



# Dietary Microbial Exposure Assessment in Adults from China and the Netherlands

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## Introduction and Objective

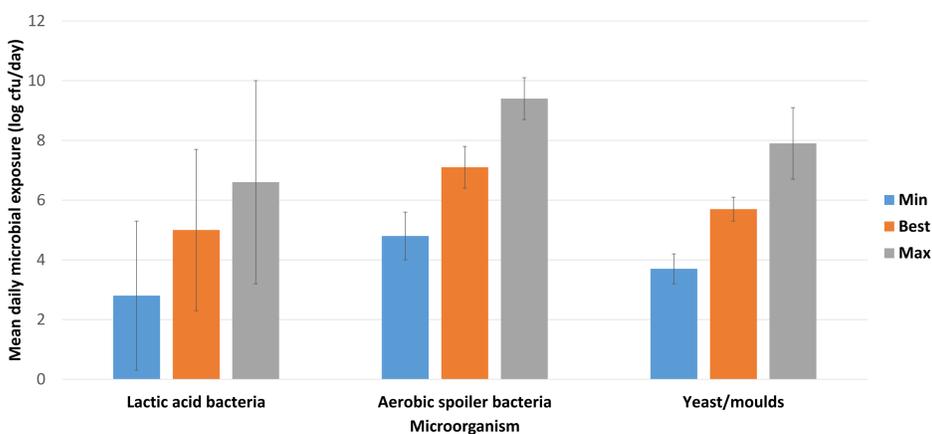
According to the revised hygiene hypothesis, exposure to microorganisms might have a protective effect against the development of allergic diseases (Liu, 2015). Earlier studies have quantified the microorganism intake through diet for the Dutch (Grijseels, 2012). However, dietary microbial intake for Chinese has not been assessed yet. The objective of this study is to evaluate the dietary microbial intake of the Chinese population and compare the intake between China and the Netherlands in order to study how the dietary pattern can affect the individual intake.

## Material and Methods

The microbial load of three dominant microbial groups in foods, being the total aerobic bacteria, lactic acid bacteria (LAB) and yeasts/moulds were estimated taking the various processing and storage condition for consumers into account (Grijseels, 2012). Three different levels of microbial loads-of the selected microorganisms were estimated accordingly. The China Health and Nutrition Survey (CHNS) 2011 provided a 3 consecutive days' 24-hour recall survey for 1250 interviewees living in Shanghai. The Dutch National Food Consumption Survey (DNFCS) conducted a 2-day 24-hour recall survey among 777 young adults aging between 18 to 30 y in the Netherlands in 2003. The dietary microbial exposure was calculated by multiplying the microbial load estimation with the consumption data of each food.

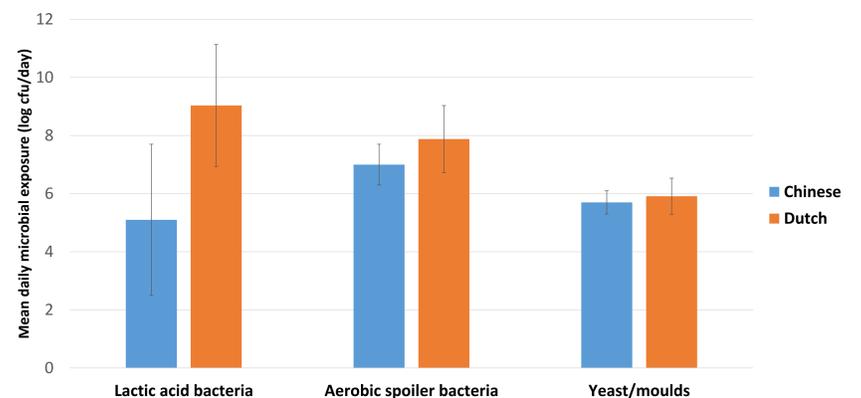
## Results

The dietary microbial exposure for Chinese is mainly determined by aerobic spoiler bacteria, whose estimated microbial intake ranged between 4.8 log cfu/day to 9.4 log cfu/day. LAB attributed least to dietary microbial intake but showed largest intake variance among three microorganism (Figure 1). Standard deviation represented the microbial intake variance between and within individuals.

