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Case Report

Prenatal Diagnosis of a Low-Level Mosaic Small Supernumerary Marker Chromosome (sSMC): Early Postnatal Clinical Follow-Up

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Abstract

Small supernumerary marker chromosomes (sSMCs) are rare chromosomal abnormalities with diverse outcomes and variable effects that can be detected prenatally. The clinical significance of low-level mosaic sSMCs is often uncertain, and postnatal follow-up is essential to assess phenotypic outcomes. A fetus in whom a low-level mosaic sSMC (8%) was detected during prenatal testing is reported. The sSMC was found in 12 out of 150 metaphases examined by conventional karyotype, followed by molecular cytogenetic analyses (chromosomal microarray analysis (CMA) and fluorescence *in situ* hybridization (FISH)). Detailed ultrasound examination during the whole pregnancy revealed no structural abnormalities or other fetal complications and the child was born at term. Postnatal clinical investigation was conducted to evaluate the phenotypic impact of the sSMC and demonstrated normal early growth and neurodevelopment during the first nine months of life. Prenatal testing revealed a *de novo* sSMC in a low-level mosaic state. Evaluation of the sSMC revealed that the origin is in the pericentromeric region of chromosome 8, consisting

predominantly of heterochromatic but also of euchromatic material. Integrating prenatal detection, molecular characterization, and postnatal clinical evaluation is crucial for managing cases with low-level prenatal mosaic sSMCs. Comprehensive follow-up is essential for better prognostic counseling and management in affected children.

Keywords
Prenatal diagnosis; low-level mosaicism; small supernumerary marker chromosome (sSMC); chromosomal microarray analysis (CMA); fluorescence *in situ* hybridization (FISH); genetic counseling

1. Introduction

Small supernumerary marker chromosomes (sSMCs) are structurally abnormal chromosomes that cannot be identified unambiguously by conventional cytogenetic analysis alone, usually due to their small size and complex structure [1]. They are characterized as additional centric chromosome fragments, equal to or smaller than chromosome 20 in size on the same metaphase spread [2]. Around 3.3 million humans in the current global population are sSMC carriers, and sSMCs can originate from any human chromosome [3]. sSMCs are found in 0.072-0.075% of prenatal cases and 0.044% of live births, although the rate is increased to 0.288% in intellectually disabled patients and to 0.125% among people with infertility issues [4-6]. Defining the phenotype-genotype correlation of sSMCs remains a challenge due to their complex origins and genetic materials. The phenotype of sSMCs is variable (mental and growth retardation, craniofacial and urogenital abnormalities, and cardiac anomalies). It depends on their size, genetic content, and degree of mosaicism, while the presence of uniparental disomy can also influence the associated phenotypes [2, 6-8]. sSMCs composed predominantly of heterochromatic material are often associated with normal development, while those containing euchromatic, gene-rich regions may lead to congenital anomalies or developmental delay. Remarkably, only 30% of sSMC carriers manifest clinical symptoms [4, 9]. The application of modern prenatal diagnostic techniques such as chorionic villus sampling (CVS), amniocentesis (AFT), and molecular cytogenetic methods, including fluorescence *in situ* hybridization (FISH), chromosomal microarray analysis (CMA), and next-generation sequencing (NGS), has improved the characterization of sSMCs. Markedly, a combination of CMA and FISH or NGS and FISH is often required to determine the chromosomal origin of an sSMC, identify the genes involved, and predict the potential phenotype [10, 11]. Mosaicism adds a layer of uncertainty: low-level mosaic sSMCs detected in prenatal CVS samples may reflect true fetal mosaicism, confined placental mosaicism, or technical/biological sampling variability, and the fraction of abnormal cells in amniotic fluid or CVS often does not predict tissue distribution after birth. Additionally, the tissue distribution of the abnormal cell line (fetal vs. placental, organ-specific), and the genetic content of the sSMC (heterochromatic vs. euchromatic, gene-containing segments) are very important for predicting the phenotypic outcome [12, 13]. Low-level mosaicism (commonly described in the literature as <10-20% of cells in the tested sample) is often associated with favorable outcomes, particularly when the marker is predominantly heterochromatin; however, exceptions exist, especially when gene-rich regions are involved. Prior studies of feto-placental mosaicism further

highlight the complexity of genotype-phenotype correlations in prenatal sSMCs and the limitations of predicting clinical outcome solely from mosaicism level [12-14]. This diagnostic uncertainty complicates both prognostic assessment and genetic counseling, as the phenotypic outcome cannot be accurately predicted based solely on the cytogenetic finding [15]. Given this heterogeneity, comprehensive cytogenetic and molecular characterization together with systematic postnatal clinical follow-up are essential to refine prognosis and provide informed genetic counseling [16, 17].

