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Trends in Genetic Testing of Products of Conception Following Pregnancy Loss: A Four- Year Retrospective Study

Katarzyna Klimaszyk
Poznan University of Medical Sciences
Katarzyna Ziółkowska
Poznan University of Medical Sciences
Małgorzata Kędzia
mkedzia@ump.edu.pl

Poznan University of Medical Sciences

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Abstract

Background

Chromosomal abnormalities are the leading cause of first-trimester pregnancy loss. Molecular diagnostics, especially chromosomal microarray analysis, have broadened the abnormalities detectable in products of conception, and genetic testing is now increasingly offered after a single miscarriage rather than only after recurrent loss.

Objective

To assess practice changes in genetic testing of products of conception at a tertiary referral gynecology& obstetric center from 1 January 2023 to 31 July 2026, focusing on the adoption of array comparative genomic hybridisation (aCGH), and to identify clinical factors linked to abnormal results.

Materials and methods

This retrospective study analysed 400 pregnancy-loss. We examined trends in testing uptake, diagnostic methods, chorionic villi availability, and genetic outcomes, and assessed associations between abnormal results and maternal age, gestational age, gravidity, and miscarriage number using multivariable logistic regression.

Results

Testing uptake rose from 10.7% (2023) to 21.9% (2024), 19.7% (2025), and 18.4% (Jan–Jul 2026), with aCGH use increasing as quantitative fluorescent PCR (QF-PCR) declined. Testing followed a first miscarriage in 54.3% of cases. Of 311 diagnostic results, 161 (51.8%) were abnormal, mainly autosomal aneuploidies, triploidy, and monosomy X. Chorionic villi were unavailable in 83 cases (20.8%). Earlier gestational age was independently associated with an abnormal result (OR 0.90/week, 95% CI 0.82–0.98; P = 0.017).

Conclusions

Genetic testing shifted toward aCGH and increasingly followed first miscarriages. High abnormality rates support testing's clinical value, while frequent tissue unavailability highlights the need for improved counselling and sample handling.

Introduction

Pregnancy loss is the most common adverse outcome of human reproduction and affects approximately 10–20% of clinically recognised pregnancies. Most miscarriages occur during the first trimester. The risk of a subsequent loss is influenced by maternal age and the number of previous miscarriages, although the prognosis for a future live birth remains favourable for most of women (Quenby et al. 2021; Coomarasamy et al. 2021; Kolte et al. 2021).

Chromosomal abnormalities are the leading cause of first-trimester miscarriage and account for approximately half of cases. Autosomal aneuploidies, monosomy X, and triploidy are the abnormalities most frequently identified in products of conception(Sugiura-Ogasawara et al. 2012; Levy et al. 2014; Sahoo et al. 2017; Finley et al. 2022; Arnadottir et al. 2025). Successful early pregnancy, however, depends not only on embryonic chromosomal integrity but also on the interaction between the embryo and the endometrium. Impaired maternal selection of embryos has therefore been proposed as an additional mechanism contributing to recurrent pregnancy loss(Brosens et al. 2022).

Genetic evaluation of products of conception has changed substantially. Conventional karyotyping is limited by the need for cell culture, culture failure, and maternal cell overgrowth. Molecular approaches, including quantitative fluorescent polymerase chain reaction (QF-PCR) and chromosomal microarray analysis, avoid some of these limitations. Array comparative genomic hybridisation (aCGH) enables genome-wide detection of chromosomal imbalances and submicroscopic copy-number variants, although it does not detect balanced rearrangements and has limited ability to identify some ploidy abnormalities(Levy et al. 2014; Sahoo et al. 2017; Dhillon et al. 2014; Schlaikjær Hartwig et al. 2023; Kolte et al. 2021).

Clinical practice has evolved in parallel with these technical developments. Genetic testing is increasingly considered not only after recurrent pregnancy loss but also after an individual miscarriage when the result may inform counselling and subsequent management. The 2026 American Society for Reproductive Medicine (ASRM) committee opinion recommends chromosome analysis of miscarriage tissue, when feasible, as a first step in the evaluation of recurrent pregnancy loss and supports array-based technology because of its technical advantages. ESHRE and RCOG also emphasise genetic evaluation within an individualised clinical approach(Regan et al. 2023; Bender Atik et al. 2022; Gracia et al. 2026).

