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## ***nirK*-TYPE DENITRIFIER COMMUNITY COMPOSITION AND DENITRIFICATION ACTIVITY IN A BUFFER STRIP**

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### **Abstract**

Excess of chemicals can be often overcome by microorganisms, even if the time required could be too long. In order to speed these processes specific microbial populations should be supported. Leaving aside the possibility to augment the size and nature of the microbial community, the most suitable approach is to manipulate the environment in a way that will promote specific microbial populations and activities.

In the case of nitrogen, especially nitrate deriving from agricultural managements, its concentration is generally found to increase in water flow. High nitrogen contents may be reduced by forcing the water flow through a buffer strip specifically designed and possibly afforested with suitable plant species. The management of this riparian buffer may definitely affect the soil microbial activities, including denitrification, as well as the composition of the community. The purpose of this study was to verify if the particular hydraulic management, the suspension of farming practices and the development of the woody and herbaceous vegetation actually produced a change in terms of denitrifying microbial community composition as compared to that of a neighbouring agricultural area.

In order to monitoring whether the required microbiota was present and functioning in the experimental buffer area, denitrification was constantly followed and the data obtained were compared to those deriving from a direct investigation on the microbial composition of the soil population. This latter analysis was performed both as a general bacterial community analysis and as a targeted determination of specific bacterial groups involved in denitrification. In particular, this investigation was focused on *nirK* gene, encoding for nitrite reductase, an enzyme essential for the conversion of nitrite to nitric oxide, and considered the key step in the denitrification process.

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