Here, we present a fetus with a low-level mosaic sSMC detected and investigated during prenatal testing. Postnatal clinical follow-up was performed in the newborn boy to assess the persistence and phenotypic consequences of the abnormality. This case highlights the variability in clinical outcomes associated with low-level mosaic sSMCs and underscores the importance of integrated prenatal and postnatal follow-up.

2. Case Report/Case Presentation

2.1 Clinical Report

A 39-year-old G2P1 woman was referred for first-trimester screening at 14 weeks of gestation. Her previous (first) child, a healthy male, had an unremarkable perinatal and developmental history, with no reported genetic or congenital abnormalities. In the present pregnancy, nuchal translucency was measured as 2 mm, and the crown-rump length (CRL) was 81 mm, consistent with gestational age. The biochemical profile revealed β-hCG: 2.426 MoM and PAPP-A: 0.576 MoM, resulting in a high-risk estimate for trisomy 21 (1:82). No structural abnormalities or soft markers were detected on the initial ultrasound. The biochemical profile combined with increased maternal age led to the amniocentesis option, which was performed at 19 weeks of gestation.

The patient underwent serial detailed ultrasound examinations at 20, 24, and 34 weeks. The fetal anatomy survey showed normal brain morphology, normal cardiac structure and function, and unremarkable development of all other organ systems. Biometric measurements (Biparietal Diameter (BPD), Head Circumference (HC), Abdominal Circumference (AC), Femur Length (FL), and Estimated Fetal Weight (EFW)) were appropriate for gestational age, ranging from the 25th to the 60^{th} percentile. Amniotic fluid volume and Doppler velocimetry indices (umbilical artery, middle cerebral artery, uterine arteries) were also within normal limits.

The antenatal course was uneventful, with no evidence of fetal growth restriction, preeclampsia, or gestational complications. At 39 + 1 weeks, the patient delivered a male neonate spontaneously, weighing 3600 g, with length 51 cm and head circumference 34.5 cm. Apgar scores were 9 and 10 at 1 and 5 minutes, respectively. Postnatal clinical examination revealed no dysmorphic features, normal muscle tone, and no congenital malformations. Routine neonatal metabolic and hearing screening were normal. The newborn was discharged on the third day of life in good general condition.

Subsequent pediatric follow-up at 2, 6, and 9 months confirmed normal growth parameters (weight and height between the 50^{th}-75^{th} percentiles) and age-appropriate neurodevelopmental and language milestones. At the most recent evaluation (9 months of age), the child demonstrated age-appropriate early growth and neurodevelopment, with no clinical abnormalities or phenotypic features suggestive of a syndromic disorder. Continued clinical follow-up has been recommended, as later-onset neurodevelopmental manifestations cannot yet be excluded. All prenatal and postnatal findings are summarized and presented in Table 1.

Table 1 Summary of prenatal and postnatal findings.

Category	Findings
Maternal/Family Background	39-year-old G2P1 mother; previous child healthy; no family history of congenital or genetic disorders.
Indication for Testing	High-risk first-trimester screening for trisomy 21 (risk 1:82); β-hCG: 2.426 MoM, PAPP-A: 0.576 MoM.
Prenatal Ultrasound	NT: 2 mm at 14 weeks; detailed anomaly scans at 20, 24, 34 weeks all normal; normal fetal anatomy and growth (25^{th}-60^{th} percentiles); normal Doppler indices.
Amniocentesis	Performed at 19 weeks of gestation.
Delivery	Spontaneous vaginal delivery at 39 + 1 weeks; male infant.
Birth Parameters	Weight 3600 g; length 51 cm; head circumference 34.5 cm; Apgar scores 9 and 10.
Postnatal Exam	No dysmorphic features; no congenital anomalies; normal muscle tone. Normal neonatal screenings.
Follow-Up	Normal early growth (50^{th}-75^{th} percentiles) and age-appropriate neurodevelopment at 2, 6, and 9 months; no clinical abnormalities identified.

NT, nuchal translucency; β-hCG, beta-human chorionic gonadotropin; PAPP-A, pregnancy-associated plasma protein A.