Nevertheless, relatively few studies have assessed how technological change has translated into routine clinical practice, including changes in testing uptake, patient characteristics, diagnostic success, and the spectrum of detected abnormalities. To our knowledge, this is the first single-centre Polish study to evaluate these elements during the implementation of chromosomal microarray testing.

The aim of this study was to evaluate changes in clinical practice relating to genetic testing of products of conception between 2023 and 2026 at a tertiary referral centre, with particular emphasis on testing uptake, changes in diagnostic methods, availability of diagnostic tissue, and the clinical and genetic characteristics of the study population.

Materials and methods

Study design and population

This retrospective observational study included patients hospitalised for pregnancy loss at the tertiary referral Gynaecology & Obstetrics center between 1 January 2023 and 31 July 2026. All episodes in which products of conception were submitted for genetic testing were assessed.

Clinical information was obtained from medical records and genetic laboratory registers. Pregnancy losses occurring beyond 22 weeks of gestation, duplicate records relating to the same diagnostic episode, and records with data insufficient for the relevant analysis were excluded. Five losses beyond 22 weeks were excluded, leaving 400 pregnancy-loss episodes for the primary analysis.

Clinical variables

The variables assessed were maternal age at pregnancy loss, gestational age, gravidity, miscarriage number, diagnostic method, and genetic test result. Maternal age was calculated from the year of birth encoded in the Polish national identification number (PESEL) and the calendar year of pregnancy loss. Maternal age was determined for all 400 patients.

Genetic testing

Chorionic villi isolated from products of conception were used for genetic testing. When fetal tissue was not identified in the fresh specimen and DNA isolation was therefore not possible, an attempt was made to retrieve suitable tissue from formalin-fixed paraffin-embedded material.

Two diagnostic approaches were used during the study period. QF-PCR targeted common aneuploidies involving chromosomes 13, 15, 16, 18, 21, 22, X, and Y. aCGH was used to evaluate genome-wide copy-number changes, including chromosomal imbalances and submicroscopic deletions and duplications. After implementation of microarray testing, QF-PCR was used as a preliminary test to identify common aneuploidies, assess ploidy abnormalities—particularly triploidy—and evaluate possible maternal cell contamination before aCGH. In a subset of cases, both methods were recorded as part of the diagnostic pathway.

Genetic results were classified as normal, abnormal, unavailable because chorionic villi were not obtained, or non-informative. Abnormal findings were further classified as autosomal aneuploidies, sex-chromosome aneuploidies, triploidy, structural abnormalities/copy-number variants, or other abnormalities.

Statistical analysis

Categorical variables are presented as counts and percentages. Quantitative variables are presented as medians with interquartile ranges (IQRs) and ranges; means and standard deviations are additionally reported where available.

Categorical variables were compared using Pearson's chi-square test or Fisher's exact test, as appropriate. Temporal trends were evaluated using the Cochran–Armitage trend test. Continuous variables were compared using the Mann–Whitney U test, and gestational-age distributions across four result groups were compared using the Kruskal–Wallis test.

A multivariable logistic regression model was fitted among cases with a diagnostic result and complete covariate data. The dependent variable was an abnormal versus normal genetic result. Maternal age, gestational age, gravidity, and miscarriage number were included as covariates. Results are reported as odds ratios (ORs) with 95% confidence intervals (CIs). A two-sided P value < 0.05 was considered statistically significant.

Ethical considerations

The study was based on retrospective analysis of anonymised clinical and laboratory data generated during routine diagnostic care. Data were analysed in aggregate without the possibility of identifying individual patients. According to the applicable institutional and national regulations for retrospective analyses of anonymised routine-care data, Bioethics Committee has confirmed that no formal ethical approval was not required.

