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The use of shotgun metagenomic sequencing for detection of *H. pylori* pre- and post-eradication: bioinformatics feasibility assessment

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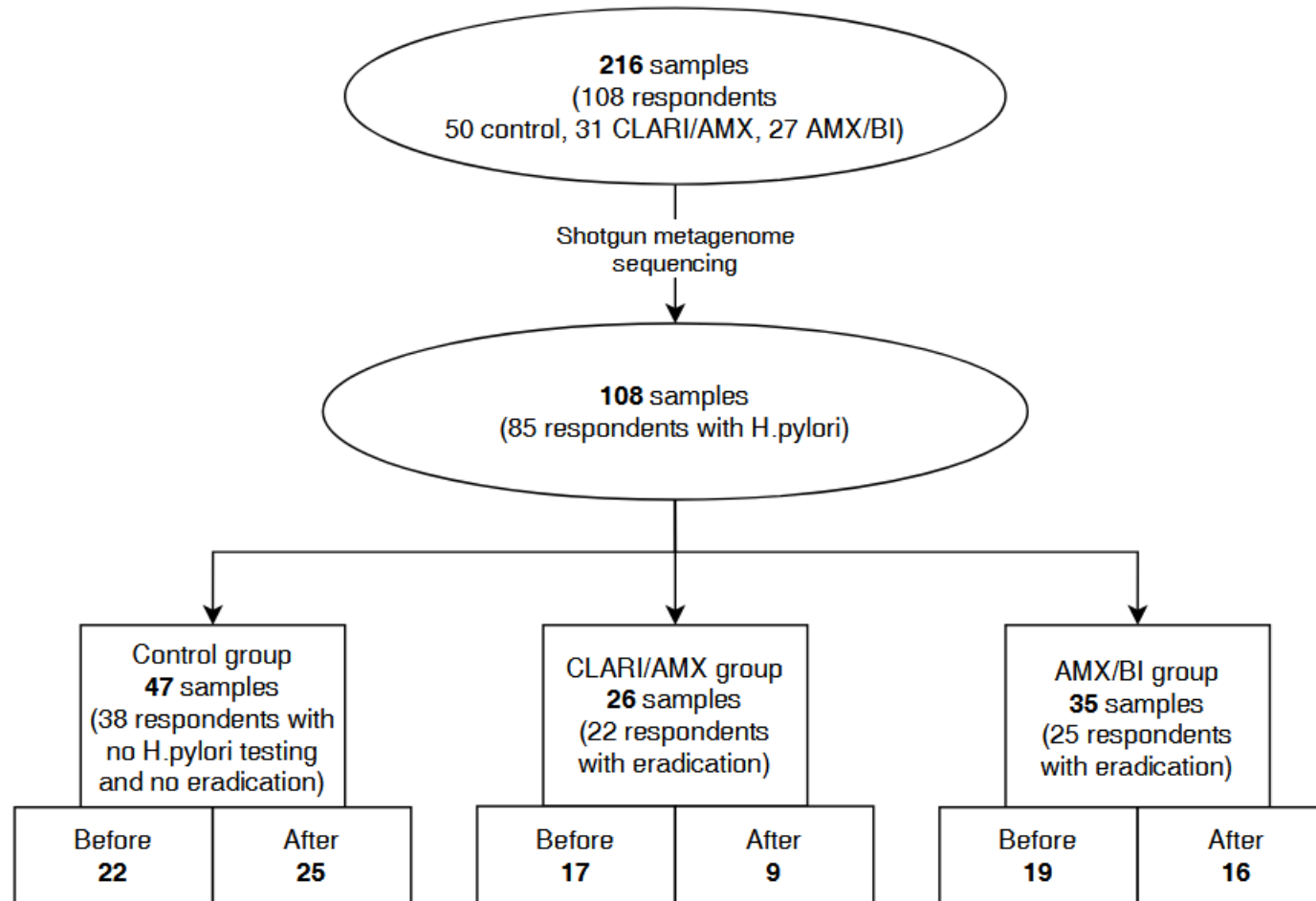
Summary

Background: Usually urea breath or stool antigen test is used for *H.pylori* detection. Shotgun metagenomic sequencing approach has not been well demonstrated.

Aim: To evaluate shotgun metagenomic sequencing and kraken2 based classification as a method for *H.pylori* identification.

Methods: Total DNA was extracted using FastDNA SPIN kit for soil, MpBio, USA. Shotgun metagenomic sequencing was performed on the DNBSEQ-G400 platform (MGI, China) using 150bp paired-end reads. At least 20 million reads were generated per sample which were quality trimmed and classified with Kraken2, using a database containing all bacterial genomes available in RefSeq (release 180 2020-12-03) and abundances were reestimated to species level with Bracken.

Results



Conclusions

- Kraken2 based shotgun metagenomics sequence classification method can be used to detect *Helicobacter pylori* species, but deeper sequencing would be required to reliably estimate their abundances.
- Different classification methods should be explored, for example, MetaPhlAn 3.0



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