Summary

The most common human chromosomal aberration is known as Down syndrome (DS). It is estimated, that between 1:1000 and 1:700 live births is affected with DS. The direct cause of DS is known to be trisomy 21. The pathomechanism of the disease, with such complicated birth defects, is still not known.

Fetal Down syndrome is diagnosed by prenatal testing. Currently, risk calculation of fetal trisomy 21 is based on the parameters evaluated during USG testing (nuchal translucency thickness and nasal bone) combined with biochemical parameters (levels of free β-human chorionic gonadotropin and pregnancy–associated plasma protein-A). For women whose calculated risk is greater than 1:300, the result is verified by invasive procedures (among others amniocentesis). These procedures allow material for cytogenetics testing to be obtained. Unfortunately, all these invasive methods are burdened with risk of complications including miscarriage.

Metabolomics is a powerful tool, which based on the analysis of small molecules allows the explanation of the details of the pathogenesis of DS and the indication of new potential markers which may improve sensitivity and specificity of noninvasive tests used in prenatal diagnosis.

The aim of the study was to finding differences in both compositions of amniotic fluid and plasma between pregnant women with fetal Down syndrome and women carrying fetus with normal karyotype. Moreover, the diagnostic potential of compounds which significantly differentiate compared groups was evaluated.

LC-MS analysis of amniotic fluid and plasma of pregnant women allowed the indication of compounds which suggested abnormal development of the fetus. Compounds from the carnitines group were detected in amniotic fluid and in plasma. They are probably connected with abnormal development of the fetal nervous system. Methylhistidine, which differentiates amniotic fluid may be a result of disturbances in the muscular system. In addition, p-cresol sulfate was detected in amniotic fluid, which seems to indicate the influence of the maternal gut microbiota on the proper development of the fetus. Moreover, differences in levels of diacetylspermine, piperine and fatty acid amides were detected.

The obtained results mainly indicate disturbances in the development of the nervous and muscular systems in fetuses with Down syndrome. In addition, metabolites detected in plasma samples obtained from pregnant women which differentiate significantly show promising diagnostic potential.