

CHANGES IN HUMAN GUT MICROBIOME COMPOSITION IN RESPONSE TO RICE BRAN ARABINOXYLAN COMPOUND

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ABSTRACT

The gut microbiome plays an essential role in health and disease and can be modulated by dietary supplementation. This study investigated the effects of rice bran arabinoxylan compound (RBAC) as a dietary supplement on the gut microbiota of healthy adults. Ten volunteers supplemented their diet with 1g of RBAC for six weeks and 3g of RBAC for another six weeks, with a three-week washout period in between. Faecal samples were collected every three weeks over twenty-one weeks, resulting in eight samples per participant. Microbiota from these faecal samples were profiled using 16S rRNA sequencing on the Illumina platform. Associations of alpha and beta diversities of the microbiota with explanatory factors, such as age, were determined using the QIIME2 platform. The statistical significance of participant as a factor was detected in alpha ($p<0.002$) and beta (weighted unifrac, $p=0.001$) diversities. Other explanatory factors including age and Australian Recommended Food Score were significantly associated with alpha ($p<0.05$) and beta ($p<0.01$) diversities. Individualised beta diversity of six participants significantly changed ($p<0.05$) during the interventional period. Seven participants showed statistically significant taxonomic changes from baseline through the experimental phases (ANCOM $W\geq 5$). These results classified four participants as responders to RBAC supplementation, with a further two participants likely responders. In conclusion, gut microbiota is highly individualised and can be modulated by RBAC as a dietary supplement, however is also influenced by diet and lifestyle factors.

Keywords: RBAC, microbiota, prebiotic