EFFECT OF LAND MANAGEMENT ON SOIL YEAST DIVERSITY

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Abstract - More knowledge about the effects of human activities on biodiversity are needed. The information of biodiversity of soil is still very limited in a hot climatic regions. Therefore, we assessed the diversity of soil yeasts and responses to land management. A total of 95 yeast strains were isolated and identified from 45 different soil samples. The samples were taken from three different sites according to the gradient of land management intensity (wildlands, orchards and agricultural fields). Overall, yeasts species composition of the different sites was very heterogeneous, and nearly half of the species were found in a single system only. We found that poor land-management has a strong negative impact on the soil biodiversity. Showed the results of molecular analysis that (21, 11 ,6) yeast species were identified respectively. Soil microbial communities in Iraq remains unexplored to a large extent, this is the first study to assess soil yeasts diversity under different management lands in Iraq and neighboring countries (the middle east).

Keywords - Yeast Diversity; Lands Management ; Soil Biota; Sustainable Agriculture; Soil Health; Hot Climatic Regions

I. INTRODUCTION

In nature, soil is one of the most intricate and diverse ecosystems on the earth (1; 2). Where it has a wide range of different organisms that interact with each other to contribute to biogeochemical cycles that make life possible (3; 1). Soil biodiversity is essential to ensure soil health and continuation of life in any ecosystem (3). Soil microorganisms play an indispensable role in ecosystems, including nutrients recycling, soil organic matter regulation and soil aggregate stabilization in addition to symbiotic relationship with plants, and that way play a major role in the productivity and sustainability of ecosystems (4; 5; 6; 7). Biodiversity loss in soil has significant environmental consequences (8) . The occurrence of yeasts in the soil promotes the growth of plants and other microbes by contributing to the recycling of key soil elements such as nitrogen and sulfur as well as their important role in maintaining soil structure (9; 10).

Most studies conducted in temperate forest soils (which are considered unmanaged cultivated land) of different parts of the world have shown that there is a significant abundance of yeast diversity (11; 12; 13). While Slavikova and Vadkertiova (14), showed that 78.4 - 86.6 % of total yeast species counts in agricultural soils (which are considered intensively managed lands) was belonging to only four species. Poor land-management practices such as Intensity of tillage and the use of inorganic fertilizers and pesticides has a significant impact on soil microbial communities (14; 15; 16). Human activities have often had a negative impact on biodiversity, which may threaten ecosystems (17).

Soil microbial communities in Iraq remains unexplored to a large extent, especially when Iraq is one of the most extreme countries in the temperature and climate change on the planet. Accordingly, this study aims to assess the diversity of soil yeasts and the impact of land management on it under different management systems.

II. MATERIALS AND METHODS

A. Study area and sampling

Iraq's agricultural sector suffers from deterioration and decline continuously under severe economic political conditions for decades. The last statistical indicate a great decrease in vegetation cover, as many orchards are converted to urban areas, which led to significant damage and losses in this sector. . In this context, there are losses of agricultural lands area with the increase of semi – arid areas throughout the country. Moreover, Iraq's ecosystems suffer from severe environmental and climatic conditions such as extreme high temperature (more than 48 ºC in some summer days) and low annual rainfall (18; 19; 20; 21). Sampling were carried out between Sep. and Oct. 2018. In total, 45 soil samples were collected from different sites in Baghdad, Iraq (33º 25 - 33º44``N , 44º16` - 44º29`E). The samples were taken from three different management systems according to the land management gradation from unmanaged natural lands (wildlands) to managed lands (orchards) and then intensively managed lands (agricultural fields), 15 samples per system. Soil samples were collected using a soil column cylinder, with a distance of not less than 10 meters between samples within one plot (sampling site). Samples were sifted from impurities and put into a glass containers sterilized and transported to the laboratory on ice for analyses.