Results

Study population

Between 1 January 2023 and 31 July 2026, products of conception from 405 pregnancy losses were submitted for genetic testing. After exclusion of five losses occurring beyond 22 weeks of gestation, 400 episodes were included.

The median gestational age was 9 weeks (IQR 8–11; range 1–22 weeks). The median maternal age was 33 years (IQR 30–38), and the mean age was 33.7 ± 4.8 years. Maternal age was determined for all 400 patients. The second pregnancy was the most frequent gravidity category (36.5%), followed by the first pregnancy (33.9%). Genetic testing was performed after a first miscarriage in 217 cases (54.3%) and after a third or subsequent miscarriage in 43 cases (10.7%) (Table 1).

Table 1
Characteristics of the study population

Characteristic	Value
Number of pregnancy-loss episodes	400
Maternal age, years, median (IQR)	33 (30–38)
Maternal age, mean ± SD	33.7 ± 4.8
Age range, years	20–49
Age groups, n (%)	
< 30 years	82 (20.5)
30–34 years	152 (38.0)
35–39 years	115 (28.8)
≥ 40 years	51 (12.8)
Gestational age, weeks, median (IQR)	9 (8–11)
Gravidity, median (IQR)	2 (1–3)
Miscarriage number, median (IQR)	1 (1–2)
First miscarriage, n (%)	217 (54.3)
Second miscarriage, n (%)	140 (35.0)
≥ 3 miscarriages, n (%)	43 (10.7)

Maternal age was determined for all 400 patients.

Uptake of genetic testing

The proportion of patients hospitalised for pregnancy loss whose tissue was submitted for genetic testing increased from 10.7% in 2023 to 21.9% in 2024, 19.7% in 2025, and 18.4% during the first seven months of 2026. The distribution differed significantly across years (χ^2=31.34, df = 3; P < 0.001), and the Cochran–Armitage test demonstrated an overall increasing trend (Z = 3.33; P < 0.001) (Table 2).

Table 2
Uptake of genetic testing of products of conception, 2023–2026

Year	Patients with pregnancy loss, n	Specimens submitted for genetic testing, n	Proportion (%)
2023	646	69	10.7
2024	617	135	21.9
2025	618	122	19.7
2026*	403	74	18.4

*Data for 2026 cover 1 January to 31 July.

Changes in diagnostic methods

QF-PCR predominated in 2023, whereas the use of aCGH increased progressively from 2024 onwards. The proportion recorded as aCGH alone increased from 27.5% in 2023 to 73.0% in 2026, while QF-PCR alone decreased from 72.5% to 27.0%. The distribution of diagnostic pathways differed significantly across years (χ^2=67.04, df = 6; P < 0.001). The trend was increasing for aCGH (Z = 5.55; P < 0.001) and decreasing for QF-PCR (Z = − 6.78; P < 0.001) (Table 3).

Table 3
Use of QF-PCR and aCGH, 2023–2026

Year	Tests, n	QF-PCR only, n (%)	aCGH used, n (%)
2023	69	50 (72.5)	19 (27.5)
2024	135	59 (43.7)	76 (56.3)
2025	122	42 (34.4)	80 (65.6)
2026*	74	20 (27.0)	54 (73.0)

*Data for 2026 cover 1 January to 31 July.

Availability of diagnostic tissue

Chorionic villi were not identified in the fresh specimen in 135 of 400 cases (33.8%). Diagnostic material was subsequently obtained from paraffin blocks in 52 cases (13.0% of the total cohort). Ultimately, no result was obtained because chorionic villi were unavailable in 83 cases (20.8%). This proportion did not differ significantly across years (χ^2=4.48, df = 3; P = 0.214) (Table 4).

Table 4
Failure to obtain chorionic villi, 2023–2026

Year	Tests, n	Chorionic villi absent at any stage, n (%)	Final absence of a result, n (%)	Result obtained after initial absence of villi, n (%)
2023	69	18 (26.1)	14 (20.3)	4 (5.8)
2024	135	58 (43.0)	32 (23.7)	26 (19.3)
2025	122	33 (27.0)	18 (14.8)	15 (12.3)
2026*	74	26 (35.1)	19 (25.7)	7 (9.5)
Total	400	135 (33.8)	83 (20.8)	52 (13.0)

A result obtained after initial absence of villi indicates testing performed on tissue retrieved from a paraffin block. *Data for 2026 cover 1 January to 31 July.

