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## OR05-3 Mir-21 Contributes to Cytokine-Induced Beta Cell Dysfunction via Inhibition of mRNAs Regulating Beta Cell Identity

[Sara Ibrahim](#), BS, [Ryan Anderson](#), PhD, [Raghavendra Mirmira](#), PhD, MD, and [Emily Sims](#), MD

Indiana University Peds Endocrinology, Indianapolis, IN, United States

Indiana University School of Medicine, Indianapolis, IN, United States

Department of Pediatrics, Indiana University School of Medicine, Indianapolis, IN, United States

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### Abstract

A hallmark of diabetes is the loss of physical or functional  $\beta$  cell mass. Alterations in  $\beta$  cell microRNA (miRNA) profiles have been described in diabetes. MiRNAs have also been shown to serve as important regulators of  $\beta$  cell development and function, implicating them in  $\beta$  cell dysfunction during diabetes development. Our lab has previously demonstrated that  $\beta$  cell microRNA 21 (miR-21) is increased in models of diabetes. However, a comprehensive analysis of the  $\beta$  cell effects of miR-21 remain poorly defined, and the effects of miR-21 on *in vivo* glucose homeostasis have never been explored. To this end, we performed a comprehensive *in silico* analysis of bioinformatics databases to identify potential  $\beta$  cell targets of miR-21, which yielded multiple targets in the Transforming Growth Factor Beta 2 (*Tgfb2*) and Fibroblast Growth Factor Receptor 3 (*Fgfr3*) pathways associated with regulation of differentiation. We hypothesize that  $\beta$  cell miR-21 plays a critical role in inhibiting  $\beta$  cell function and inducing loss of  $\beta$  cell identity. To validate targets *in vitro*, we developed a model whereby miR-21 is upregulated using a dose dependent lentiviral Tetracycline-on system in INS1 cells. Overexpression of miR-21 led to a reduction in expression levels of several members of the *Tgfb2* and *Fgfr3* pathways as well as multiple transcription factors associated with  $\beta$  cell function and identity, and an increase in aldehyde dehydrogenase transcripts, consistent with  $\beta$  cell dedifferentiation. To verify direct interactions between miR-21 and candidate target mRNAs, a biotin pulldown experiment was performed using a 3' biotinylated mature miR-21 construct and a 3' biotinylated cel-miR-67 control construct. Several mRNAs associated with  $\beta$  cell identity were enriched in the pulldown, indicating a direct interaction with miR-21. Lineage tracing was performed within an *in vivo* zebrafish model of  $\beta$  cell specific oxidative stress in which  $\beta$  cells expressed a nuclear GFP signal. Whole body knock down of miR-21 by morpholino microinjection showed a protective effect in stressed  $\beta$  cells and rescued against a dedifferentiated phenotype. To test the effect of miR-21 on glucose tolerance *in vivo*, inducible  $\beta$  cell specific knockout ( $\beta$ miR-21KO) and overexpression ( $\beta$ miR-21) mice were generated



by crossing *Ins1tm1(CreERT2)*Thor mice with miR-21 floxed mice and miR-21-CAG-Z-EGFP mice, respectively. When compared to littermate controls, intraperitoneal glucose tolerance tests (IPGTT) exhibited hyperglycemia in  $\beta$ miR-21 mice and euglycemia in  $\beta$ miR-21KO mice. Metabolic studies, including glucose stimulated insulin secretion (GSIS) and insulin tolerance tests (ITT) are ongoing in our mouse models. Our results implicate miR-21 as a regulator of  $\beta$  cell dedifferentiation during diabetes development.

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