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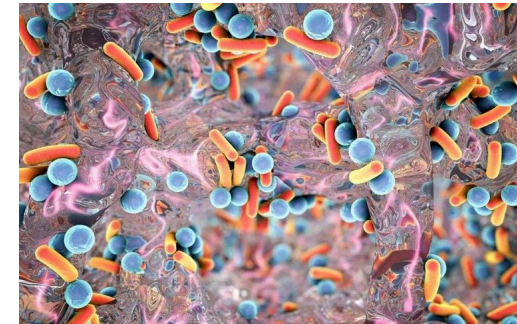
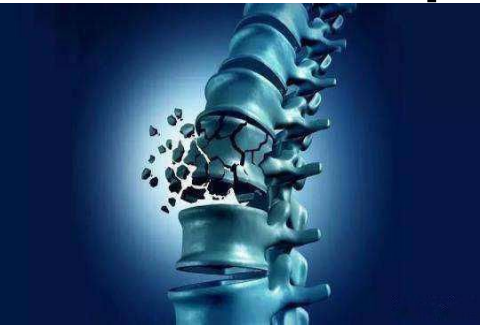
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# **Changes in the gut microbiota of osteoporosis patients based on 16S rRNA gene sequencing: a systematic review and meta-analysis**

**Key words: Osteoporosis; Microbiome; Intestinal; 16S rRNA sequencing.**

# Research Summary

This systematic review and meta-analysis mainly focused on the changes of gut microbiota in patients with osteoporosis

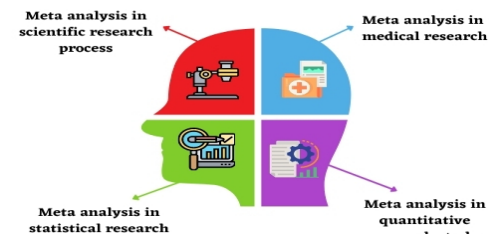


Based on 16s rRNA Gene Sequencing:

- Gut microbiota diversity
- Relative abundance of gut microbiota
- Lefse analysis

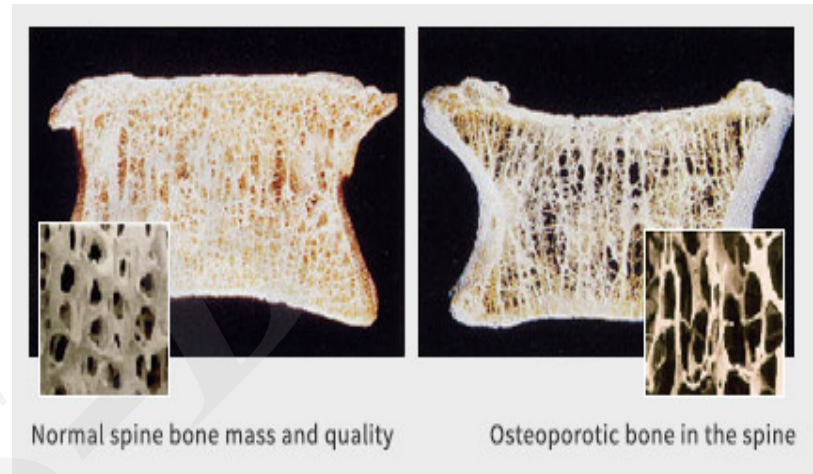


## IMPORTANCE OF META ANALYSIS



# ***Innovation points***

- **The First meta-analysis to demonstrate an association between gut microbiota and osteoporosis**
- **Summary of the diversity of gut microbiota and the results of lefse analysis**
- **Emphasis of the Relative abundance of gut microbiota**



# ***Innovation points***

**A series of comprehensive figures and tables were generated to summarize the changes of intestinal microbiota in osteoporosis patients and healthy people**

**Figure 1 | Forest map of alpha diversity differences by Chao and Shannon's diversity index.**

**Figure 2 | Forest plot of F/B ratio.**

**Table 3 | Changes at the taxonomic level in phyla associated with intestinal flora.**

**Table 4 | Differences in the relative abundance of gut bacteria at the genus level between osteoporosis patients and healthy.**

**Table 5 | Controversial results.**