

# The gut microbiota of healthy aged Chinese is similar to the healthy young

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## Abstract

The influence or consequence of a healthy gut microbiota to the healthy aging process is controversial. Here we collected and examined the gut microbiota of a cross-sectional cohort of more than 1000 very healthy Chinese individuals who spanned the ages from 3 to over 100. Analysis of 16S rRNA gene sequencing results, using a compositional data analysis paradigm, where ordination, differential abundance and correlation can be analyzed in a unified and robust framework, showed several surprising results compared to other cohorts. First, the overall composition of the healthy aged group was similar to that of people decades younger. Second, the major changes in the gut microbiota profiles were found to occur before age 20. Third, the gut microbiota reached an equilibrium around age 30 that was maintained for life. Fourth, the gut microbiota of males appeared to be more variable than that of females. Taken together, the present findings provide novel insight into the temporal relationship between gut microbiota profiles and healthy ageing in this and similar populations.

(Jones and Johnson, 1986; Emmanuel and others, 1989)

or

Emmanuel and others (1989) showed that ..., whereas Jones and Johnson (1986) found that ...

When giving a quote or referring to a specific fact or formula in a book or from an article of more than 8 pages, the citation should include the page number. Examples:

(Chayes, 1956, p. 55) or (Matheron, 1975, p. 229).

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## References

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