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CORRELATIONS BETWEEN SOIL MICROBIAL FLORA, PLANTS AND FARM ANIMALS HEALTH IN ORGANIC FARMING

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Abstract

This study regards organic and biodynamic agriculture as forms of nature expression without interference with synthetic substances. The work is about the soil microbiology, feed plants health and the quality parameters of animal products. The author had made a parallel between the mechanisms of antibiotic resistance in humans and animals and those that generate: soil microbial disorders, plant vulnerability to pest attack and the receptivity of farm animals to infectious diseases. The factors involved in these phenomena were herbicides, pesticides and synthetic fertilizers. Using the principles of homeopathic treatments, associated with the biodynamic farming doctrines for the rehabilitation of denatured soils, on new scientific basis, the study demonstrated the possibility of recovering degraded land from human actions.

Key words*: animal health, biodynamic agriculture, soil microorganisms.*

INTRODUCTION

Despite the fact that world agricultural production is steadily increasing, as a consequence of the increase in the world's population, more and more signals announce a collapse of the productive capacity of the soil with dramatic consequences for the future. Faced with these challenges, many companies have tried in recent decades to find solutions for avoiding a food catastrophe.

The variables are the following: soil health, fodder plant diseases, animal diseases and ultimately public health. Methods of control used up to now: pesticides, herbicides, antiparasitics, antibiotics, pH and GMOs reduce their efficiency from year to year. As a result, scientists are trying to find solutions to develop healthy and renewable farming methods, while pursuing the recovery of land compromised by conventional practices used in the past.

Starting from the concept of biodynamic agriculture (Steiner, 2012) enunciated by Rudolf Steiner in 1924 and subsequently applied in practice both in Europe and the USA, more and more farmers approached agricultural sciences at an unconventional angle, considered for decades to be a pseudoscience. In recent years, due to the advances made in the study of human microbiome, rhizomicrobiome and nanotechnology, these practices have begun to be reconsidered (Teruo and Parr, 1994). This study has demonstrated that biodiversity is the essence of balance in nature (Chhabra, 2017). Interaction between microbial flora populations often determines the biodiversity of plants.

Any human action designed to eliminate certain species considered harmful, both microscopically and macroscopically, inevitably leads to a global dysfunction of the biotope with adverse consequences already known in agriculture (Sohag et al., 2010). Recent data show that up to 10 billion bacteria and 10 million fungi (de Vrieze, 2015) can be found in the soil around each rhizosphere. Microbes have multiple functions in the soil: they can provide plants with nutrients and minerals from the soil, produce growth stimulating hormones, stimulate the immune system of plants, and trigger or mitigate stress responses.

MATERIALS AND METHODS

Four farms from different pedoclimatic areas were selected to track the soil, plant, animal or human route. The first location was in the Burnaz Plain on the Teleorman River bank, the second in Bărăgan Lehliu – Dor Mărunt area, the third on the bank of the Bârsa brook, on a

plot belonging to Vulcan village, and the fourth in the region of the Precarpathian hills in the Breaza area. Corn fodder and wheat have been grown in the meadow or in the plain areas. In the hilly region the basic crop was that of vegetables. Each ranch, with the exception of the vegetable one, owns a beef and/or a dairy farm. Soil samples were collected from each farm after protocols agreed by statisticians. Twenty dominant bacterial species and five mushroom species were identified. Laboratory examinations were done in the pedology laboratory in Pécs. In addition to qualitative tests, two simple and inexpensive methods were used to measure microbial activity in the soil: the respirometry method and the cotton strip test method (image analysis and tensometer) (Gunasekhar et al., 2007).

In November 2015 samples of compost soil with cow dung were collected and were placed in a cow horn. The horn was buried in the ground with the bottom down to about 20 cm deep. The central area of the plot was chosen as the place of choice for soil sampling and horn burial. In April each horn was dug out and the content was placed in a container of five hundred liters of water. The liquid was mixed continuously for an hour, using the Hanemann method, in order to obtain a dynamization dilution (Bellavite, 2005). With the help of sprinklers, the solution was sprinkled on three hectares of cereal crop for each cattle farm (six containers per hectare) and on 1000 m^2 of vegetable farm. A second identification of the microbial flora was performed one year after the first harvest. At the same time, the productive characteristics of the parcels were determined, following the quality of the vegetal material, the degree of parasitic attack, the health status of the animals fed with these fodders and the quality of the products obtained from them (Miller-Ensminger, 2018).