Genetic test results

A diagnostic result was obtained in 311 of 400 cases (77.8%). An abnormal result was identified in 161 cases (40.3% of the total cohort and 51.8% of diagnostic results), and a normal result in 150 (37.5% of the total cohort and 48.2% of diagnostic results). No result was obtained because chorionic villi were unavailable in 83 cases (20.8%), and six results (1.5%) were non-informative(Fig. 1). Among diagnostic results, the proportion of abnormal findings did not differ significantly across years (χ^2=2.22, df = 3; P = 0.528) (Table 5).

Table 5
Genetic test results by year

Year	Tests, n	Normal, n (%)	Abnormal, n (%)	No result, n (%)	Non-informative, n (%)	Abnormal among diagnostic results, n (%)
2023	69	24 (34.8)	27 (39.1)	14 (20.3)	4 (5.8)	27/51 (52.9)
2024	135	45 (33.3)	58 (43.0)	32 (23.7)	0 (0.0)	58/103 (56.3)
2025	122	55 (45.1)	47 (38.5)	18 (14.8)	2 (1.6)	47/102 (46.1)
2026*	74	26 (35.1)	29 (39.2)	19 (25.7)	0 (0.0)	29/55 (52.7)
Total	400	150 (37.5)	161 (40.3)	83 (20.8)	6 (1.5)	161/311 (51.8)

A diagnostic result was defined as a normal or abnormal result. *Data for 2026 cover 1 January to 31 July.

Clinical characteristics by diagnostic result

Among cases with a diagnostic result, maternal age, gravidity, and miscarriage number did not differ significantly between normal and abnormal result groups. Gestational age was lower in the abnormal-result group (median 9 weeks, IQR 8–10) than in the normal-result group (median 10 weeks, IQR 9–11; P = 0.012) (Table 6).

Table 6
Clinical characteristics according to genetic test result

Characteristic	Normal result (n = 150)	Abnormal result (n = 161)	P value
Maternal age, years, median (IQR)	33 (30.25–36)	34 (30–38)	0.187
Gestational age, weeks, median (IQR)	10 (9–11)	9 (8–10)	**0.012**
Gravidity, median (IQR)	2 (1–3)	2 (1–3)	0.739
Miscarriage number, median (IQR)	1 (1–2)	1 (1–2)	0.961

Comparisons were performed using the Mann–Whitney U test.

Spectrum of chromosomal abnormalities

A total of 161 abnormal results were identified. The most frequent individual findings were triploidy (n = 26), trisomy 21 (n = 16), trisomy 16 (n = 16), monosomy X (n = 14), trisomy 15 (n = 13), and trisomy 22 (n = 12). Structural abnormalities/copy-number variants accounted for 26 cases (Table 7).

Table 7
Types of chromosomal abnormalities

Abnormality	2023, n	2024, n	2025, n	2026*, n	Total, n
Triploidy	7	9	5	5	26
Trisomy 21	1	7	5	3	16
Trisomy 16	4	7	5	0	16
Monosomy X	2	5	5	2	14
Trisomy 15	0	6	4	3	13
Trisomy 22	3	4	5	0	12
Trisomy 18	1	2	1	1	5
Trisomy 13	0	3	0	1	4
Trisomy 4	0	1	3	0	4
Trisomy 14	0	1	0	2	3
Trisomy 20	2	0	0	1	3
Trisomy 10	0	0	2	1	3
Trisomy 9	0	0	1	1	2
Trisomy 2	0	2	0	0	2
Trisomy 5	1	0	0	0	1
Trisomy 3	0	0	1	0	1
Klinefelter syndrome (47,XXY)	1	0	0	0	1
Other sex-chromosome abnormalities	0	2	1	1	4
Other structural abnormalities/CNVs	4	5	9	8	26
Unclassified abnormal result	1	4	0	0	5
Total	**27**	**58**	**47**	**29**	**161**

*Data for 2026 cover 1 January to 31 July. CNV copy number variation

After grouping the abnormalities, autosomal aneuploidies accounted for 47.2% of abnormal results. Triploidy and structural abnormalities/CNVs each accounted for 16.1%, and sex-chromosome aneuploidies for 11.8% (Table 8).

