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# Protocols for "Shotgun Metagenomics of 361 elderly women reveals gut microbiome change in bone mass loss"

Forked from Protocols for "Shotgun Metagenomics of 361 elderly women reveals gut microbiome change in bone mass loss"

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1 Works for me [dx.doi.org/10.17504/protocols.io.bq6hmzb6](https://dx.doi.org/10.17504/protocols.io.bq6hmzb6)

BGI GIGA 1 more workspace

wangqi

## ABSTRACT

Bone mass loss contributes to the risk of bone fracture in the elderly. Many factors including age, obesity, estrogen and diet, are associated with bone mass loss. Mice studies suggested that the gut microbiome might affect the bone mass by regulating the immune system, however there has been little evidence from human studies. Bone loss increases after menopause. Therefore, we have recruited 361 Chinese post-menopausal women to collect their fecal samples and metadata to conduct metagenome-wide association study (MWAS) to investigate the influence of the gut microbiome on bone health. Gut microbiome sequencing data were produced using BGISEQ500 sequencing, Bone mineral density (BMD) was calculated using Hologic dual energy X-ray machine, body mass index (BMI) and age were also recorded. This collected data allows exploration of the gut microbial diversity and their links to bone mass loss, as well as microbial markers for bone mineral density. In addition, these data are potentially useful in studying the role the gut microbiota might play in bone mass loss and in exploring the bone mass loss process.

## DOI

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<https://dx.doi.org/10.17504/protocols.io.bq6hmzb6>

## FORK NOTE

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#### ABSTRACT



Bone mass loss contributes to the risk of bone fracture in the elderly. Many factors including age, obesity, estrogen and diet, are associated with bone mass loss. Mice studies suggested that the gut microbiome might affect the bone mass by regulating the immune system, however there has been little evidence from human studies. Bone loss increases after menopause. Therefore, we have recruited 361 Chinese post-menopausal women to collect their fecal samples and metadata to conduct metagenome-wide association study (MWAS) to investigate the influence of the gut microbiome on bone health. Gut microbiome sequencing data were produced using BGISEQ500 sequencing, Bone mineral density (BMD) was calculated using Hologic dual energy X-ray machine, body mass index (BMI) and age were also recorded. This collected data allows exploration of the gut microbial diversity and their links to bone mass loss, as well as microbial markers for bone mineral density. In addition, these data are potentially useful in studying the role the gut microbiota might play in bone mass loss and in exploring the bone mass loss process.



## FILES

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**BGISEQ-500 Sequencing**  
**Version 1**  
by Xinming Liang, Beijing Genomics Institute
- 

**Quality control for metagenomics data**  
**Version 1**  
by Qi Wang
- 

**DNA extraction for human microbe samples.**  
**Version 1**  
by Lilan Hao
- 

**BGISEQ-500 WGS library construction**  
**Version 1**  
by Xinming Liang, Beijing Genomics Institute
- 

**The calculation of gut metabolic modules from gene profile**  
**Version 1**  
by wangqi