2.2 Cytogenetic and Molecular Studies (Karyotype, FISH, CMA)

A 39-year-old woman underwent amniocentesis at 19 weeks of gestation. Whole genomic DNA was extracted from the amniotic fluid using QIAGEN DNeasy Blood & Tissue Kit according to manufacturer's instructions. The extracted DNA was used for rapid aneuploidy testing (QF-PCR) and CMA analysis. QF-PCR was initially carried out to exclude common aneuploidies (chromosomes 13, 18, 21, X, and Y), showing a normal disomic pattern. CMA analysis was performed using the Affymetrix Cytogenetics Whole-Genome CytoScan 750K array platform. The results were analyzed using the Chromosome Analysis Suite Software (ChAS ver3.1, Affymetrix, Thermo Fisher Scientific, Waltham, MA, USA) according to the human genome assembly GRCh37:Feb.2009 hg19. The analysis did not reveal any copy number imbalances of clinical significance.

Conventional karyotype analysis was also performed on cultured amniocytes from the fetus, showing the presence of an sSMC in 8% of metaphases analyzed (12/150), while the remaining cells showed a normal male chromosome content; the karyotype was according to ISCN (2024) mos 47,XY,+mar[12]/46,XY[138] (Figure 1).

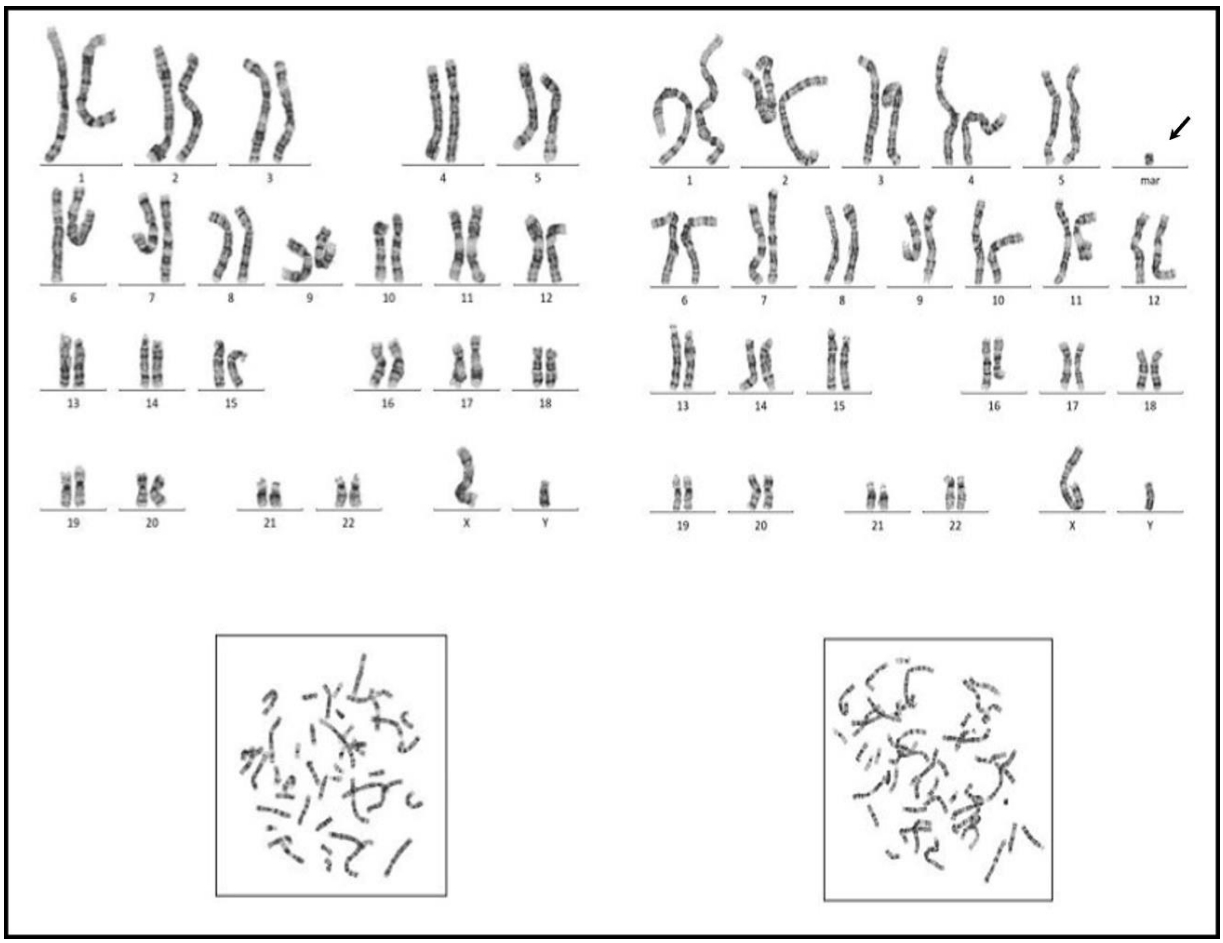

Figure 1 Conventional karyotype of the proband. Cultured amniocytes metaphase showing the presence of a small supernumerary marker chromosome (sSMC) in low-level mosaicism (12/150 metaphases analyzed). The sSMC is indicated by an arrow.

