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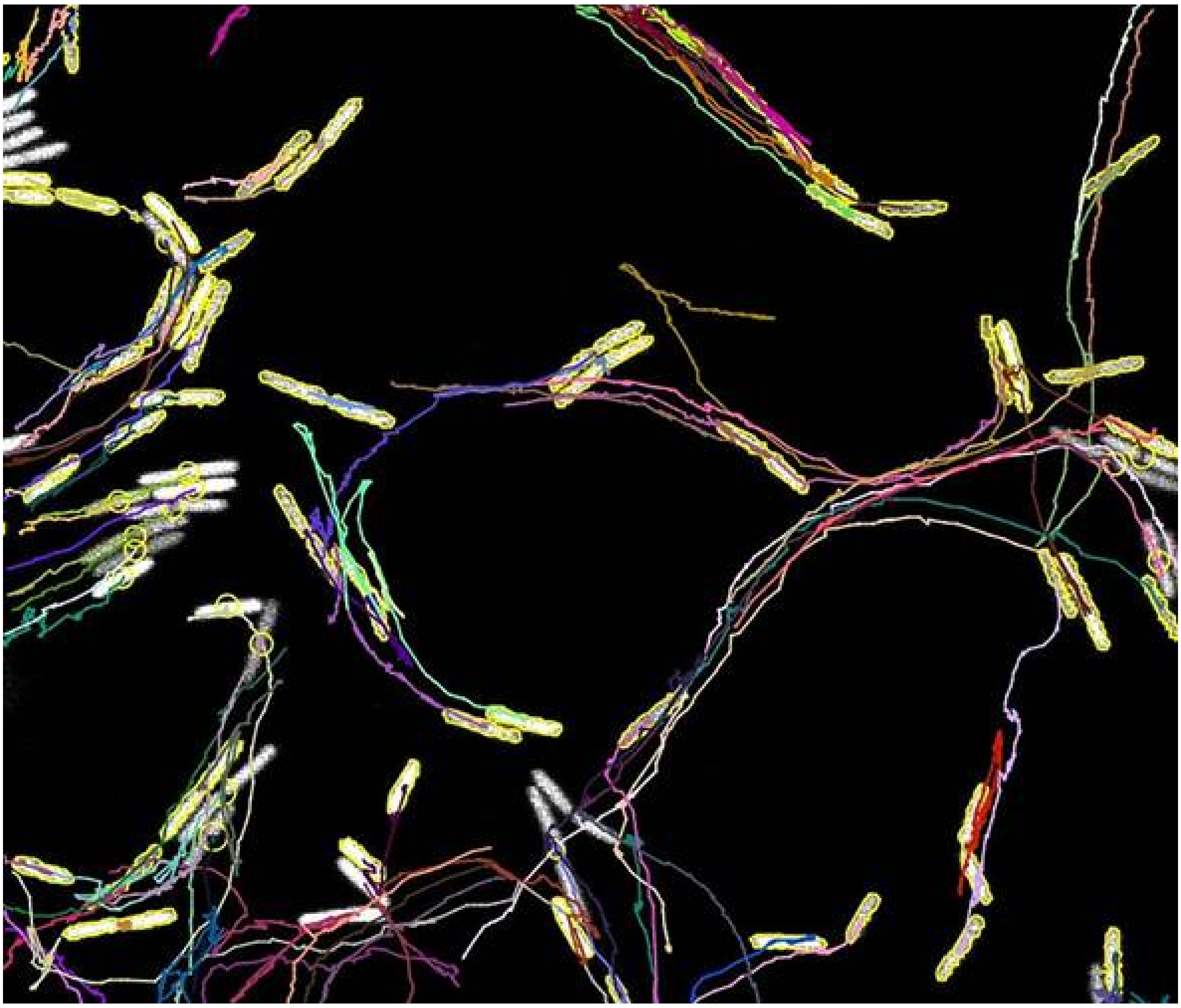

Foto: Se hace camino al andar. Celeste Dea. 1er puesto. Concurso fotográfico SAMIGE 20 años.

182 - Microbiología Ambiental, Agrícola y del Suelo

APPLICATION OF BOVINE EXCRETA IN A PASTURE AND FEEDLOT SYSTEM: EFFECT ON THE SOIL MICROBIOME AND N2O EMISSIONS

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Soil microorganisms are involved in more than 90 % of soil functions, including nutrient cycling and decomposition of organic matter. Some microbial processes, such as nitrification and denitrification, produce nitrous oxide (N_2O) as an intermediate, which contributes to greenhouse gas emissions as well as nitrogen losses from the system. N_2O emissions are often associated with nitrogen fertilisation, but in livestock systems, the dominant source is livestock deposition. To develop mitigation strategies, it is important to know the effect of the beef cattle diet, mediated by the excreta, on the soil and soil microbial communities. With this objective in mind, the influence of environmental factors, management and urine and faeces deposition on the structure of soil microbial communities during a rearing and fattening cycle in two production systems (pasture and feedlot) and their relationship with N_2O emissions was evaluated. Periods of the year associated with N_2O emission peaks were chosen from two seasons: summer and spring, and aligned with periods before, during and after the emission peaks. Analysis of microbial communities was carried out by targeted sequencing of the 16S rRNA gene for Bacteria and Archaea and the ITS region for Fungi. An exploratory non-metric multivariate analysis based on the Bray-Curtis distance was carried out to observe the clustering of the microbial community between the sources of variation studied (season, system, type of depositions), This study showed a clear separation of samples according to the pastoral and feedlot systems. However, the diversity of the microbial population, as measured by Shannon and Simpson indices, was similar across the two systems and types of depositions. Some microorganisms showed significant differences between systems, season, and deposition, However, there were no taxa that increased in abundance at peak emission and could thus be identified as the cause of the N_2O emissions. However, two amplicon sequence variants, ASV2 and ASV13, classified as Cladosporium cladosporioides and Alternaria alternata, respectively, were found to be more abundant pre-peak than post-peak of N_2O emission. In conclusion, the structure of microbial communities was affected by the fattening system, and was related to the environmental variables measured, including N_2O emissions. No significant differences were found in the diversity of the soil microbial communities during the rearing and fattening cycle in the pasture and feedlot systems on urine and faeces deposition concerning the control soil. Changes in the abundance of certain taxa of microorganisms related to the emission peaks were found, however, it was not possible to detect individual taxa whose abundance could explain the increase in N_2Oemissions. We propose the N_2O emission peak was provoked by the coordinated activity of several functionally redundant taxa.

Palabras clave: soil microbiome-greenhouse gases-nitrogen.