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Osteoporosis Gene Interactome: A comprehensive *in silico* analysis

Bharat Singh[1] and Yasha Hasija[1]

[1]Department of Biotechnology, Delhi Technological University, Shahbad Daulatpur, Main Bawana Road, Delhi 110042, INDIA

Presenting author: bharat30.1990@gmail.com

Abstract

Today it is a challenge for clinicians and researchers to understand the comprehensive relationship between molecular and physical functioning of genes towards the progression of disease. Although genomic advancements have produced significant data to identify the genes involved in many complex diseases but a loop exists since a single gene is not attributable to a particular concept. In our work, we tried to find key neighbours involved in osteoporosis by analysing osteoporosis disease module (interactome) using both experimental and clinical methodologies which may also contain mechanisms that are collective with other disease modules. Our idea was strengthened by the findings of previous GWAS p-value studies wherein the level of gene expression was different in both diseased as well as normal conditions. We thus, constructed a gene-gene and protein-protein interaction network for 104 genes linked with 173 genetic variants (single nucleotide polymorphisms) that revealed significant hub proteins which might be fundamentally linked to disease pathogenesis. We further performed gene ontology and functional enrichment analysis followed by KEGG pathway analysis to analyze and validate the role of these genes for their pathophysiological and functional activities. Our analysis revealed the polymorphism in SOST and LRP5 genes as significant conservative SNPs which might have a substantial role in the onset of osteoporosis and its development.

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