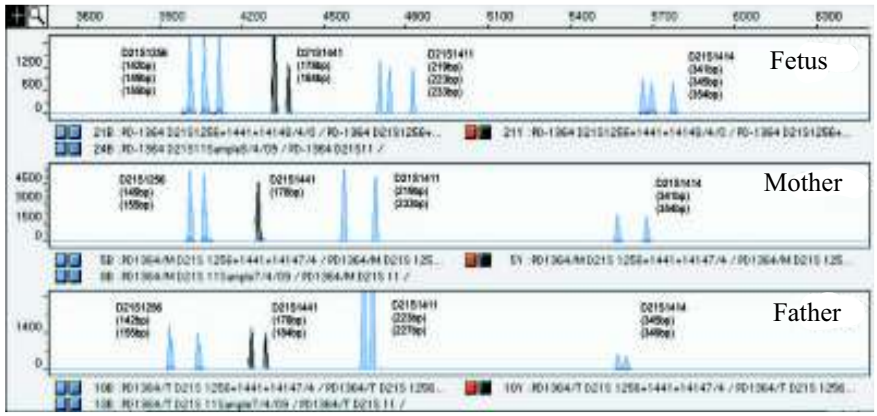

Figure 2. Electrophoreogram of the QF-PCR analysis from a fetus with trisomy 21. STR markers D21S1256, D21S1411 and D21S1414 showed triallelic pattern with a 1:1:1 ratio, while STR marker D21S1441 showed diallelic pattern with a 2:1 ratio. The comparison of STR alleles (given in base pairs) of the fetus, his father and mother revealed maternal meiotic I error of extra chromosome 21.

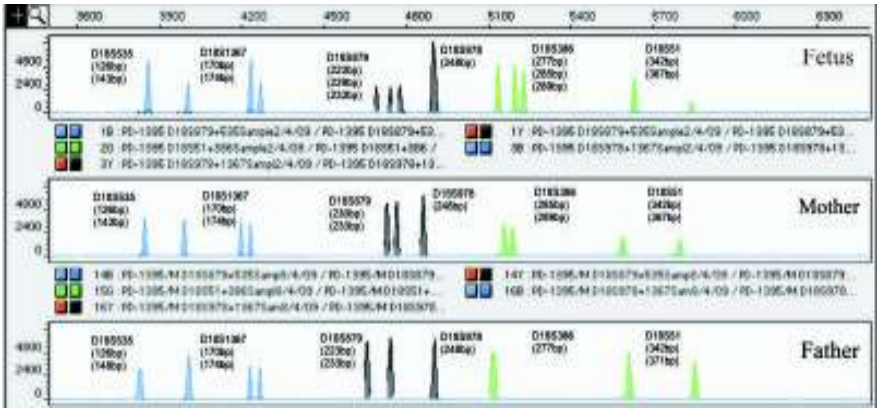

Figure 3. Electrophoreogram of three multiplex QF-PCR analysis from a fetus with trisomy 18. STR markers D18S879 and D18S386 showed triallelic pattern with a 1:1:1 ratio. Markers D18S535, D18S1367 and D18S51 showed diallelic patern with a 2:1 ratio, while D18S978 was uninformative showing only one peak. The comparison of STR alleles (given in base pairs) of the patient, his father and mother revealed maternal meiotic I error of extra chromosome 18.

ACKNOWLEDGMENT

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