RESULTS AND DISCUSSIONS

The bacterial species identified in the previous year were also found in the following year, with the difference in population proliferation that changed sensitively. The species found in the soil were: *Acidobacterium capsulatum, Azotobacter agilis, Azotobacter salinestris, Azotobacter chroococcum, Arthrobacter aurescens, Bacillus thuringiensis, Bacillus coagulans, Bacillus subtilis, Thiobacillus thiooxidans, Thiobacillus denitrificans, Chromatium okenii, Frankia asymbiotica, Methanobrevibacter smithii adhaesiva, Rhizobium aggregatum, Methylobacterium organophilum, Nitrobacter vulgaris, Rhodopseudomonas palustris, Rhodobacter sphaeroides, Xanthomonas perforans* (Table 1, Table 2 and Table 3).

The identified mushroom families were: *Aspergillus, Rhizopus, Trichoderma, Penicillium, Fusarium*.

Table 1. Bacterial species ratio in farm 1

Bacterial species	2016 (%)	2017 (%)
1. Acidobacterium capsulatum	5.5	9.5
2. Azotobacter agilis	0.1	0.3
3. Azotobacter salinestris	10.1	5.4
4. Azotobacter chroococcum	1.7	2
5. Arthrobacter aurescens	1	0.5
6. Bacillus thuringiensis	14.7	5.8
7. Bacillus coagulans	5.1	8.1
8. Bacillus subtilis	2.8	1.8
9. Thiobacillus thiooxidans	5.3	9.4
10. Thiobacillus denitrificans	3.6	8.3
11. Chromatium okenii	2.8	1.3
12. Frankia asymbiotica	0.9	0.4
13. Methanobrevibacter smithii adhaesiva	4.8	3.1
14. Rhizobium aggregatum	1.5	2.1
15. Methylobacterium organophilum	2.3	3.4
16. Nitrobacter vulgaris	6.1	10.8
17. Rhodopseudomonas palustris	8.8	14.3
18. Rhodobacter sphaeroides	4.7	3.5
19. Xanthomonas perforans	6.1	3.8
20. Holophaga foetida	12.1	6.2

Table 2. Bacterial species ratio in farm 2

Bacterial species	2016 (%)	2017 (%)
1. Acidobacterium capsulatum	6.1	7.2
2. Azotobacter agilis	0.3	0.5
3. Azotobacter salinestris	8.7	7.2
4. Azotobacter chroococcum	2.2	1.3
5. Arthrobacter aurescens	1	1.5
6. Bacillus thuringiensis	15	11
7. Bacillus coagulans	7.8	5.8
8. Bacillus subtilis	4.3	4.1
9. Thiobacillus thiooxidans	3.1	2.8
10. Thiobacillus denitrificans	2.4	8.6
11. Chromatium okenii	4	3.3
12. Frankia asymbiotica	0.1	0.2
13. Methanobrevibacter smithii adhaesiva	6.2	7.9
14. Rhizobium aggregatum	3.9	3.6
15. Methylobacterium organophilum	1.8	1.1
16. Nitrobacter vulgaris	8.4	12.4
17. Rhodopseudomonas palustris	5.2	7.2
18. Rhodobacter sphaeroides	3	9.3
19. Xanthomonas perforans	2.5	2.6
20. Holophaga foetida	14	2.4

Table 3 – Bacterial species ratio in farm 3

Bacterial species	2016	2017
1. Acidobacterium capsulatum	7.5	2.9
2. Azotobacter agilis	0.5	4.1
3. Azotobacter salinestris	8	6.3
4. Azotobacter chroococcum	3.9	2.2
5. Arthrobacter aurescens	1.2	1.9
6. Bacillus thuringiensis	12.5	6.4
7. Bacillus coagulans	9.1	11.7
8. Bacillus subtilis	5.6	6.1
9. Thiobacillus thiooxidans	0.7	5.4
10. Thiobacillus denitrificans	1.2	8.9
11. Chromatium okenii	3	4
12. Frankia asymbiotica	1	0.5
13. Methanobrevibacter smithii adhaesiva	11	7
14. Rhizobium aggregatum	7.8	6.7
15. Methylobacterium organophilum	0.6	1.1
16. Nitrobacter vulgaris	0.8	0.4
17. Rhodopseudomonas palustris	18	9
18. Rhodobacter sphaeroides	2.8	5.8
19. Xanthomonas perforans	1.2	5.2
20. Holophaga foetida	3.6	4.4

By the respirometry method, microbial biomass was determined in the soil on the twelve day of incubation. On soils treated with dynamized solution, microbial biomass increased significantly between 200% and 250%. Testing the resistance of cotton tape on buried fibers for 35 days with the tensometer, as well as image analysis by the color intensity measurement technique, confirmed an increased enzyme activity in experimental plots.

