**The composition of microbial community and denitrifying bacteria in full-scale woodchip fields**

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Full-scale woodchip fields, in which woodchips are the source of organic carbon for heterotrophic denitrifying microbes, are simple and cost-efficient end-of-pipe method to manage nitrate-rich aquaculture effluents. Currently, the microbial communities, as well as the key denitrifying microbes, are poorly known in woodchip fields, and the alternative nitrate reduction processes producing nitrous oxide or ammonium have been mainly neglected. To get deeper insight into the function and composition microbial communities, we studied three full-scale woodchip fields treating effluents of rainbow trout farms. The microbial community was characterized by IonTorrent PGM sequencing of 16S rRNA gene, genetic potential for nitrate reduction was determined with qPCR targeting key denitrification genes, and nitrate reduction process rates were measured using stable isotope technique. In addition, the nitrate reducing microbial communities were characterized by sequencing of *nir*S and *nir*K genes. The microbial community composition varied between three studied sites and quantification of ITS revealed fungi in the fields. The most abundant prokaryotic taxa were Epsilonbacteraeota, Bacteroidetes and Betaproteobacteria, and same core proteobacterial groups were found to drive denitrification across all sites. Incoming nitrate was consumed efficiently at all three woodchip fields: measured daily rates varied between 4.3 to 6.9 g N m3 -1 d-1, and complete denitrification was the dominant process. Quantification of denitrification genes *nir*S, *nir*K and *nos*ZI+II demonstrated equally high genetic potential for nitrate reduction at all studied woodchip fields, suggesting that nitrate concentration and hydraulic retention time were the main factors controlling nitrate removal.