Construction of PADPIN: Protein-Protein Interaction Networks in Peripheral Artery Disease

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Abstract

Background

Peripheral artery disease (PAD) is usually caused by atherosclerosis in the peripheral arteries, which the plaque builds up in the wall of an artery. PAD affects approximately 8 to 12 million people in United States, especially those over the age of 50 and its prevalence is now almost comparable to that of coronary artery disease. Risk factors contributing to PAD include smoking, diabetes and Hypertension. With the goal of trying to increase blood flow around blockages, clinical trials using drugs and gene delivery aimed at stimulating vascular growth and remodeling (angiogenesis and arteriogenesis) have been performed for more than a decade but have not been successful.

Results

We combine several databases and machine learning methods to construct the PADPIN, protein-protein interaction networks of PAD. We focus on three main biological processes in PADPIN: angiogenesis, arteriogenesis and immune response. We use GSEA (gene set enrichment analysis) to analyze existing multiple large-scale high-throughput gene expression datasets from mouse PAD muscle samples.

Conclusions

A systematic analysis of molecules, pathways, protein-protein interactions, and GSEA analysis will provide much needed guidance for experimental validation, prevention and treatment of PAD in the future.