

P38 – Soil microbiome before and after fertilization with bovine manure

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Background: Dairy manure is commonly used for the fertilization of agricultural soils, and it includes the intestinal microbial community influenced by the feed and possible drug residues used for therapy. The excessive use of antimicrobials in animal husbandry and subsequent land application of animal wastes may introduce massive quantities of antimicrobials and resistant bacteria into the soil environment.

Objective: The objective of this paper is to evaluate the possible change of the soil microbiome after fertilization with manure coming from intensive dairy farms.

Methodology: Samples of manure and soil (before and after 30 days from fertilization) were collected from intensive dairy farms.

Microbioma of samples was determined by a culture independent approach based on NGS sequencing. All samples were also screened for detecting and quantifying the most commonly used antimicrobials (i.e. beta-lactams, fluoroquinolones, polymyxins and macrolides) by HPLC methods.

Results: All samples were negative for the antimicrobials screened. The manure microbioma was homogenous among different farms and regions of Northern Italy, but very different from the soil one. In manure, a higher presence of *Porphyromonadaceae*, *Lachnospiraceae*, *Clostridiaceae*, *Pseudomonadaceae* and *Ruminococcaceae* families was observed, whereas in soil the *Chitinophagaceae* family was the most commonly detected. After fertilization, the microbioma composition of soil was not changed, however the absence of drugs concentration in manure may have had a role in this.

Conclusions / Implications for practice: This is one of the first study evaluating the modifications of the microbial communities of dairy manure and agricultural soil before and after fertilization in Northern Italy.

References

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