To further characterize the chromosomal origin of the marker chromosome, FISH analysis was performed using centromere-specific and locus-specific probes for chromosome 8 (i.e., D8Z2, RP11-503E24, RP13-116A4). The FISH pattern indicated that the sSMC originated from chromosome 8, involving pericentromeric regions (ish der(8)(:p12→q11.1:)(RP11-,503E24+,D8Z2+,RP13-,116A4-)) and consisting predominantly of heterochromatic material with only minimal euchromatic involvement. The BAC probe RP11-503E24 maps to chromosome 8p11.21 (hg19: 42,384,567-42,555,145) and showed a positive signal on the marker chromosome, whereas RP13-116A4 maps to chromosome 8q11.21 (hg19: 48,482,616-48,530,952) and did not hybridize to the marker chromosome. These findings indicate that the breakpoint in 8p is distal from RP11-503E24-most likely in 8p11.2 and the break in 8q is located between centromere 8 and RP13-116A4 (Figure 2). Banding cytogenetic analysis on peripheral blood of both parents was performed. A total of 110 metaphases were analyzed for each parent, revealing normal karyotypes (46,XY and 46,XX, respectively), with no evidence of a mosaic marker chromosome (Figure 3). Therefore, the sSMC was considered the most likely *de novo* finding, although parental germline mosaicism cannot be completely excluded. The final fetal karyotype was designated as mos 47,XY,+mar[12]/46,XY[138]dn.ish der(8)(:p12→q11.1:)(RP11-503E24+,D8Z2+,RP13-116A4-).

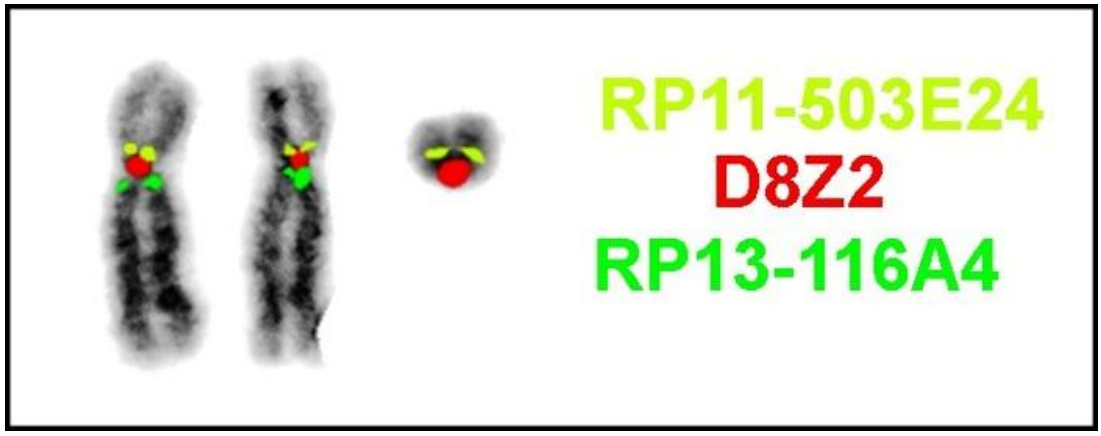

Figure 2 FISH on the sSMC. Fluorescence *in situ* hybridization (FISH) using chromosome 8-specific probes. The centromeric probe D8Z2 (red), the BAC probe RP11-503E24 (yellow-green), and the BAC probe RP13-116A4 (green) were used. The marker chromosome showed positive hybridization signals for D8Z2 and RP11-503E24, whereas no signal was observed for RP13-116A4, indicating that the sSMC originated from the pericentromeric region of chromosome 8.