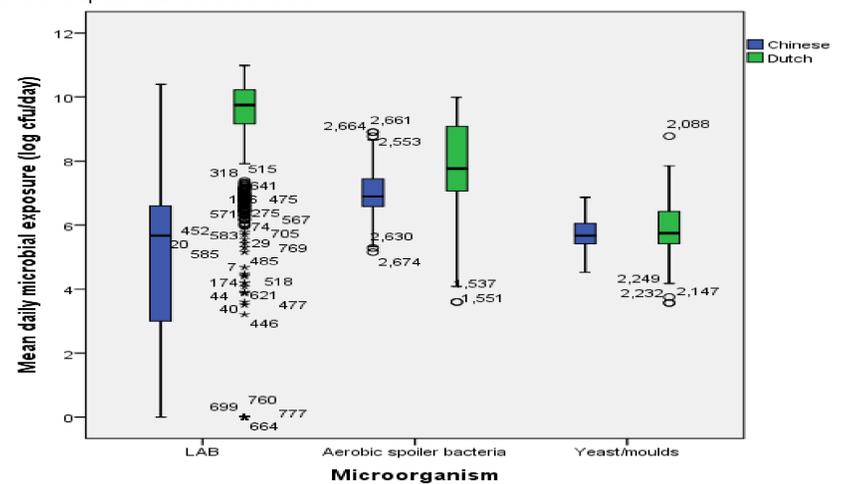


**Figure 1.** Estimation of mean microbial intake of different microorganism based on 24-hour recall for Shanghai citizens according to CHNS 2011 Error bar depicts standard deviation

The most abundant microorganisms between the Chinese and Dutch diet. LAB was responsible for most of the microbial exposure in the Netherlands. The mean daily dietary LAB exposure of Dutch was 10,000 times (4 logs) higher than that of Chinese (Figure 2). The interquartile range (IQR) of Chinese LAB intake was approximately two times larger than that of Dutch (Figure 3).



**Figure 2.** Estimation of mean microbial intake of different micro-organism based on best microbial estimation from CHNS 2011 and DNFCS 2003 (van Baar, 2012) & (Grijseels, 2012); Error bar depicts standard deviation



**Figure 3.** Mean of dietary exposure of Chinese adults and Dutch adults to LAB, aerobic spoiler bacteria and yeast/moulds base on best estimation of microbial intake

Yoghurt, estimated LAB load of 8 log cfu/g, was the most important contributor of dietary LAB exposure for both countries. With the same LAB estimates compared with yoghurt, cheese was the second important source of LAB exposure in the Netherlands. However, cheese only attributed 1% of the LAB exposure in China because of its low popularity in the Chinese diet showing the effect of dietary pattern variance on microbial exposure (Table 1).

**Table 1.** Comparison of the most relevant foods of LAB intake for China and the Netherlands

Food	China	Food	Netherlands*
	Total LAB exposure contribution (%)		Total LAB exposure contribution (%)
Yoghurt	94	Yoghurt	58
Sauerkraut	5	Cheese	28
Cheese	1	Fresh cheese	9

\*According to van Baar (2012)

## Conclusion

- Aerobic spoiler bacteria is the most abundant microorganism in the Chinese diet
- Dietary microbial intake of Dutch is generally higher than Chinese
- Dutch daily consumes 10,000 times (4 log cfu/day) more LAB than Chinese
- Yoghurt attributes to 94% of LAB dietary intake in China

## Reference

- Liu, A. H. (2015). Revisiting the hygiene hypothesis for allergy and asthma. *Journal of Allergy and Clinical Immunology*, 136(4), 860-865.
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