The primary production obtained on the tested land parcels as compared to the witness one showed superior quality of the plant material used for silos with better consistency and an increase in the amount of gluten from the seeds. The palatability of the silo improved, the animals showing a higher appetite than those in the witness group. As far as the secondary production is concerned, the quality of the carcasses in Angus cows was higher by 5 - 8% compared to those fed with the feed on the witness group (Figure 2). The morbidity of juveniles was 0 whereas in the witness group there were 5 cases of illness (group of 25 heads). The amount of milk harvested from the experimental plots was 8 -10% higher than the witness one (Figure 1), the microbial load and the number of somatic cells, lower.

In terms of soil fertility, three large groups of microorganisms have been identified, that live in different proportions. The first is that of positive microorganisms involved in soil regeneration. The second is that of negative organisms that contribute to soil degeneration.

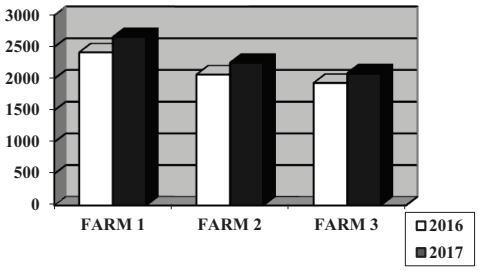

Figure 1. Evolution of milk production
2016 – FARM 1: 105 dairy cows *23 l/day
FARM 2: 86 dairy cows *24 l/day
FARM 3: 69 dairy cows *28 l/day
2017 – FARM 1: amount of milk higher 10%
FARM 2: amount of milk higher 9%
FARM 3: amount of milk higher 8%

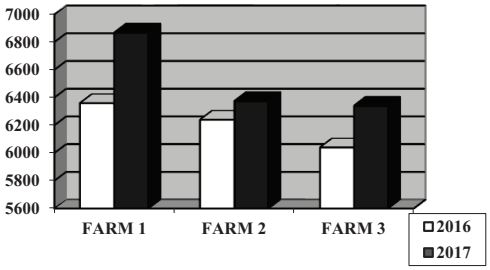

Figure 2. Evolution of the carcasses quality
2016 – FARM 1: 20 Angus cows *318 kg/carcass
FARM 2: 20 Angus cows *312 kg/carcass
FARM 3: 20 Angus cows *302 kg/carcass
2017 – FARM 1: quality of carcasses higher 8%
FARM 2: quality of carcasses higher 6%
FARM 3: quality of carcasses higher 5%

The third one has a neutral but also opportunistic manifestation. It join the first group or the second group according to small changes in the environment. By multiplying these microorganisms we can potentiate the effect of the first or of the second. Conventional agriculture can destroy soil rhizobioma (microbial ecosystem) by using foreign substances, such as fertilizers and pesticides, without compensating for these effects.

Although the studies are still in a preliminary stage, many variables needing to be controlled, we can say that by the "potentialization" of the matter by dynamization, the soil microorganisms populations transfer positive properties to the inorganic substrate, affecting the structure and fertility of the soil. During plant domestication, they were selected for crop-related attributes, but not for plant-friendly associations with a beneficial microbiome.

Agriculture can destroy soil rhizobioma (microbial ecosystem) by using soil modifications, such as fertilizers and pesticides, without compensating for their effects. On the contrary, healthy soil can increase fertility in a number of ways, including supplying nutrients such as nitrogen and also protecting against pests and viral, bacterial or fungal diseases.

CONCLUSIONS

The composition of rhizobiome can change rapidly in response to changes in the environment. By Hanemannian, dinamization of the compost solution, opportunist organisms join the positive action helping to recover compromised soils.

Even minor changes in the amount of certain bacteria can have a major effect on plant defense and physiology.

On the contrary, healthy soil can increase fertility in several ways: providing nutrients such as nitrogen and protecting against pest and viral, bacterial or fungal diseases.

A more diversified soil microbe stimulates plant biodiversity and results in increased yields and reduced animal disease.

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TECHNOLOGIES OF THE AGRO FOOD PRODUCTS PROCESSING