Relationships between maternal gene polymorphisms in one carbon metabolism and adverse pregnancy outcomes: a prospective mother and child cohort study in China

Shuxia Wang¹, Yifan Duan¹, Shan Jiang¹, Ye Bi¹, Xuehong Pang¹, Changqing Liu¹, Zhenyu Yang¹, and Jianqiang Lai¹

¹Affiliation not available

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Abstract

Objective: To investigate relationships between maternal genes involved in one carbon metabolism and adverse pregnancy outcomes. Design: Prospective mother and child cohort study Setting: Wuqiang, China Population or Sample: Pregnant women (n=939). Methods: A structured questionnaire was used to collect pregnancy outcomes. The maternal serum folate concentration was measured by using Abbott Architect i2000SR chemiluminescence analyzer in the first prenatal care visit. The type of DNA was processed by Sequenom MassARRAY iPLEX Platform. Main Outcome Measures: Pregnancy outcomes (PTB, LBW and SGA), DNA genotyping of methylenetetrahydrofolate reductase (MTHFR), methionine synthase reductase (MTRR), methionine synthase (MTR) and thymidylate synthetase (TYMS). Results: Totally, 849 dyads of women and infants were included in the analysis. The prevalence of PTD, LBW, and SGA were 3.76%, 1.58%, and 5.31% respectively. The average serum folate concentration was 11.95 ng/ml and the folate deficiency rate was 0.47%. There were no significant associations between MTHFR C677T, MTHFR A1298C, MTRR A66G, MTR A2756G, TYMS rs3819102 alleles and PTD, LBW, SGA (P>0.05). Conclusion: In the population with adequate folate status and low prevalence of adverse pregnancy outcomes, MTHFR C677T, MTHFR A1298C, MTRR A66G, MTR A2756G, TYMS rs3819102 alleles may not be related to PTD, LBW, and SGA. Funding: Program for Healthcare Reform from the Chinese National Health and Family Planning Commission. Keywords: Polymorphism, MTHFR, MTR, TYMS, Preterm delivery, Low birth weight, Small-for-gestational-age Tweetable abstract No significant relationships were found between MTHFR, MTRR, MTR, TYMS and PTD, LBW and SGA in the population with adequate folate status.

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