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THE INFLUENCE OF AMELIORATION MEASURES ON THE STRUCTURE AND ACTIVITY OF SOIL MICROBIAL COMMUNITIES IN EXPERIMENTAL FIELD MAXINENI-CORBU NOU

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Abstract: *The main purpose of the study presented in this paper was to assess the influence of amelioration measures on the soil microbial communities and their physiological activities in experimental field from Maxineni-Corbu Nou. Since in literature there are few data and information on the relationships between the amelioration processes and soil microbiological activity in saline soils, researches aiming to highlight the changes that occur, both in their activity and qualitative and quantitative distribution of microorganisms in relation to soil desalination were developed. The concept of intensive amelioration of saline soils includes both the application of a set of agropedoameliorative measures based on drainage and irrigation, adapted to specific conditions and restoration of biological activity. To highlight the main aspects of microbiological activity in saline soils, measurements in the experimental field Maxineni-Corbu Nou from Braila county were done. This field was established in 1977 and had as primary objective the intensive improvement of saline soils. Previous researches have been carried out in this region to describe the natural peculiarities and the main physical, chemical and biological properties of the salinized soils and to apply the most appropriate measures for preventing their degradation. The present research assessed the effects of these measures by monitoring the development of bacterial and fungal communities, as well as the physiological activities, expressed by the potential level of soil respiration. This new method was recently applied to the study of these soils, instead of other methods based on the evaluation of dehydrogenase activity. The paper brings to date the information concerning the actual state of the soils from experimental field Maxineni-Corbu Nou, with respect to microbial community, important by their implication in most processes that usually take place into the soil. The research is carried out within the postdoctoral research national project PN II RU - PD Contract 192/10.08.2010.*

Key words**:** *bacteria, fungi, soil respiration*

INTRODUCTION

As regarding the experimental field Maxineni-Corbu Nou, this is strongly affected by soil degradation processes as a result of major changes that occurred since the total impoundment of rivers Siret, Buzau and Ramnicu Sarat. The state is constantly improving due to an appropriate draining system.

From the physico-geographical point of view, the territory of the experimental field is situated in the Low Plain of Siret and includes a series of specific microrelief forms characteristic to alluvial accumulative areas.

The representativeness of experimental field is assured by the existence of major issues at both micromorphological and other natural conditions with a wide swing in area of the Low Plain of Siret and other alluvial areas.

Researches on both microbial activity in these soils, and on changes caused by the application of specific measures for improving the development and diversity of microorganisms, while diminishing the effects of stress exerted by the high content of soluble salts, exchangeable sodium, etc., have been restricted. However, most researches have highlighted the important role of biological activity in restoring and maintaining the fertility of these soils degraded by salinization.

MATERIAL AND METHODS

The experimental field consisted in several parcels, related to the type of arrangement (without drainage, open channels, drainage with pipes and rice field).

The soil samples were collected on the genetic horizons of H2 plot (P1 soil profile), representative for the improvement of soils located in depressions, formed on stratified alluvial deposits with clayly texture, and A4 plot (P2 soil profile), representative for the improvement of soils situated on large hillocks formed on layered alluvial deposits with loamy-sandy texture.

Soil sampled from each genetic horizon of the two profiles was analyzed from a microbiological point of view. Thus, soil decimal dilutions were plated on solid specific culture media, respectively PDA for fungi and Topping for heterotrophic bacteria. Petri plates were incubated and developed colonies counted.

Taxonomic composition of microbial populations was established according to determinative manuals: BERGEY's (HOLT et al., 1994) for bacteria, DOMSCH & GAMS (1970) and SAMSON & HOEKSTRA (1988) for fungi.

The global microbial activity was estimated by substrate induced respiration method (STEFANIC, 1992) and expressed as the quantity of CO_2 evolved from microbial metabolism.

RESULTS AND DISCUSSIONS

Analysis of data revealed that microbial communities structure and activity presented specific features for each soil profile as a function of environmental parameters generated by previous melioration measures.

Generally, higher values of microbiological parameters were registered for P1 profile than for P2 profile.

Potential level of soil respiration was high in Ap and Am horizons of P1 profile and moderate in the deeper C horizons (Fig. 1). A moderate microbial activity was measured in Ap and Amsa horizons, then it decreased with the depth to low levels of 30.213 mg CO_2x100 g^{-1} registered in C horizon (Fig. 2).

