



The intensity of IUGR-induced transcriptome deregulations is inversely correlated with the onset of organ function in a rat model

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Résumé en anglais

A low-protein diet applied during pregnancy in the rat results in intrauterine growth restricted (IUGR) fetuses. In humans, IUGR is associated with increased perinatal morbidity, higher incidence of neuro-developmental defects and increased risk of adult metabolic anomalies, such as diabetes and cardiovascular disease. Development and function of many organs are affected by environmental conditions such as those inducing fetal and early postnatal growth restriction. This phenomenon, termed "fetal programming" has been studied unconnectedly in some organs, but very few studies (if any) have investigated at the same time several organs, on a more comparative basis. However, it is quite probable that IUGR affects differentially most organ systems, with possible persistent changes in gene expression. In this study we address transcriptional alterations induced by IUGR in a multi-organ perspective, by systematic analysis of 20-days rat fetuses. We show that (1) expressional alterations are apparently stronger in organs functioning late in foetal or postnatal life than in organs that are functioning early (2) hierarchical classification of the deregulations put together kidney and placenta in one cluster, liver, lungs and heart in another; (3) the epigenetic machinery is set up especially in the placenta, while its alterations are rather mild in other organs; (4) the genes appear deregulated in chromosome clusters; (5) the altered expression cascades varies from organ to organ, with noticeably a very significant modification of the complement and coagulation cascades in the kidney; (6) we found a significant increase in TF binding site for HNF4 proteins specifically for liver genes that are down-regulated in IUGR, suggesting that this decrease is achieved through the action of HNF transcription factors, that are themselves transcriptionnally induced in the liver by IUGR (x 1.84 fold). Altogether, our study suggests that a combination of tissue-specific mechanisms contributes to bring about tissue-driven modifications of gene cascades. The question of these cascades being activated to adapt the organ to harsh environmental condition, or as an endpoint consequence is still raised.

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