

## Yigu decoction has an influence on quantitative proteomics.

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### Introduction

Osteoporosis (OP) is a systemic bone disease marked by a loss of bone mass, degradation of the microstructure of bone tissue, increased brittleness, and an increased risk of fracture. OP is associated with significant consequences and has a high incidence rate and a protracted illness course. Yigu Decoction (YGD) is a traditional Chinese medicine chemical prescription used to treat OP. In OP, however, the process is unclear. The possible bone-protective mechanism of YGD was investigated in an osteoporotic rat model using a Tandem Mass Tag (TMT) quantitative proteomics approach. By modulating target proteins involved in many signalling cascades, YGD can considerably improve the Bone Mineral Density (BMD) of osteoporotic rats and may perform a therapeutic role. As a result, these findings contribute to a better understanding of the OP mechanism and provide an experimental foundation for the clinical use of YGD in OP treatment. Low bone mass, bone tissue breakdown, and discomfort are all symptoms of Osteoporosis (OP).

Low bone mass, bone tissue metamorphism, bone structure breakdown, reduced bone strength, and an increased risk of fracture are the most common symptoms. Reduced Bone Mineral Density (BMD) and increased bone brittleness are signs of low bone mass. Bone tissue metamorphism and bone structure degradation are bone homeostasis changes produced by decreased osteoblast production and increased osteoclast proliferation, and OP's end point event is fracture, most commonly vertebral fracture, hip fracture, or forearm fracture.

The proteome is the collection of proteins produced by an organism. It differs from cell to cell and changes over time and across distinct cellular states, such as after a particular therapy. Proteomics-based mass spectrometry (MS) can now accurately assess the complete cellular proteome; but, in some circumstances, it may be more useful to focus on specific groups of proteins of interest (the so-called POIs) [1].

POIs can be diverse, include members of a chemically modified subset, a newly generated one, a pool of membrane proteins, or a secreted subset of the entire proteome, for example [2]. Indeed, analysing a smaller portion of the proteome has the advantage of allowing one to identify and quantify more proteins that may be in low abundance in respect to the background of the full proteome [3]. It would be simple to

focus on the secretome, which represents all proteins secreted beyond the cell membrane into the extracellular matrix, in the research presented in this publication, which is focused on the influence of a plant extract on wound healing [4]. Cytokines, coagulation factors, growth factors, cell-cell adhesion, and other signalling molecules are among the secreted proteins; the secretome is straightforward to collect, and using proper precipitation procedures, samples with an appropriate protein concentration for proteomic analysis can be prepared [5].

### Conclusion

The effect of YGD on protein expression in bone tissue was investigated using TMT-based proteomics technology and proteome microarray technology. The findings revealed that YGD was engaged in various signalling pathways associated to OP, as well as several proteins involved in signalling pathway control. This backed up the conclusions achieved in certain papers and supported our YGD research concept. That is, YGD regulates a variety of target proteins, engages in signal transduction across numerous signalling pathways, and has a therapeutic role. At the same time, we discovered a link between the differentially expressed protein DPP4 and OP, although more research into how DPP4 participates in signal pathway transduction and influences the occurrence and progression of OP is needed. The potential of this plant-derived polysaccharide to trigger the manufacture or release of specific proteins from keratinocytes, in particular, makes its application in the treatment of skin lesions even more appealing.

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