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Alteration of the gut microbiome of the common carp (Cyprinus carpio L., 1758) mediated by probiotics and yeast prebiotic

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INTRODUCTION

In aquaculture, Common carp (Cyprinus carpi) is considered one of the major fresh-water fish species, with a global production of more than 4 million tonnes, representing more than 7.7% of total finfish production (FAO, 2020). Antibiotics are commonly implemented in aquaculture to overcome pathogens and diseases development, however, they are not known for their negative impact on beneficial microbes (Wang et al., 2020). The rise of antibiotic resistance and consumer safety concerns are key factors that have motivated scientists to seek for alternative control strategies, such as probiotics and prebiotics in aquaculture. The aims of the current study were to examined the impact of dietary supplementation with probiotics and yeast prebiotic on intestinal microbiota of common carp, *Cyprinus carpio.*

MATERIALS AND METHODS

A total of 96 carps with average body weight of 932±163 g were distributed into 12 fish tanks (800 L), 8 fish/tank. Fish received different types of experimental diets, including the basal diet only (CD), basal diet supplemented with the probiotic *Pediococcus acidilactici* (PA), the yeast probiotic *Saccharomyces cerevisiae* (SC), or the yeast cell wall prebiotic (YANG) at a concentration of 0.1% (1 g/ kg) for 42 days. At the end of the trial, fish digesta were withdrawn and the total bacterial community in the gut of common carp was analysed using Illumina's NGS targeting the 16S rRNA gene.

RESULTS

The Krona phyla richness pie chart (Figure 1) showed that 11 bacterial phyla were recorded in fish fed YANG, with the top three phyla being Fusobacteria, Firmicutes and Proteobacteria. In addition, 10 phyla were found in faecal samples from carp fed PA, with the top three phyla being Proteobacteria, Firmicutes and Fusobacteria. Furthermore, carps fed SC recorded 9 phyla, the top three phyla being Fusobacteria, Firmicutes and Proteobacteria. However, carp fed the basal diet only showed 14 phyla, with the most abundant phyla being Fusobacteriota, Bacteroidota and Proteobacteria.

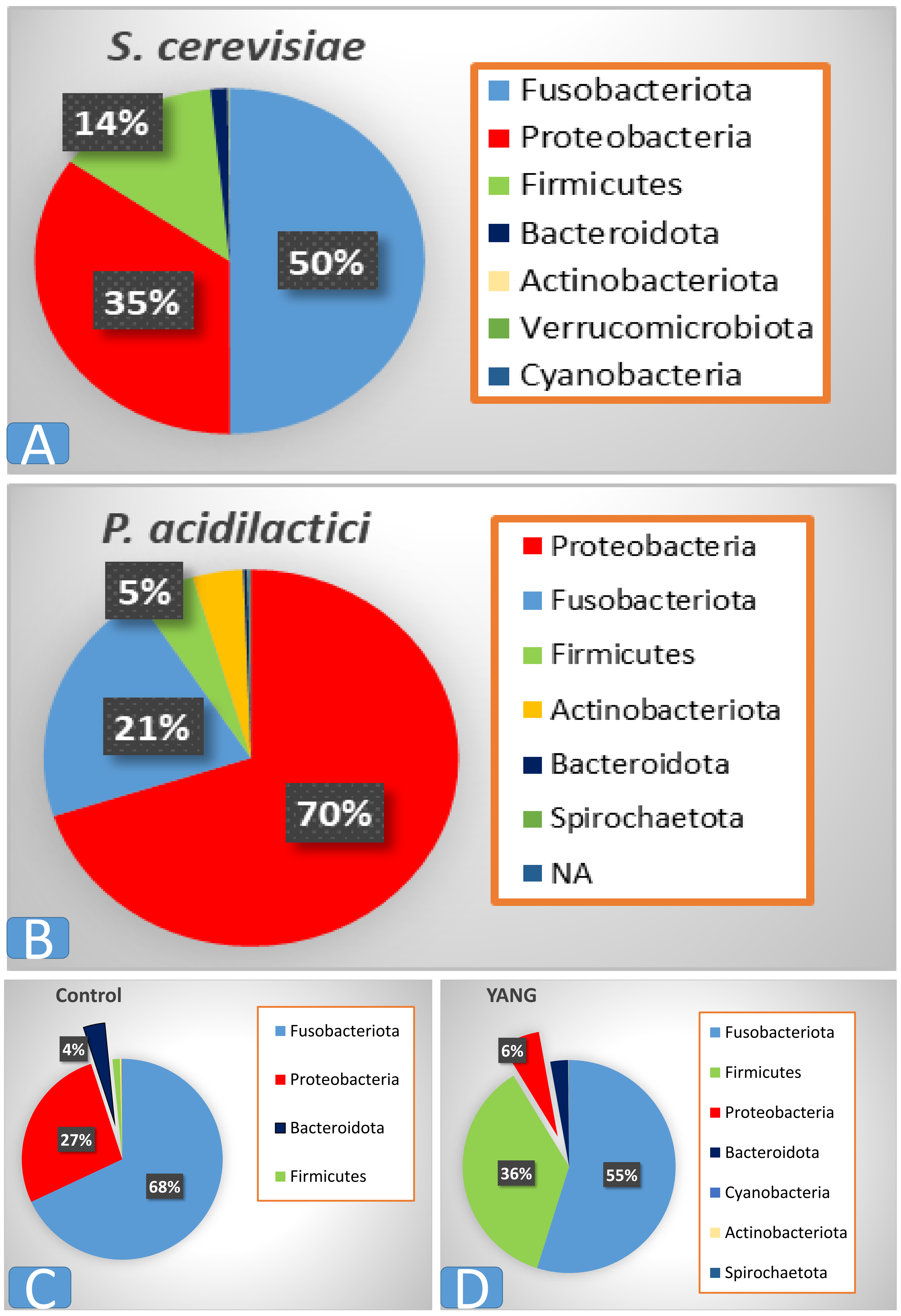

Figure 1. Krona pie chart is adjusted at the phylum level. The charts are showing the abundant of intestinal bacterial community of carps fed with (A): *S. cereviciae*, (B): *P. acidilactici*, (C): the control diet only, or (D): yeast prebiotic.

CONCLUSION

The study concluded that the tested feed supplements could cause considerable alterations in the composition of the gut microbiome of the carps reared in recirculating system.

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