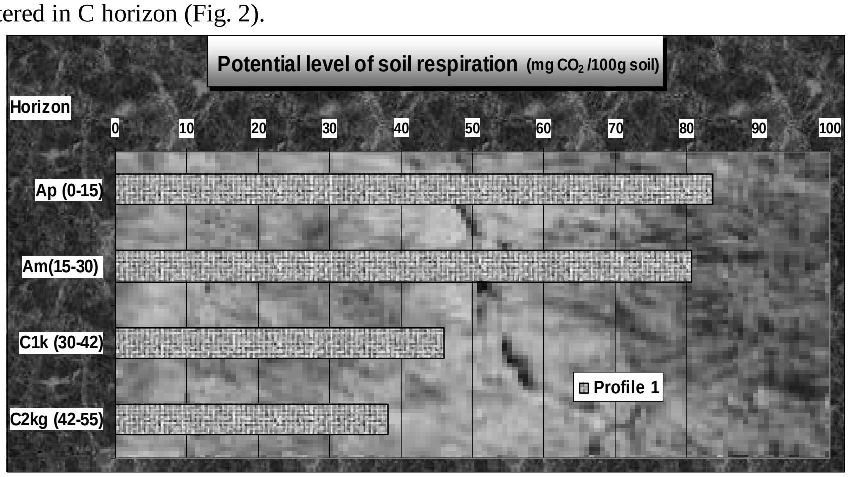

Figure 1. Potential level of soil respiration in soil profile P1 from Maxineni-Corbu Nou

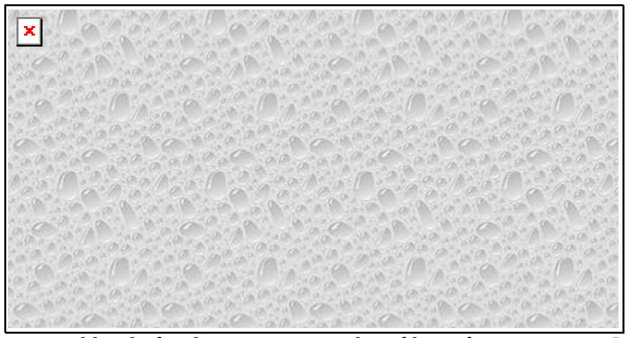

Figure 2. Potential level of soil respiration in soil profile P2 from Maxineni-Corbu Nou

Bacterial counts revealed the abundant development of this group of microorganisms, with higher values in upper horizons, better aerated than deeper ones. The abundant bacterial microflora in P1 profile (Fig. 3) was represented by 10 species belonging to genera *Bacillus, Pseudomonas, Arthrobacter, Azotobacter* and by actinomycetes from series Albus and Fuscus. Bacteria less numerous from P2 profile (Fig. 4) was represented by 11 species of the same genera, 9 of them common with those from P1 but only actinomycetes from series Albus (Table 1).

The species *Azotobacter chroococcum* isolated from both soil profiles from Maxineni-Corbu Nou, considered as a microbial indicator for improved conditions (MIHALACHE et al., 1989a), was also reported after the first stage of melioration of these soils (MIHALACHE et al., 1989b).

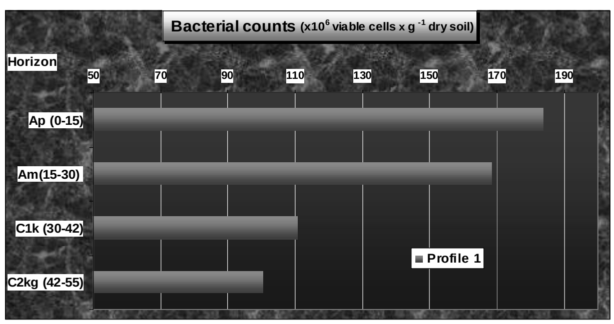

Figure 3. Bacterial counts in soil profile P1 from Maxineni-Corbu Nou

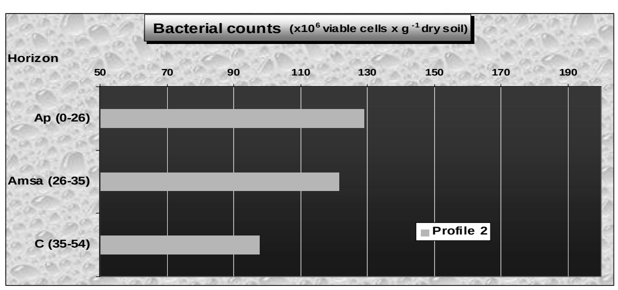

Figure 4. Bacterial counts in soil profile P2 from Maxineni-Corbu Nou

Fungal counts in P1 profile (Fig. 5) presented high values Ap and Am horizons, then decreased to moderate and low effectives in C horizons.

In P2 profile, high numbers of fungi at upper A horizons but low in C horizon (Fig. 6).

A number of 15 species were identified in P1 and 16 in P2 profile, with 5 common species. Many of them are cosmopolitan and belong to genera *Penicillium*, *Aspergillus*, *Fusarium* or *Cladosporium*. The presence of representatives of these genera was also reported in former analyses in soils from Maxineni-Corbu Nou (MIHALACHE, 2000).