Table 8
Classification of chromosomal abnormalities

Category	2023, n	2024, n	2025, n	2026*, n	Total, n (%)
Autosomal aneuploidies	12	31	22	11	76 (47.2)
Sex-chromosome aneuploidies	3	7	6	3	19 (11.8)
Triploidy	7	9	5	5	26 (16.1)
Structural abnormalities/CNVs	4	5	9	8	26 (16.1)
Other abnormalities	1	6	5	2	14 (8.7)
Total	**27**	**58**	**47**	**29**	**161 (100.0)**

Percentages were calculated using all 161 abnormal results as the denominator. *Data for 2026 cover 1 January to 31 July. Copy number variation (CNV)

Genetic result and miscarriage number

No significant association was observed between miscarriage number and the distribution of normal and abnormal diagnostic results (χ^2=2.26, df = 3; P = 0.521) (Table 9).

Table 9
Genetic test result according to miscarriage number

Miscarriage number	n	Normal, n (%)	Abnormal, n (%)	No result, n (%)	Non-informative, n (%)
1	213	78 (36.6)	87 (40.8)	43 (20.2)	5 (2.3)
2	137	53 (38.7)	53 (38.7)	30 (21.9)	1 (0.7)
3	30	12 (40.0)	11 (36.7)	7 (23.3)	0 (0.0)
≥ 4	12	3 (25.0)	8 (66.7)	1 (8.3)	0 (0.0)

This analysis included 392 cases with available miscarriage-number data.

Diagnostic method and miscarriage number

The choice of recorded diagnostic pathway did not differ significantly according to miscarriage number (χ^2=8.15, df = 6; P = 0.227) (Table 10).

Table 10
Diagnostic method according to miscarriage number

Miscarriage number	n	QF-PCR only, n (%)	aCGH, n (%)
1	213	97 (45.5)	116 (54.4)
2	137	50 (36.5)	87 (63.5)
3	30	14 (46.7)	16 (53.3)
≥ 4	12	2 (16.7)	10 (83.3)

This analysis included 392 cases with available miscarriage-number data.

Gestational age and genetic result

Gestational-age distributions differed modestly across result categories (Kruskal–Wallis H = 9.67; P = 0.022). The lowest median gestational age was observed in cases with no result because chorionic villi were unavailable (Table 11).

Table 11
Gestational age according to genetic test result

Genetic result	n	Gestational age, weeks, median (IQR)	Range
Normal	146	9 (8–11)	5–22
Abnormal	159	9 (8–10)	6–16
No result because chorionic villi were unavailable	81	8 (7–10)	5–17
Non-informative	6	10 (10–10.8)	8–15

This analysis included 392 cases with available gestational-age data.

Additional diagnostic yield of chromosomal microarray analysis

Among 210 pregnancies analysed by aCGH, 54 (25.7%) demonstrated clinically relevant chromosomal abnormalities that could not have been identified using QF-PCR alone. These abnormalities comprised chromosomal imbalances and pathogenic copy-number variants located outside the chromosomal targets routinely assessed by QF-PCR.

Multivariable logistic regression

The regression analysis included 305 cases with complete clinical data and a diagnostic genetic result. Gestational age was the only variable independently associated with an abnormal result (OR 0.90 per additional week, 95% CI 0.82–0.98; P = 0.017). Maternal age, gravidity, and miscarriage number were not

independently associated with the result (Table 12). The overall likelihood-ratio test was P = 0.060 and McFadden's pseudo-R^2 was 0.021, indicating that the included variables explained only a small proportion of outcome variability.