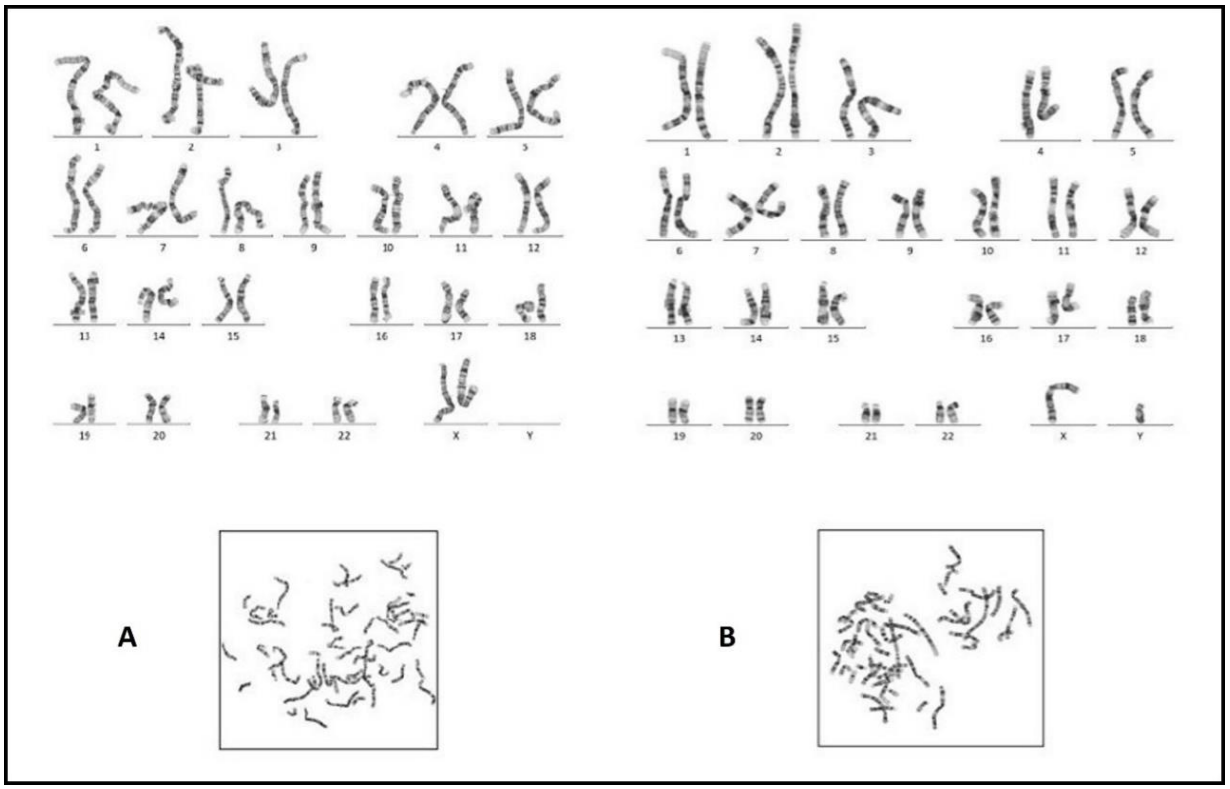

Figure 3 Conventional karyotypes of the parents of the proband. Peripheral blood conventional karyotypes of both parents show normal karyotypes: A. 46,XX (mother), and B. 46,XY (father) without any structural chromosomal abnormalities or any marker chromosomes, indicating that the sSMC in the proband was considered most likely *de novo*, although parental germline mosaicism cannot be completely excluded.

The combination of cytogenetic and molecular analyses confirmed the presence of a low-level mosaic sSMC derived from the predominantly heterochromatic chromosome 8 with only minimal

euchromatic involvement. The BAC RP11-503E24 is mapped to chr8:42,384,567-42,555,145 (hg19). According to [18], the triplo-sensitive region in the short arm of chromosome 8 starts between 40.23 and 40.75 Mb. Thus, the sSMC(8) observed here does not appear to include dosage-dependent genes, which could lead to phenotypic abnormalities.

2.3 Statement of Ethics

This study was performed in accordance with the Declaration of Helsinki. Ethical approval was not obtained for this human study because the individual's mother provided consent for publication of their data. All parents, guardians, or next of kin provided written informed consent for the minors to participate in this study. Written informed consent was obtained from the legal guardian of the individual(s) for publication of the details of their medical case and any accompanying images.