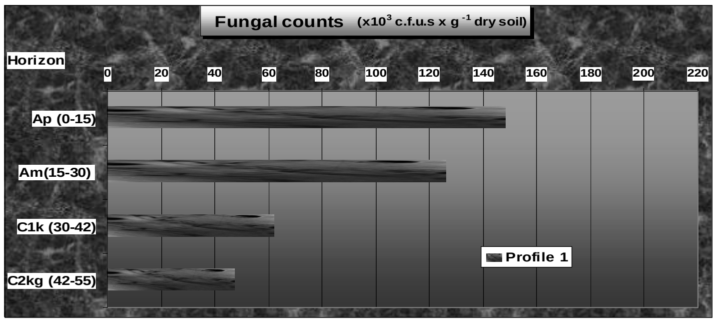

Figure 5. Fungal counts in soil profile P1 from Maxineni-Corbu Nou

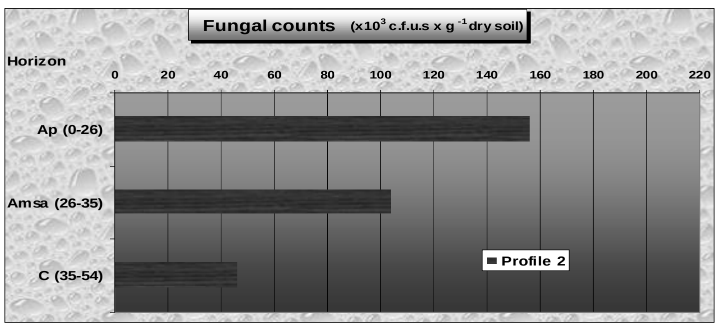

Figure 6. Fungal counts in soil profile P2 from Maxineni-Corbu Nou

Table 1

Bacterial species in P1 and P2 soil profiles from Maxineni-Corbu Nou

Bacterial species	
P1	**P2**
Bacillus cereus	***Bacillus circulans***
Bacillus megaterium	***Bacillus megaterium***
Bacillus circulans	***Bacillus cereus***
Pseudomonas sp.	***Pseudomonas fluorescens***
Pseudomonas pseudogleyi	***Bacillus subtilis***
Arthrobacter simplex	***Pseudomonas sp.***
Arthrobacter globiformis	***Arthrobacter globiformis***
Pseudomonas fluorescens	***Bacillus cereus* var. *mycoides***
Azotobacter chroococcum	***Arthrobacter simplex***
Bacillus cereus* var. *mycoides	***Azotobacter chroococcum***
	Arthrobacter simplex
Actinomycetes Series Albus and Fuscus	**Actinomycetes Series Albus**

Table 2

Fungal species in soil profiles P1 and P2 from Maxineni-Corbu Nou

Fungal species	
P1	**P2**
Penicillium glabrum	***Penicillium* sp.**
Aspergillus fumigatus	***Aspergillus terreus***
Aspergillus terreus	***Fusarium oxysporum***
Penicillium verrucosum	***Cladosporium herbarum***
Fusarium oxysporum	***Aspergillus fumigatus***
Rhizopus stolonifer	***Cladosporium cladosporioides***
Cladosporium herbarum	***Absidia corymbifera***
Cladosporium sphaerospermum	***Alternaria alternata***
Penicillium janthinellum	***Fusarium culmorum***
Absidia glauca	***Coemansia pectinata***
Acremonium strictum	***Torula herbarum***
Mucor racemosus	***Phyalophora fastigiata***
Scopulariopsis brevicaulis	***Geotrichum candidum***
Fusarium equiseti	***Aureobasidium pullulans***
Mortierella sp.	***Acremonium strictum***
	Calcarisporium arbuscula

CONCLUSIONS

Microbiological analyses revealed the beneficial effect of measures applied in soils from Maxineni-Corbu Nou, creating conditions for development of soil bacteria and fungi.

Bacterial and fungal communities were better developed in A horizons from the soil surface and less in deeper horizons.

Bacterial species belonged to genera *Bacillus, Pseudomonas, Arthrobacter, Azotobacter* and to actinomycetes from series Albus and Fuscus, 9 of them common in both soils.

The species *Azotobacter chroococcum* considered as a microbial indicator for improved conditions was isolated from both soil profiles from Maxineni-Corbu Nou.

Fungal species belong usually to genera *Penicillium, Aspergillus, Fusarium* or *Cladosporium.*

Soil respiration follows the development of microbial populations, with higher intensity of metabolic activities and CO_2 released in soil upper horizons than to the depth.

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