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TCDD exposure during critical period of gonadal sex determination could interfere with methylation pattern of Igf2-H19 ICR and affect steroidogenesis genes in male placenta

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Dioxins are prototype environmental endocrine disrupting chemicals (EDCs). Reproductive and endocrine toxicity of TCDD is the most serious and sensitive end point. In our present exploratory study, SD rats were intrauterine exposed to TCDD during critical period of gonadal sex determination. Epigenetic and molecular techniques were used to measure methylation pattern of imprinted genes and expression levels of steroidogenesis genes in the placenta. Results show that intrauterine exposure to TCDD can cause adverse pregnancy outcomes, including stillbirth, absorption and malformation. Placental weight, fetal weight, body length, tail length, AGD and CAL were also affected. Methylation pattern in Igf2-H19 imprinting control region of male placenta was changed in the TCDD- exposed (100, 500ng/kg) groups. The mRNA expression levels of P450scc, CYP17 and 3β-HSD, key genes in steroidogenesis, were decreased in TCDD- exposed male fetal placenta compared to the control group. Disturbance of the establishment and/or maintenance of the imprint marks may cause methylation errors and contribute to adverse pregnancy outcomes, which may also be a reason for the decrease of fetal weight. TCDD exposure during gonadal sex determination could interfere with steroid hormone generation and further affect the development of male reproductive system. In conclusion, TCDD causes adverse pregnancy outcomes by changing DNA methylation pattern of imprinted genes and interfering with steroidogenesis in male placenta, taking into account that TCDD is an endocrine disruptor, steroid hormone signaling pathways may be involved in the changes of DNA methylation pattern.

Biography

Jing Ma is a PhD student from Department of occupational and environmental health, School of Public Health, Tianjin Medical University. Her research mainly focuses on TCDD- induced epigenetic transgenerational inheritance of DNA methylation patterns of imprinted genes and steroidogenesis genes. All authors work collaboratively on this project.