3. Discussion

The mechanisms leading to the formation of small supernumerary marker chromosomes (sSMCs) are heterogeneous and remain incompletely understood. Several mechanisms have been proposed, including meiotic nondisjunction, trisomy rescue, postzygotic chromosome mis-segregation, and, in selected complex cases, chromothripsis [19]. However, the underlying mechanism cannot be determined in the present case.

Until today, >7,500 cases of sSMCs have been reported in the literature [18]. In general, sSMCs represent a very heterogeneous group of structural chromosomal abnormalities with highly variable clinical consequences. Common clinical features that are recorded in sSMC(8) cases include developmental delay, mental retardation, intellectual disability, severe hypotonia, attention deficit hyperactivity disorder (ADHD), skeletal abnormalities and atypical facial appearance, in different severities. Multiple factors such as chromosomal origin, gene content, level of mosaicism, and tissue distribution of the abnormal cell line can affect the subsequent phenotype [4, 12, 20]. According to [18], the triplo-sensitive region in the short arm of chromosome 8 starts between 40.23 and 40.75 Mb. Thus, the sSMC(8) observed here does not appear to include dosage-dependent genes, which could lead to phenotypic abnormalities.

Only a few cases of low-level mosaic sSMCs have been reported prenatally, and their postnatal outcomes range from normal development to mild or more severe manifestations. The overall risk of abnormal phenotypic outcomes in prenatal cases with sSMC presence is estimated at approximately 13% [3].

Prognostic evaluation and following genetic counseling are further complicated by low-level mosaicism, as the percentage of abnormal cells detected in amniocytes or CVS does not necessarily reflect the fetal tissue composition due to biological and sampling variability. Several studies have indicated that mosaic levels below 10-20% often have limited phenotypic expression, particularly when confined to extraembryonic tissues. The same studies show that low-level mosaicism is more often associated with favorable outcomes, particularly when the marker is largely heterochromatic [5, 13]. Nevertheless, exceptions in the literature, especially when the sSMC contains euchromatic DNA with known dosage-sensitive genes, emphasize the need for individualized interpretation and thorough genetic counseling [15]. Therefore, both prenatal detection and postnatal confirmation are essential to accurately assess the clinical relevance. Additionally, although uniparental disomy (UPD) should be considered in selected cases with apparently *de novo* sSMCs, chromosome 8 is not

associated with a well-established clinically relevant imprinting disorder. Therefore, additional UPD testing was not considered necessary in the present case.

Chromosome 8-derived sSMCs constitute a small subset of all reported cases (approximately 70 cases in the existing literature) and show diverse clinical presentations depending on the specific pericentromeric segment involved. For example, the involvement of 8q12.2 critical gene has been associated with severe phenotypic characteristics among the reported cases [21]. The pericentromeric regions of chromosome 8 consist mostly of heterochromatin, with limited euchromatin in 8p11-p12 and 8q11.1. Around 18 reported cases involving 8p11.2/q11.21 exist in the literature, with the severity of the clinical outcome relying solely on the precise size and gene content of the duplicated region [2, 9, 22-24].

In the present case, the sSMC was identified through conventional karyotype in 8% of analyzed metaphases (12 out of 150), consistent with a low-level mosaic abnormal cell line. FISH established its chromosomal origin and demonstrated that it arose from the pericentromeric region of chromosome 8, which was mostly heterochromatin and involved only minimal euchromatin. The BAC probe RP11-503E24 (8p11.21; hg19: 42,384,567-42,555,145) hybridized to the marker chromosome, whereas RP13-116A4 (8q11.21; hg19: 48,482,616-48,530,952) did not, indicating that the breakpoint lies between these two loci. Accordingly, based on the FISH mapping results, the retained euchromatic segment is not expected to encompass any currently established dosage-sensitive genes. As expected, CMA did not identify the marker chromosome, most likely because the abnormal cell line (8%) was below the detection threshold of the platform and because pericentromeric regions are suboptimally represented in array-based analyses. This case highlights the complementary role of conventional cytogenetics, FISH, and CMA in the investigation of prenatally detected sSMCs. While CMA is highly effective at detecting clinically relevant copy number imbalances, it may miss low-level mosaic marker chromosomes, making conventional karyotyping and FISH indispensable for their characterization. The subsequent postnatal normal phenotype is in agreement with this genomic low-mosaic result, in combination with the absence of ultrasound abnormalities during pregnancy. Additionally, the newborn did not show any congenital anomalies or dysmorphic features, and early developmental milestones remained age-appropriate during the first nine months of life, supporting the existing literature on the benign outcome of low-level mosaic pericentromeric sSMCs with limited euchromatic content [13]. Nevertheless, continued follow-up is required, as neurodevelopmental disorders associated with chromosome 8-derived sSMCs may become apparent later in childhood.