Table 12
Multivariable logistic regression of factors associated with an abnormal genetic result

Variable	OR	95% CI	P value
Maternal age, per year	1.04	0.99–1.09	0.153
Gestational age, per week	0.90	0.82–0.98	0.017
Gravidity	1.05	0.79–1.39	0.749
Miscarriage number	1.01	0.68–1.49	0.963

The model included 305 cases with complete covariate data and a diagnostic result.

Discussion

This study documents changes in routine clinical practice relating to genetic testing of products of conception during the implementation of chromosomal microarray analysis at the tertiary referral Gynaecology & Obstetrics center. The principal findings were an increase in testing uptake, a progressive shift from QF-PCR towards aCGH, testing after a first miscarriage in more than half of cases, an abnormal result in approximately half of diagnostic analyses, and failure to obtain a result because chorionic villi were unavailable in about one fifth of the cohort.

The increase in testing and the high proportion of analyses performed after a first miscarriage suggest a change in referral practice. Earlier studies of genetic testing after pregnancy loss focused predominantly on recurrent miscarriage(Ogasawara et al. 2000; Sugiura-Ogasawara et al. 2012). Greater awareness among clinicians and patients, together with broader access to molecular diagnostics, may have contributed to earlier testing. Current guidelines remain focused on recurrent pregnancy loss: the 2026 ASRM committee opinion recommends chromosome analysis of miscarriage tissue, when feasible, as a first step in the evaluation of recurrent pregnancy loss and supports array-based technology because of its technical advantages(Gracia et al. 2026). ESHRE and RCOG similarly emphasise genetic evaluation within an individualised diagnostic pathway(Gracia et al. 2026; Bender Atik et al. 2022; Regan et al. 2023). Our observation that testing was frequently undertaken after a first loss describes local practice; it should not be interpreted as evidence that universal testing after every first miscarriage is indicated.

The organisation and financing of testing are important when interpreting these findings. During the study period, genetic analysis of products of conception was provided as a commercial service paid for by patients. Therefore, the decision to undergo testing have been influenced by financial resources as well as clinical indications. The choice between QF-PCR and the more comprehensive aCGH pathway

may also have been affected by cost. This creates a potential selection bias: the study population may differ from women who did not undergo testing and may not represent all patients with pregnancy loss. It also illustrates how limited public funding may restrict the implementation of professional recommendations. Formal health-economic studies are required before conclusions can be drawn about the cost-effectiveness of broader publicly funded testing.

An abnormal result was obtained in 51.8% of diagnostic analyses. This is consistent with large series showing that chromosomal abnormalities account for approximately half of early pregnancy losses (Levy et al. 2014; Sahoo et al. 2017; Finley et al. 2022; Arnadottir et al. 2025). Autosomal aneuploidies, triploidy, and monosomy X predominated, in keeping with established patterns. The whole-genome sequencing study by Arnadottir et al. similarly detected chromosomal abnormalities in approximately half of the analysed pregnancy-loss set and further demonstrated the diversity of sequence-level abnormalities lost in early pregnancy (Arnadottir et al. 2025).

The progressive replacement of QF-PCR by aCGH reflects wider changes in cytogenomic practice. Microarrays do not require cell culture and can identify submicroscopic copy-number changes that targeted methods cannot detect (Levy et al. 2014; Sahoo et al. 2017; Dhillon et al. 2014; Shao et al. 2021). In the present cohort, aCGH enabled the identification of complex structural abnormalities and copy-number variants. Nevertheless, no single method detects all relevant abnormalities. aCGH does not identify balanced rearrangements and has limitations for some ploidy abnormalities, supporting the laboratory strategy of complementary preliminary QF-PCR. The 2026 ASRM opinion likewise notes that available platforms have distinct advantages and limitations and supports array-based analysis of miscarriage tissue (Gracia et al. 2026).