B. Isolation of yeasts

The serial dilution method was used of all the soil samples, 1 g from each soil sample were placed in tube and 6 – fold diluted with sterile water. the suspension were shaken in an orbital shaker at 200 rpm for 1 hr. 100 µl was plated on the surface of plates. Glucose yeast extract peptone agar (GPYA)

was used for isolation of yeasts, 3 replicates (subsamples) were analyzed from each dilute. Based on environmental conditions was selected of incubation temperature at 27 ±1 ºC. Colonies were examined and counted after 3 days, viable count of yeasts colonies were achieved macro-microscopic differentiation of yeast (22). The values were statistically analyzed using ANOVA.

C. DNA extraction and identification of yeasts Genomic DNA was extracted from the samples using the FastDNA®kit (MP Biomedicals LLC, lrvine, CA). Completed the procedure using the yeast protocol and manufacturer company instructions. PCR technique was used to detect yeasts species using specific primers for the D1 / D2 domain of 26S rRNA gene was amplified using the primers NL1 (5`-GCA TAT CAATAA GCG GAG GAA AAG-3`) and NL4 (5`-GGT CCG TGTTTC AAG ACG G-3`) (MWG Biotech). The internal transcribed spacer (ITS) sequences were obtained using the forward primer ITS1 (5`-TCC GTA GGT GAA CCT GCG G-3`) and the reverse primer ITS 4 (5`-TCC TCC GCT TAT TGA TAT GC-3`) (MWG Biotech). Sequences were carried out using an Applied Biosystems DNA sequencer using standard protocols. Sequence alignment were made using Meg Aliga DNA STAR Lasergene. All sequences obtained were compared with sequences from GenBank database (http:// www. ncbi. nlm. nih. gov/BLAST) using BLASTN search algorithm.

III. RESULTS AND DISCUSSION

In this work, the effect of lands management on soil yeast diversity was studied from different sites in Baghdad. A total of 95 yeast strains were isolated from 45 different soil samples. The number of yeast isolates obtained from orchards, agricultural fields and wild lands soil samples were (47, 39, 9) respectively. Whereas, the average number of yeasts obtain was (5.75×10^3 , 2.82×10^3, 0.73×10^2) CFU g-1 of soil respectively with no significant ($p > 0.05$) difference between the samples at the system level. The yeast quantity were higher in orchards than in agricultural field soils, while significantly decreased in wild soils (Figure 1). These results indicate that land management and other factors directly affect the yeast activity in the soil.

Table 1 shows the results of molecular analysis of yeast species obtained using a specific primers for 26S rRNA gene and (ITS) sequences. In the orchard soils, it has been recorded 22 yeast species belonging to 11 genera (Aureobasidium , Bulleromyces, Candida,Cryptococcus, Debaromyces, Lindnera , Pichia , Rhodotorula , Schwanniomyces , Torulaspora , Trichosporon). In contrast, 10 yeasts species belonging to 5 genera (Aureobasidium, Candida, Cryptococcus, Rhodotorula, Saccharomyces) were obtained from the agricultural fields. When comparing these results roots of plants contain a variety of fungi that have symbiotic relationships with each other (26; 27). Therefore, the agricultural system is one of the most important factors to maintain the diversity of soil biota.

shows a significant decrease of the yeasts diversity in agricultural fields (diversity loss exceeds 50%) (Figure 1,2). These results agree with Slavikova and Vadkertiova (14) that the yeast diversity in agricultural soils (intensively tilled soil) was significantly lower when compared with unmanaged lands. Wagg et. al (8) also mentioned the intensification of land use leads to change in soil microbial communities. Agricultural fertilizers and pesticides have a strong impact on biodiversity and the activity of microorganisms in soil (23). As Banerjee et, al (7) indicated That farming using organic fertilizers and without tillage has led to an increase in the diversity and abundance of soil fungi, while the intensification of farming has a strong negative impact on soil microbiome.

