APPLICATION NOTE

MATERNAL CELL CONTAMINATION DETECTION
USING DEVYSER COMPACT V3 (8-A017.3)

Invasive prenatal diagnosis involves testing material that is obtained by chorionic villus or amniocentesis sampling. These sampling procedures may result in contamination of the sample with maternal cells, leading to a serious risk of misdiagnosis. As described in various guidelines[1,3], it is of high importance to analyse the maternal sample alongside the prenatal sample and asses the level of maternal cell contamination (MCC) before the prenatal report is issued.

This application note describes how to use the Devyser Compact kit to determine the level of MCC in a prenatal sample.

Follow the instructions in the Devyser Compact v3 IFU (7-A023) with the following modifications:

Chapter 7.2 Sample Preparation and PCR Amplification

- Dilute the extracted fetal sample DNA to 4 ng/µL resulting in 20 ng/PCR.
- In parallel with the fetal sample DNA, a maternal DNA sample should be analyzed. This is performed in order to simplify the identification of informative markers to be used for detection of MCC. Dilute the maternal sample DNA to 4 ng/µL resulting in 20 ng/PCR.

Chapter 8. Results and analysis

- Identify the informative markers to be used for detecting MCC. Informative markers are identified by comparing the fragment lengths (base pair) of the maternal alleles to the fragment lengths of alleles from the fetus for all markers using the criteria outlined below:

Maternal alleles

The long allele (204 bp) is not suitable since it is also present in the fetal sample.

The short allele (200 bp) is not suitable since it is of the same size as a stutter peak in the fetal sample.

Fetal alleles

The long allele (204 bp) is of maternal origin.

The short allele (192 bp) is of paternal origin.

Figure 1

- Be generally observant of PCR artifacts as described in Chapter 8, and be aware of them when selecting informative markers.
- A maternal allele is not suitable if it is also present in the fetal sample (Figure 1)
- A maternal allele is not suitable for comparison if located within a stutter peak (Figure 1) of a fetal allele for a given marker.
- The fetal and maternal alleles should be well-separated i.e. the alleles are separated by more than one marker specific repeat, typically 4 bp (Figure 2).
- If the electrophoretic trace displays background signals, markers in this area should be used with caution or not at all.
- It is recommended that at least two informative markers are used for the MCC determination.

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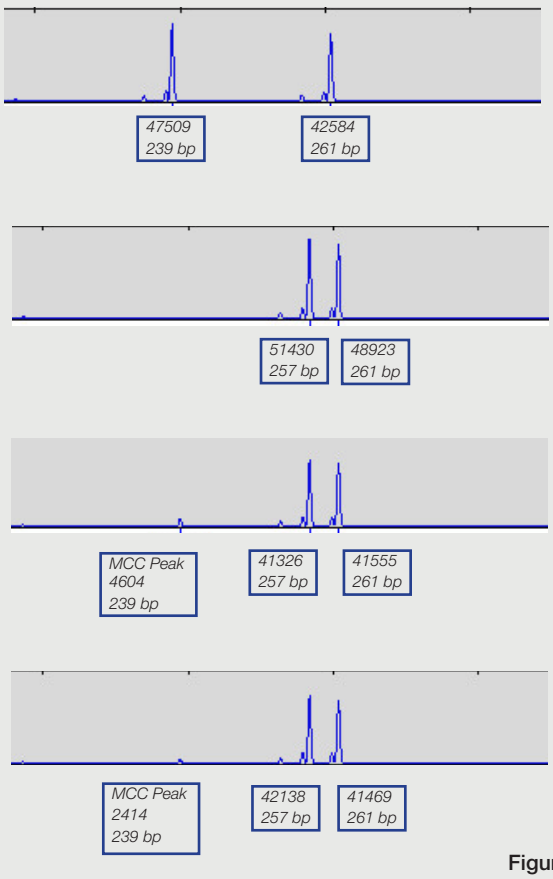
Calculating % MCC

- Add the MCC peak manually if it has not been automatically detected by the software.
- Estimate the level of MCC for each of the selected markers by using the following formula:
  %MCC = (Area MCC peak / Area Fetal peak of paternal origin) x 100
- Estimate the level of MCC in the analyzed samples by calculating the mean of the %MCC from all the individual informative markers.



Maternal alleles

The short allele (239 bp) is suitable since it is not present in the fetal sample.

The long allele (261 bp) is not suitable since it also present in the fetal sample.

Fetal alleles

The long allele (261 bp) is of maternal origin.
The short allele (257 bp) is of paternal origin.

Fetal sample with 10% MCC

Fetal sample with 5% MCC

Figure 2

References

1. Allen S, Mountford R, Butler A, Mann K and Treacy B. 2008. Practice guidelines for the Testing for maternal cell contamination (MCC) in prenatal samples for molecular studies. Clinical Molecular Genetics Society (CMGS)

2. Schrijver I, Cherny S.C. and Zehnder J.L. 2007. Testing for maternal cell contamination in prenatal samples. J. Mol. Diagnostics 9 (3): 394-400

3. Nagan N, Faulkner N.E., Curtis C and Schrijver I. 2011. Laboratory Guidelines for Detection, Interpretation, and Reporting of Maternal Cell Contamination in Prenatal Analyses. J. Mol. Diagnostics 13 (1): 7-11

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