

The Role of TNFAIP1 in Regulation of LPS-induced Pathway

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Background :

Porphyromonas gingivalis /lipopolysaccharide (P.g/LPS) induces inflammatory diseases via TNF- α -mediated transcription factors. Our recent data showed that TNFAIP1 (TNF- α induced protein 1) is related to TNF- α in response to LPS. However, The involvement of TNFAIP1 in the LPS-induced pathway is largely unknown.

Aim :

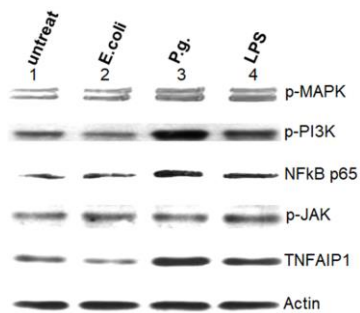
To determine transcriptional regulation of TNFAIP1 gene

Materials and Methods :

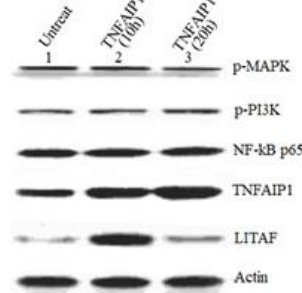
- human macrophage THP-1 cells, mouse macrophage RAW264.7 cells
- Cloning of human or mouse TNFAIP1 cDNA and TNFAIP1 promoter DNA into plasmid of pCDNA3 and pGL3-basic
- Western blot to determine LPS stimulated downstream pathway
- ELISA to quantify TNF- α /Caspase 1
- Protein Array to determine apoptotic gene expression

Results :

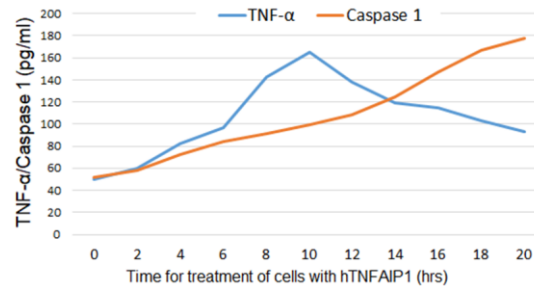
1. Increasing NFkB (p65), TNFAIP1, MAP kinase, and PI3K by P.g/LPS stimulation



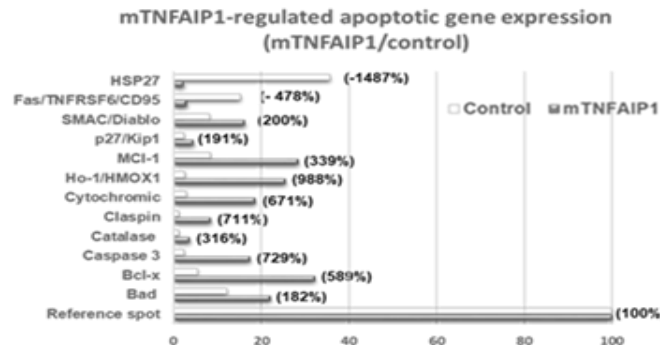
2. The overexpression of humanTNFAIP1 did not activate MAP kinase, PI3K, and NF-kB, except LITAF.



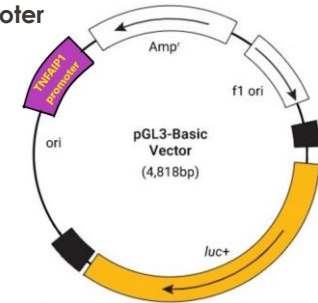
3. TNF- α production rose to the top (10 hrs), gradually drop to 20 hrs, while Caspase 1 increased.



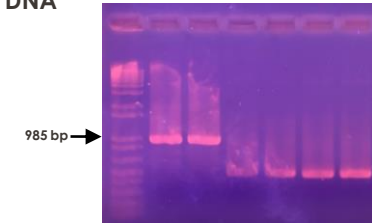
4. Overexpression of mouse TNFAIP1 cDNA caused increasing Bad, Bcl-x, Caspase 3, Catalase, Claspin, Cytochromic, Ho-1/HMOX1/HSP32, MCl-1, P27/Kip1, SMAC, reducing Fas/TNFRSF6/CD and HSP27



5. The recombinant plasmid DNA of TNFAIP1 promoter



6. Confirmation of the cloned TNFAIP1 promoter DNA



7. The proposed interaction of TNFAIP1 promoter with transcription factors



Conclusion:

- MAP kinase or PI3K as upstream factor and LITAF as downstream factor in TNFAIP1-dependent pathway
- Overexpression of TNFAIP1 induces apoptotic proteins

Future research plan:

- Further analysis of TNFAIP1 promoter activity; To determine factors that control TNFAIP1 promoter activity as possible targets for inhibition of P.g/LPS-induced inflammatory diseases