An important contribution of the present study is the assessment of the additional diagnostic value of aCGH within the diagnostic pathway used at our institution. In our laboratory, QF-PCR was routinely performed as the initial molecular investigation, while aCGH was undertaken after exclusion of the common aneuploidies and triploidy detectable by QF-PCR. Despite this preselection, aCGH identified 54 clinically relevant chromosomal abnormalities among 210 analysed pregnancies (25.7%). These abnormalities were located outside the diagnostic scope of QF-PCR and therefore represent additional genetic diagnoses that would not have been established using targeted aneuploidy testing alone. This finding highlights the considerable incremental diagnostic yield of aCGH analysis and provides practical evidence supporting its implementation as the preferred comprehensive method for genetic evaluation of products of conception whenever resources permit.

A clinically important finding was the absence of a final result because chorionic villi were unavailable in 20.8% of cases. Fresh tissue initially lacked identifiable villi in one third of specimens, although paraffin-embedded tissue enabled testing in 52 cases. These findings emphasise the importance of tissue selection, pathological support, and coordination between clinical and genetic laboratories. Patients should be counselled that submission of tissue does not guarantee a diagnostic result. The use of cell-free fetal DNA, as evaluated in the Copenhagen Pregnancy Loss Study, represents a potential

complementary approach, but it is not yet a replacement for routine tissue analysis(Schlaikjær Hartwig et al. 2023).

Earlier gestational age was the only variable independently associated with an abnormal genetic result. Each additional week was associated with an approximately 10% reduction in the odds of detecting an abnormality. This finding is biologically plausible because severe chromosomal abnormalities often result in developmental arrest early in gestation (Levy et al. 2014; Sahoo et al. 2017; Finley et al. 2022; Brosens et al. 2022; Arnadottir et al. 2025; Ogasawara et al. 2000). The low pseudo-R^2 indicates, however, that the clinical variables included in the model explained only a small proportion of the variation in genetic results.

Maternal age was not independently associated with an abnormal result in the analysed cohort. This finding must not be interpreted as evidence that maternal age is unrelated to aneuploidy or miscarriage risk. The study included only patients who had already experienced pregnancy loss and whose tissue was submitted for testing; it did not compare women with and without miscarriage. The result therefore describes the absence of an independent association between age and the genetic outcome within this selected cohort. The relatively narrow age distribution and the limited proportion of women aged 40 years or older may also have reduced the ability to detect an association.

We also found no significant association between miscarriage number and the frequency of abnormal results. Thus, our data did not reproduce the observation by Ogasawara et al. that the proportion of abnormal embryonic karyotypes decreases as the number of previous miscarriages increases(Ogasawara et al. 2000). Differences in patient selection, the predominance of first and second miscarriages in our cohort, sample size in the higher-order miscarriage groups, and the use of contemporary molecular techniques may account for the discrepancy.

The strengths of this study include the analysis of real-world practice over four years, inclusion of the period during which microarray testing was implemented, and simultaneous assessment of testing uptake, tissue availability, genetic outcomes, and clinical factors. The study also has important limitations. Its retrospective, single-centre design limits generalisability. Testing was self-funded, and patients who did not choose or could not afford testing were not represented. The study did not capture the reasons for testing or for selecting a specific method. Missing clinical data resulted in different denominators for some analyses. Potentially relevant factors such as paternal age, body mass index, smoking, and comorbidities were not available. Finally, the study was not designed to assess whether testing improves psychological outcomes, subsequent management, live-birth rates, or cost-effectiveness.

In conclusion, genetic testing of products of conception became increasingly integrated into clinical practice during the study period, with a marked shift from QF-PCR towards aCGH and frequent testing after a first miscarriage. Approximately half of diagnostic results were abnormal, supporting the aetiological value of testing, while the substantial rate of unavailable chorionic villi highlights an important limitation that should be addressed in pre-test counselling and tissue-handling pathways. The

commercial nature of testing may have influenced access and patient selection. Multicentre studies incorporating health-economic and patient-reported outcomes are needed to define the optimal role and equitable provision of genetic testing after pregnancy loss.

Declarations

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Ethics approval: This is an observational retrospective study. The Poznan University of Medical Science Research Ethics Committee has confirmed that no ethical approval is required.