Moreover, the results of current study indicates that diversity in wildlands is very low (diversity decreased by approximately 73% compared to orchards) (Figure 1,2). Six species, all of which belong to only three genera (Candida, Cryptococcus, Pichia) although these lands are unmanaged (Table 1). This can be explained by the fact that the most wildlands in Iraq is a semi – arid region (more than 80% of the country) (19; 20). Which are an environment characterized by low nutrient concentrations and water content (24), and scarcity of vegetation (22). Borowik & Wyszkowska (25), found that the optimum soil moisture for growth of fungi was at the level of 60% . Thiele-Bruhn et. al,(23) also indicated that microbial diversity of soil depends on plant diversity and vice versa. As the

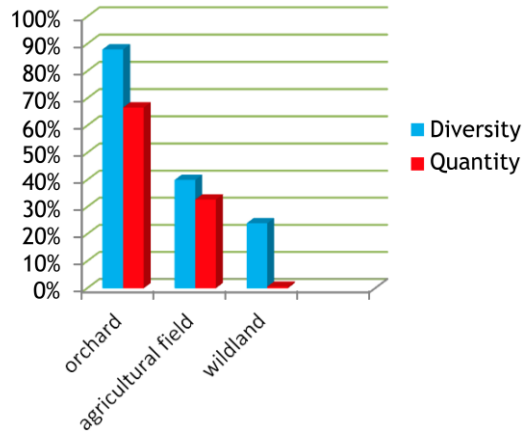


Fig.1. showing the relative abundance and diversity of yeasts communities collected from three different management systems, Baghdad (Iraq) in 2018.

The most frequent genera were Cryptococcus (33.6% of total isolates) followed Candida (15.7%), while

Bulleromyces albus, C. railenensis, Cr. humicola, Cr. terricola and Trichosporon asahii were occurred as single isolates (Table 1). These results are in agreement with (22; 28) that Cryptococcus is the most frequently yeast in nature.

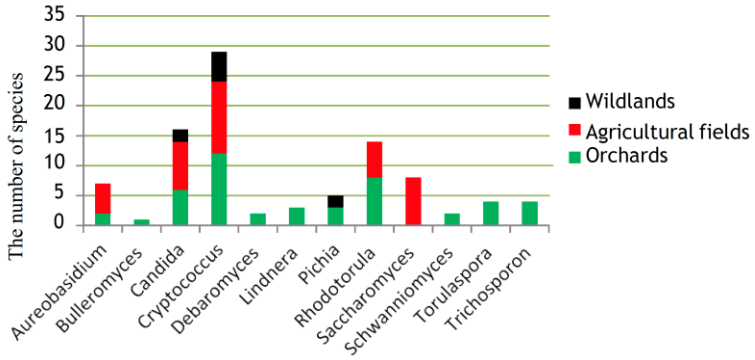


Fig. 2. Total yeast community with the number of species in the three systems, Baghdad, Iraq (2018).

Yeast species	Orchards Managed lands	Agricultural fields Intensively managed lands	Wildlands Unmanaged lands
Aureobasidium pullulans	2	5	--
Bulleromyces albus	1	--	--
Candida glabatra	3	2	1
C. labiduridarum	--	2	--
C. railenensis	1	--	--
C. tropicalis	2	4	1
Cryptococcus albidus	3	3	--
Cr. flavescens	1	--	2
Cr. humicola	1	--	1
Cr. laurentii	2	5	--
Cr. skinneri	4	4	2
Cr. terricola	1	--	--
Debaromyces hansenii	2	--	--
Lindnera saturnus	3	--	--
Pichia delftensis	1	--	2
P. kudriazevii	2	--	--
Rhodotorula glutinis	3	--	--
Rh. mucilaginosa	2	3	--
Rh. rubra	3	--	--
Saccharomyces boulardii	--	3	--
S. cerevisiae	--	5	--
Schwanniomyces polymorphus	2	--	--
Torulaspora globosa	4	--	--
Trichosporon asahii	1	--	--
T. porosum	3	--	--

Table 1. Species list and isolates number for the soil yeasts isolated from a three different management systems.

Finally, Adopting alternative farming systems such as sustainable agriculture and no-till farming are good solutions to promote soil health and ecosystem and reduce harmful environmental impacts. in order to maintain the health and safety of soil, we must pay attention to the soil biodiversity By using organic farming and limiting the use of pesticides and inorganic fertilizers, in addition to protecting natural forests (being a source of biodiversity richness) and orchards.

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