4. Conclusions

This case illustrates key challenges in genetic counseling for families when low-level mosaic sSMCs are identified prenatally. Although the combined use of conventional karyotyping, FISH and CMA significantly improves the characterization of prenatally detected sSMCs, each technique has specific limitations and they cannot fully predict the degree of postnatal tissue mosaicism or developmental outcome. Therefore, integrated prenatal and postnatal follow-up remains essential. Systematic neonatal examination and ongoing pediatric follow-up have so far shown no clinical consequences, providing reassurance to the family and contributing valuable evidence to the limited literature on chromosome 8-derived mosaic sSMCs. Continued long-term follow-up remains important to assess later neurodevelopmental outcomes.

This case report is subject to several limitations, including the inherent inability to determine tissue-specific mosaicism postnatally and the lack of whole-genome sequencing-based breakpoint resolution, which may have further clarified the exact euchromatic content of the marker. Nonetheless, the concordance of cytogenetic findings, normal CMA results, and postnatal development strongly supports the benign nature of this specific chromosomal variant.

In conclusion, the combination of conventional karyotyping, FISH, and molecular techniques such as CMA improves the characterization of sSMCs and guides genetic counseling, especially in prenatally detected sSMCs. In prenatal settings, uncertainty regarding prognosis can cause significant parental anxiety; thus, detailed postnatal follow-up and multidisciplinary communication are critical. This report adds evidence to the scientific community supporting that low-level mosaic sSMCs derived from pericentromeric regions-particularly of chromosome 8-are often associated with a normal clinical outcome. The favorable clinical outcome emphasizes the importance of cautious interpretation of such findings and highlights the need for continued data collection to refine genotype-phenotype correlations.

Author Contributions

Conceptualization, E.L. and S.V.; writing-original draft preparation, M.B.; writing-review and editing, M.B., E.L., K.T., T.L., and S.V.; supervision, S.V. All authors have read and agreed to the published version of the manuscript.

Competing Interests

The authors have declared that no competing interests exist.

AI-Assisted Technologies Statement

Artificial intelligence (AI) tools were used solely for basic grammar correction and language refinement in the preparation of this manuscript. Specifically, OpenAI's ChatGPT was employed to improve the readability and linguistic clarity of the English text. All scientific content, data interpretation, and conclusions were developed independently by the author. The authors have thoroughly reviewed and edited the AI-assisted text to ensure its accuracy and accept full responsibility for the content of the manuscript.

References

1. Liehr T, Claussen U, Starke H. Small supernumerary marker chromosomes (sSMC) in humans. Cytogenet Genome Res. 2004; 107: 55-67.
2. Liehr T, Klein E, Mrasek K, Kosyakova N, Guilherme RS, Aust N, et al. Clinical impact of somatic mosaicism in cases with small supernumerary marker chromosomes. Cytogenet Genome Res. 2012; 139: 158-163.
3. Warburton D. *De novo* balanced chromosome rearrangements and extra marker chromosomes identified at prenatal diagnosis: Clinical significance and distribution of breakpoints. Am J Hum Genet. 1991; 49: 995-1013.

