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Title: The predictive model for perinatal asphyxia risk evaluation in the neonates

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Body: Background: Perinatal asphyxia (PA) is often associated with nonreversible adverse neurological outcome. Modern tests for PA diagnostic have low predictive values. The aim of this study was to define the genetical based predictive model for early preventive diagnostic of PA. Methods: We performed a case-control study of 201 neonates PA cases and 110 from control group. The I/D, A1166C, G308A, C677T polymorphism of ACE, AT2R1, TNF-a, MTHFR genes were detected using PCR and RFLP analysis. Statistical analysis was performed to assess the effects of all analyzed genes and their combinations (logistic regression (SPSS_17.0) and MDR model (MDR_2.0)). Results: The frequency of all investigated genotypes with mutant alelle was significantly higher among PA cases.

The statistical model including all investigated genes had the higher predictive value (Percentage Correct=76,5). We have found positive entropy which determined synergy interaction between ACE and AT2R1 genes.

Conclusion: We suggest that using predictive model baised on I/D, A1166C, G308A, C677T polymorphism of ACE, AT2R1, TNF-a, MTHFR genes and their combination may increase early diagnostic of PA.