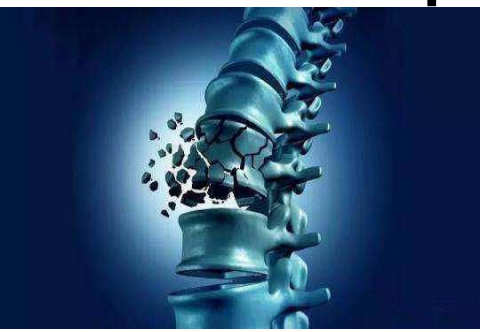
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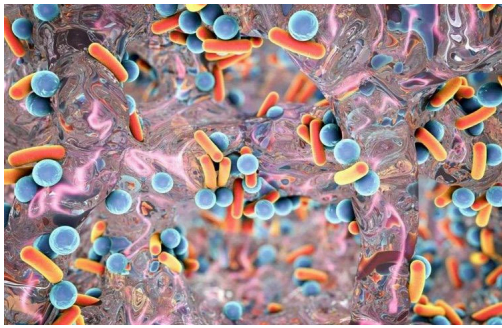
Changes in the gut microbiota of osteoporosis patients based on 16S rRNA gene sequencing: a systematic review and meta-analysis

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

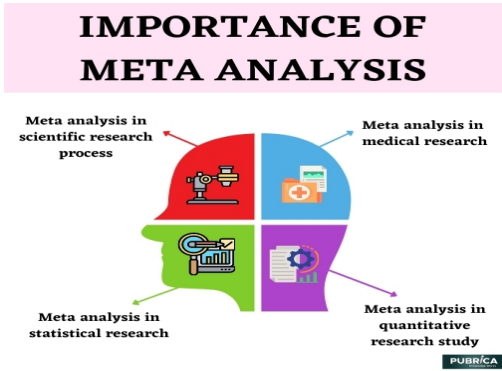




Based on 16s rRNA Gene Sequencing:

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





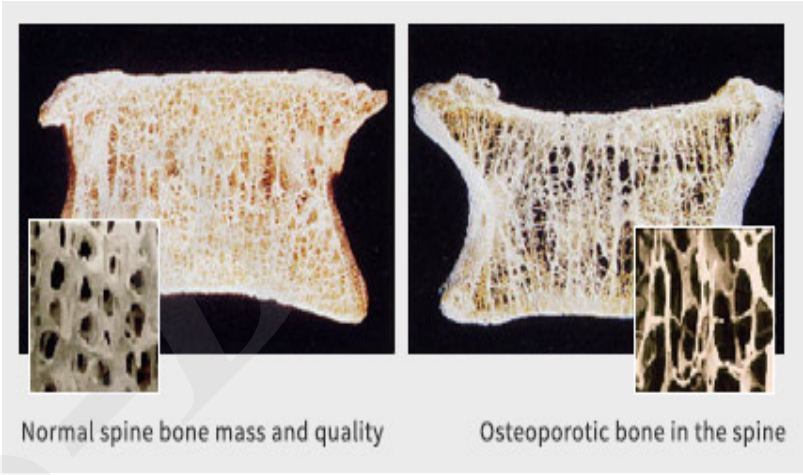
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Innovation points

- **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.

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