Maternal energy restriction in early gestation affects *MYOG* network topology of bovine skeletal muscle

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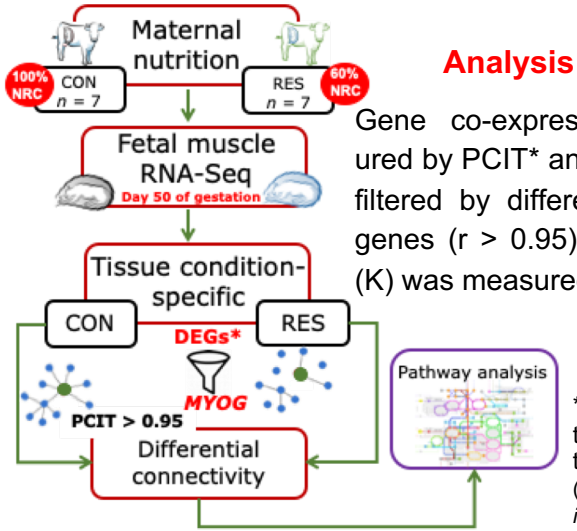
Introduction

Maternal nutrition has long-term consequences on muscle development through transcriptomic changes. However, the relationship between genes and its role in the regulation of specific pathways is still limited.

To determine the relationship between maternal nutrition, gene expression, and the pathways that control skeletal muscle development, we performed a **gene co-expression network (GCN) analysis**.

Materials & Methods



Analysis Workflow

Gene co-expression was measured by PCIT* and gene pairs were filtered by differentially expressed genes (r > 0.95). The connectivity (K) was measured as $K_{CON} - K_{RES}$.

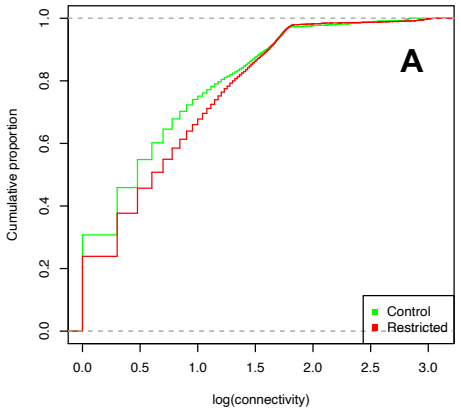
*PCIT = partial correlation and information theory algorithm (Reverter & Chan. *Bioinformatics*, 2008).

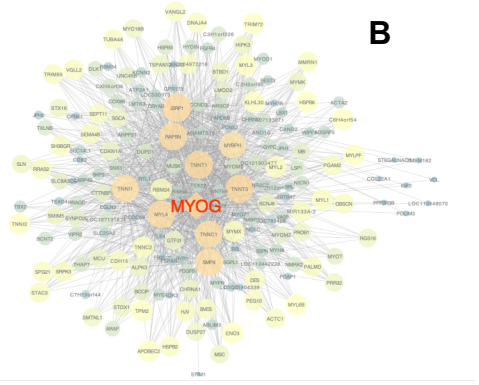
Results

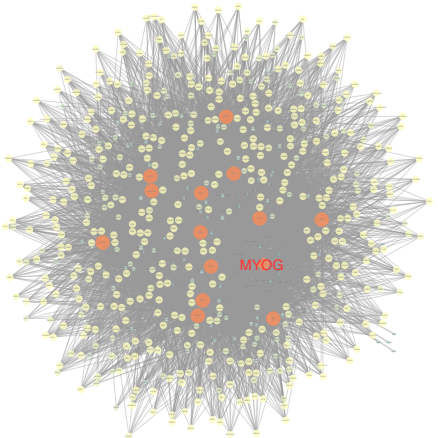
The RES networks showed a gain of connectivity **(A)**.

MYOG, a transcription factor required for myogenesis, was identified among the hub genes in both groups; however, it was 70.5% more connected and 33% more expressed in the RES when compared with CON.

Signaling pathways, such as FoxO and AMPK, underlay the **CON** group (*n* = 1,393 genes, **B**), whereas fatty acid metabolism, mTOR, and insulin were over-represented in the **RES** group (*n* = 2,453 genes, **C**).







Conclusion

Energy restriction leads to a gene rewiring that can affect gene expression, muscle development and metabolism by affecting gene-specific sub-networks.

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