Protein-protein Interaction Analysis of Contributing Molecules in Dura mater Healing Process

Hendrikus Masang Ban Bolly[1,3,*], Yulius Hermanto[4],
Ahmad Faried[2], Muhammad Zafrullah Arifin[2],
Trajanus Laurens Yembise[3], Firman Fuad Wirakusumah[5]

[1]Doctoral Program in Medicine, Faculty of Medicine, Padjadjaran University, Bandung West Java Indonesia
[2]Department of Neurosurgery, Faculty of Medicine, Padjadjaran University- Hasan Sadikin Hospital, Bandung-West Java Indonesia
[3]Department of Surgery, Faculty of Medicine, Cenderawasih University, Jayapura Papua, Indonesia
[4]Neurosurgery Division, Surgery Department, Faculty of Medicine, Riau University, Riau Indonesia
[5]Department of Obstetrics and Gynecology, Faculty of Medicine, Padjadjaran University - Hasan Sadikin Hospital, Bandung West Java Indonesia

Abstract : Background: Dura mater is a special tissue that fulfills a critical function in brain anatomy and physiology. This tissue contains numerous cells, stem cells, and growth factors. This research investigates the protein interaction contributing to dura mater healing process. **Methods:** We use the available analysis software to perform the protein-protein interaction (PPI) analysis (http://gpsprot.org/index.php). GPS Protein is an interactive platform for visualizing human protein interaction by integrating HIPPIE and CORUM databases. We excluded HIV-1 proteomic and RNAi databases, instead focused on human PPI (Confidence level 0.75). Two proteins were inputted as query to identify the potential protein network in Dura mater healing according to previous studies, i.e. *fibroblast growth factor-2* (FGF2) and *transforming growth factor beta-1* (TGFβ1). **Results:** PPI results shows a high level (confidence level > 0.75) of protein-protein interaction of TGFβ1 to 197 other proteins (Confidence level ranges: 0.49 - 0.87), and PPI of FGF2 to 26 other proteins (Confidence level ranges: 0.0-0.97). TGFβ1 interactions showed the important interactions to some remodeling proteins. TGFβ1 encoded regulates cell proliferation, differentiation, growth, expression modulation and the activation of other growth factors. It also induces epithelial-to-mesenchymal transition (EMT) and cell migration. **Conclusion:** This bioinformatics approach is the more efficient and cheaper method for analyzing the molecular aspect of protein that has a special contribution in Dura mater healing process. These results could beneficial in focusing further researches for more complex laboratory examinations.

Keywords : Bioinformatic, dura mater, healing, protein interaction, transforming growth factor beta-1.

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