<u>Cite this as:</u> Li-ning SU, Xiao-qing SONG, Zhan-xia XUE, Chen-qing ZHENG, Hai-feng YIN, Hui-ping WEI, 2018. Network analysis of microRNAs, transcription factors, and target genes involved in axon regeneration. *Journal of Zhejiang University-Science B (Biomedicine & Biotechnology)*, 19(4):293-304.

https://doi.org/10.1631/jzus.B1700179

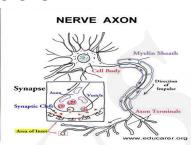
Network analysis of microRNAs, transcription factors, and target genes involved in axon regeneration

Key words: Transcription factors, MiRNAs, Target genes, Axon, Network

Research Summary

This review mainly focused on identifying several genes, microRNAs (miRNAs), and transcription factors (TFs) that influence axon regeneration.

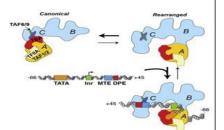






- Axon-associated miRNAs and predictions of miRNA targets
- Prediction of axon-associated TFs
- FFLs and miRNA-TF-target gene networks

Functional enrichment analysis

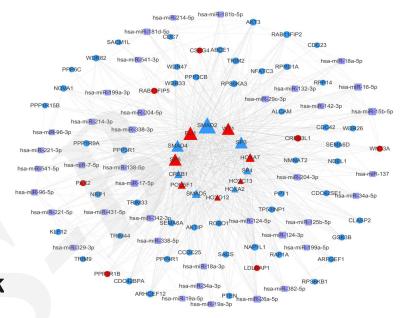


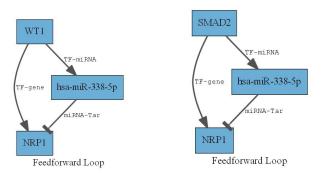


Innovation points

- Obtain genes, microRNAs, and transcription factors involved in axon regeneration.
- Summary the regulatory network and feed-forward loops involved.

• Emphasis seven important genes six important miRNAs and eight important TFs which appear to play an important role in axon regeneration.





Innovation points

A series of comprehensive tables were generated to summarize.

Table 1 | Axon-related and miRNA target genes.

Table 2 Genes overlapping between Genes Cluster 1 (axon-related DEGs) and Genes Cluster 2 (axon-related miRNA target genes) and miRNA-target gene interactions.

Table 3 Transcription factors overlapping between DEGs and human transcription factors (TFs Cluster 1).

Table 4 | Important nodes selected based on their closeness centrality and etwork.