In vivo and in vitro muscle metabolic profiles of TIEG1 KO muscle mice using spectroscopy techniques (MRS / NMR)

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Introduction: TGFβ inducible early gene-1 (TIEG1) is a member of the Krüppel-like family of transcription factors (KLF10). Deletion of TIEG1 results in muscle fiber hypertrophy, texture profile changes, dysfunction of mitochondrial biogenesis and defects in functional properties.

Aim: To further analyze the effect of TIEG1 gene on muscle metabolism.

Methods and Results: 12 WT and 12 TIEG1 KO mice were used for *in vivo* spectroscopy acquisitions 9.4T (Bruker). A home built coil was developed. Resonance frequencies were 400 MHz for the proton and 162 MHz for the phosphorus. Localized 1H and 31P spectroscopy were performed with PRESS sequence providing quantification of different metabolites. While 1H-NMR spectra showed no significant difference for choline, creatine, taurine and extramyocellular lipids between WT and TIEG1 KO. 31P spectra revealed a significant difference for phosphocreatine and ATPγ.

For metabolomics analysis ^{1}H-NMR spectra were obtained from soleus (N=18) and EDL (N=18) muscles isolated from WT and TIEG1 KO with a 600MHz spectrometer (Bruker, 14T). Heatmaps were generated to visually depict changes in metabolites ($p < 0.05$) as a function of mouse genotype. For both TIEG1 KO soleus and EDL muscles, there were more down regulated metabolites compared to WT muscles.

Conclusion: The present study has demonstrated a new role for TIEG1 in the homeostasis of the muscle metabolome and specifically in energetic metabolism.