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ANÁLISE DO TRANSCRITOMA DO PÂNCREAS DE RATAS COM HIPERGLICEMIA PROGRAMADA PELO DIABETE MATERNO

Relatório de Pós-doutorado realizado na Universidade Estadual Paulista (UNESP), Faculdade de Medicina, Botucatu.

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RESUMO

Introdução: A exposição intrauterina ao diabete pode afetar o desenvolvimento levando a efeitos a longo prazo na saúde da prole. Os desfechos mais comuns são o desenvolvimento de alterações metabólicas, estruturais e funcional no pâncreas endócrina. Considerando que o diabete materno prejudica o metabolismo da glicose e a função pancreática nos descendentes tanto de mulheres quanto em animais de laboratório, há necessidade de identificar marcadores moleculares para estudar e entender os mecanismos fisiopatológicos envolvidos nas repercussões nas ilhotas pancreáticas destes descendentes. **Objetivo:** Analisar o transcritoma do pâncreas endócrino de ratas diabéticas e de suas descendentes, que são advindas da hiperglicemia programada pelo diabete materno. **Materiais e método:** Ratas fêmeas da linhagem *Sprague Dawley* foram submetidas à indução do diabete pela administração de *streptozotocin* [droga beta (β)-citotóxica - grupo Dmod] ou tampão citrato (grupo não-diabético Controle) na fase neonatal e, após confirmação do diabete na vida adulta, as ratas foram acasaladas para obtenção de descendentes, as quais foram avaliadas na vida adulta (grupo FDmod). Aos 120 dias de vida, ratas-mães diabéticas e sua prole feminina adulta foram anestesiadas para serem submetidas à laparotomia para coleta do pâncreas e isolamento das ilhotas pancreáticas. O RNA foi extraído das ilhotas pancreáticas e o perfil de transcritos foi avaliado pela técnica de *microarray***. Resultados:** Foram encontrados um total de 749 genes diferencialmente expressos entre os grupos Dmod x Controle, sendo 407 *up* regulados e 342 *down* regulados. Em relação à comparação FDmod x Controle, um total de 672 genes estavam diferencialmente expressos, destes 334 *up* regulados e 338 *down* regulados. Na comparação entre Dmod x FDmod, 3926 foram diferencialmente expressos, sendo 2251 *up* regulados e 1675 *down* regulados. De acordo com o diagrama de Veen, 5 genes apresentaram interseção entre as comparações e os principais genes diferencialmente expressos foram identificados de acordo com o *fold change*. **Conclusão:** A análise do transcritoma das ilhotas pancreáticas de ratas diabéticas e de suas filhas mostrou diferenças no perfil de genes diferencialmente expressos no modelo de diabete intergeracional avaliados nesse estudo. Análises mais aprofundadas são necessárias para identificar as principais vias alteradas e os principais genes envolvidos nestas alterações.

Palavras-chave: diabete, pâncreas, transcritoma, programação fetal, ratas.

SUMÁRIO

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