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Figures

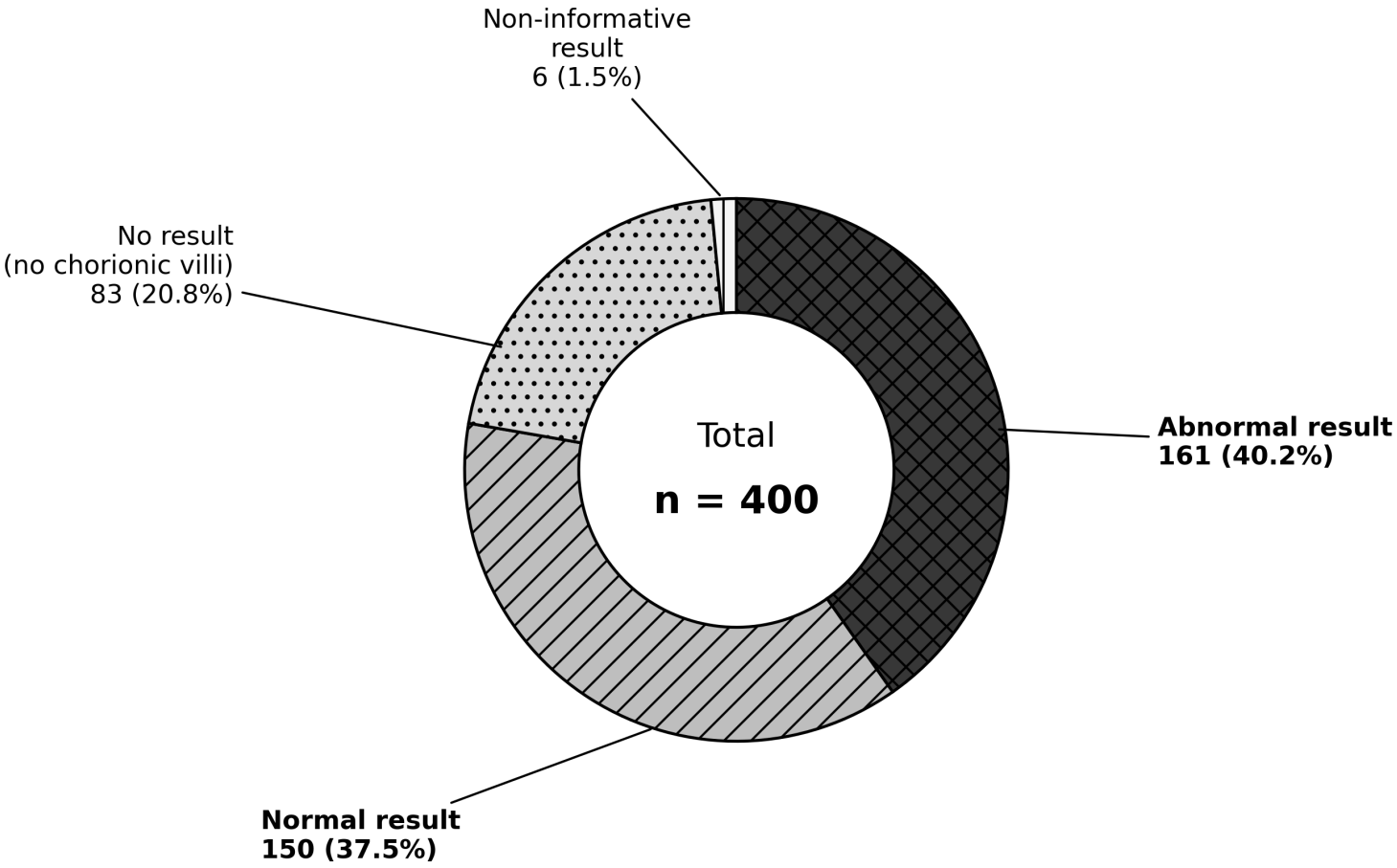


Figure 1

Distribution of genetic test results in the selected cohort of 400 pregnancy-loss episodes: abnormal result, 161 (40.3%); normal result, 150 (37.5%); no result because chorionic villi were unavailable, 83 (20.8%); non-informative result, 6 (1.5%)