The role of perm1 (PGC1 and ERR-induced Regulator in Muscle 1) in cardiac ischemia and Reperfusion

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Background
Transcriptional networks play a central role in metabolic pathway. Perm1 (PGC1 and ERR-induced Regulator in Muscle 1) is a protein induced by PGC1a and ERRs and also regulates the selective PGC1/ERR target genes, such as glucose, lipid metabolism, mitochondrial biogenesis, energy transfer, and contractile function. Myocardial ischemia and reperfusion (I/R) is a kind of stress to change cardiomyocyte intrinsic metabolism. This situation induced complicated transcriptional signal regulation and protein interaction. This experiment aims to elucidate the role of Perm1 in myocardial ischemia and reperfusion.

Method
Wild type (WT) and Perm1 homogenous knockout (KO) mice were used. Three to six month mice received sham and left anterior descending coronary artery (LAD) temporary ligation surgery. Under 37^{o}C body temperature, LAD was ligated for ischemia 30min and the knot was released for reperfusion 24 hours. After that, TTC staining and protein analysis were applied for further result.

Result
The mice were divided to four groups, WT/sham (n=3), KO/sham (n=3), WT/IR (n=3), and KO/IR (n=3). TTC staining result showed KO mice tended to be more severe infarction area than WT mice after one day ischemia/reperfusion (24.4% in WT vs 35.1% in KO, p=.0158). In protein analysis, PGC1a and Oxphos did not reveal significant change compared with Sham and I/R surgery. Perm1 was downregulated in WT I/R group compared with WT sham group. ERRs, PPARa, and catalase tended to be downregulated in KO I/R group compared with WT I/R group.

Conclusion
Perm1 may play a key role in antioxidant and metabolism regulation in

transcriptional factor initially. Further metabolism pathway analysis is required.