4. Liehr T, Weise A. Frequency of small supernumerary marker chromosomes in prenatal, newborn, developmentally retarded and infertility diagnostics. Int J Mol Med. 2007; 19: 719-731.
5. Malvestiti F, De Toffol S, Grimi B, Chinetti S, Marcato L, Agrati C, et al. *De novo* small supernumerary marker chromosomes detected on 143 000 consecutive prenatal diagnoses: Chromosomal distribution, frequencies, and characterization combining molecular cytogenetics approaches. Prenat Diagn. 2014; 34: 460-468.
6. Jafari-Ghahfarokhi H, Moradi-Chaleshtori M, Liehr T, Hashemzadeh-Chaleshtori M, Teimori H, Ghasemi-Dehkordi P. Small supernumerary marker chromosomes and their correlation with specific syndromes. Adv Biomed Res. 2015; 4: 140.
7. Woo HY, Cho HJ, Kong SY, Kim HJ, Jeon HB, Kim EC, et al. Marker chromosomes in Korean patients: Incidence, identification and diagnostic approach. J Korean Med Sci. 2003; 18: 773-778.
8. Marchina E, Forti M, Tonelli M, Maccarini S, Malvestiti F, Piantoni C, et al. Molecular characterization of a complex small supernumerary marker chromosome derived from chromosome 18p: An addition to the literature. Mol Cytogenet. 2021; 14: 6.
9. Starke H, Nietzel A, Weise A, Heller A, Mrasek K, Belitz B, et al. Small supernumerary marker chromosomes (SMCs): Genotype-phenotype correlation and classification. Hum Genet. 2003; 114: 51-67.
10. Sun M, Zhang H, Li G, Guy CJ, Wang X, Lu X, et al. Molecular characterization of 20 small supernumerary marker chromosome cases using array comparative genomic hybridization and fluorescence *in situ* hybridization. Sci Rep. 2017; 7: 10395.
11. Xue H, Huang H, Wang Y, An G, Zhang M, Xu L, et al. Molecular cytogenetic identification of small supernumerary marker chromosomes using chromosome microarray analysis. Mol Cytogenet. 2019; 12: 13.
12. Grati FR. Chromosomal mosaicism in human feto-placental development: Implications for prenatal diagnosis. J Clin Med. 2014; 3: 809-837.
13. Navarrete-Meneses MP, Ochoa-Mellado I, Gutiérrez-Álvarez R, Martínez-Anaya D, Juárez-Figueroa U, Durán-McKinster C, et al. Cytogenomic characterization of small supernumerary marker chromosomes in patients with pigmentary mosaicism. Front Genet. 2024; 15: 1356786.
14. Chen CP, Chen M, Su YN, Huang JP, Chern SR, Wu PS, et al. Mosaic small supernumerary marker chromosome 1 at amniocentesis: Prenatal diagnosis, molecular genetic analysis and literature review. Gene. 2013; 529: 169-175.
15. Militaru MS, Babliuc IM, Bloaje-Florică VL, Danci VA, Filip-Deac I, Kutasi E, et al. The Impact of chromosomal mosaicisms on prenatal diagnosis and genetic counseling-a narrative review. J Pers Med. 2024; 14: 774.
16. Liehr T, Ewers E, Kosyakova N, Klaschka V, Rietz F, Wagner R, et al. Handling small supernumerary marker chromosomes in prenatal diagnostics. Expert Rev Mol Diagn. 2009; 9: 317-324.
17. Joksic I, Toljic M, Milacic I, Stankovic A, Karadzov Orlic N, Mikovic Z. Small supernumerary marker chromosomes in prenatal diagnosis-molecular characterization and clinical outcomes. Front Genet. 2024; 14: 1326985.
18. Liehr T. Small supernumerary marker chromosomes [Internet]. Jena, Germany: Institute of Human Genetics; 2026. Available from: https://cs-tl.de/DB/CA/sSMC/0-Start.html.

19. Pellestor F. Chromothripsis: How does such a catastrophic event impact human reproduction? Hum Reprod. 2014; 29: 388-393.
20. Dharmadhikari AV, Pereira EM, Andrews CC, Macera M, Harkavy N, Wapner R, et al. Case report: Prenatal identification of a *de novo* mosaic neocentric marker resulting in 13q31.1→qter tetrasomy in a mildly affected girl. Front Genet. 2022; 13: 906077.
21. Amouroux C, Vincent M, Blanchet P, Puechberty J, Schneider A, Chaze AM, et al. Duplication 8q12: Confirmation of a novel recognizable phenotype with Duane retraction syndrome and developmental delay. Eur J Hum Genet. 2012; 20: 580-583.
22. Gole LA, Biswas A. Characterization of a small supernumerary marker chromosome as r(8) at prenatal diagnosis by MFISH. Prenat Diagn. 2005; 25: 73-78.
23. Shao HY, Miao ZY, Liu XY, Hou XF, Wu H. Molecular cytogenetic characterization of mosaicism for a small supernumerary marker chromosome derived from chromosome 8 associated with congenital hypoplasia of the tongue and review of the literature. Taiwan J Obstet Gynecol. 2020; 59: 323-326.
24. Rothenmund H, Chudley AE, Dawson AJ. Familial transmission of a small supernumerary marker chromosome 8 identified by FISH: An update. Am J Med Genet. 1997; 72: 339-342.