Comparison of diversity and activity of soil bacteria inhabiting maize field and grassland with similar location and soil properties – a case study

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Introduction

Revealing of the genetic diversity and metabolic activity of soil microbial communities in agricultural environments is of great importance to keep sustainable land management more effective considering maintenance of soil fertility, soil health and environmental safety. The aim of this case study was to get information about the basic state of the soils of the „Soil Biome Project" in long term field experiment in the perspective of the following studies. In addition to the long term maize field experiment represented by two distinct non-fertilized maize fields, a local fallow area characterized by imperfect succession and low floral diversity, and a natural grassland characterized by high floral diversity were examined *(Fig. 1)*.

Figure 1. Locations of sampling sites near Budapest (Hungary)

Figure 2. Soil profiles at the studied maize fields (left maize field 1; right maize field 2)

Results and discussion

Altogether 19 samples were processed with DGGE method; a total of 89 bands were detected, each sample contained 19-35 bands, and diversity did not show any trends along with the depth.

On the UPGMA dendogram *(Fig. 3)*, based on the DGGE patterns:

- surface samples from Martonvásár (1_1; 2_1; 3_1) clustered together;
- the AC horizon of the local control (3_2; 3_3) showed similarity to the absolute control (BIP2_1-5);
- samples from Bicske differed from all the cultivated (in the past, or the present) soils (even in A horizon), and formed a distinct cluster (with the AC samples of the local control);
- maize field 1 and 2 C (1_5; 2_3; 2_4) and AC (1_3; 1_4; 2_2) samples did not form clusters according to the horizon.

The history of the area could be a major driver of this result: field 1 probably was covered with a grove before agricultural use.

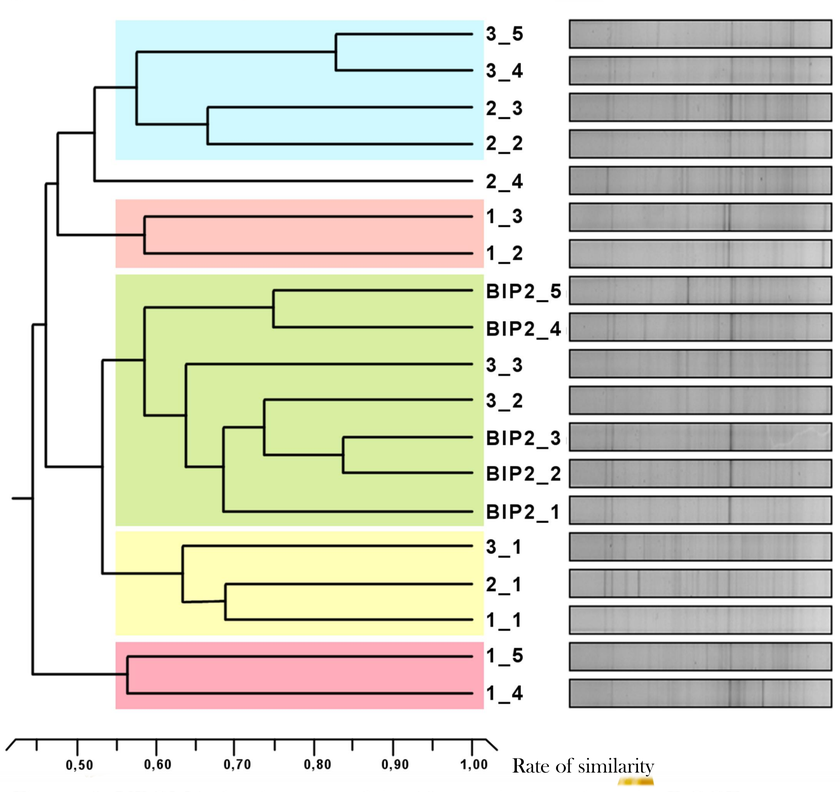

Figure 3. UPGMA dendrogram of the 19 samples based on the DGGE patterns

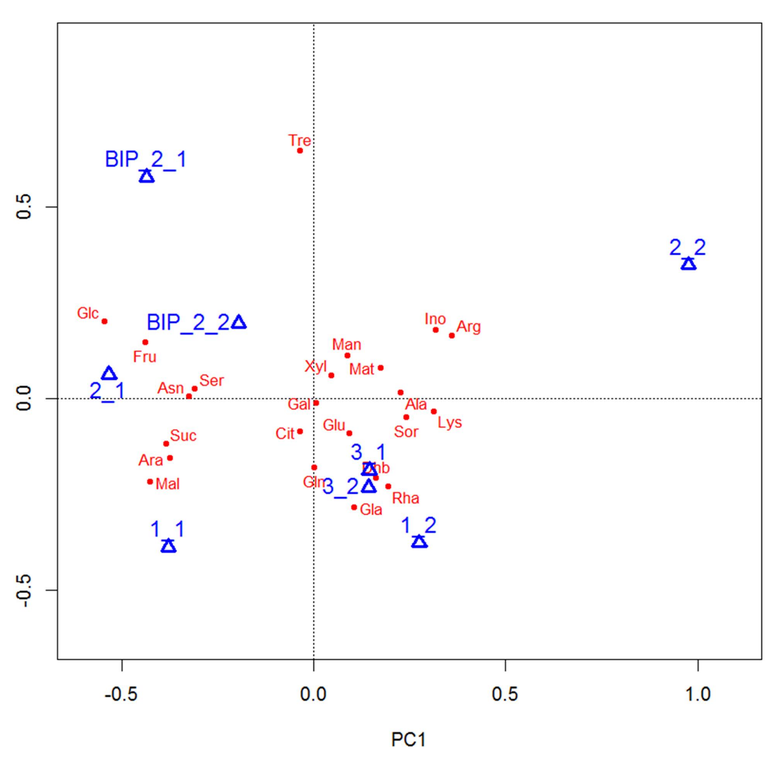

Figure 4. PCA biplot of the soil catabolic activity (MicroResp): samples (blue) from the upper soil horizons (A and AC horizons), substrates (red)

The PCA, based on the MicroResp™ substrate induced respiration measurement of the 19 samples, clearly separated the upper soil samples, except for local fallow control samples (3_1; 3_2) *(Fig. 4)*.

Fig. 5 shows the most important factors (carbon sources) of separation, based on the PCA (*Fig. 4*).

The A horizons always showed higher activity, than ACs. Catabolic activity of the surface control of the natural grassland (BIP2_1) was always extremely high compared to the A horizon samples from Martonvásár – even compared to the fallow area *(Fig. 5)*.

These findings could be explained with diverse flora and dense root system of the natural grassland.

Table 1. The pH and $CaCO_3$-content of the soil samples

	1_1	1_2	1_3	1_4	1_5	2_1	2_2	2_3	2_4
pH (H_2O)	6,92	7,21	7,91	7,99	8,36	7,90	8,16	8,38	8,43
pH (KCl)	6,32	6,38	7,47	7,67	7,77	7,50	7,72	7,69	7,81
$CaCO_3$ [%]	0,00	0,00	2,12	26,79	42,40	3,59	29,25	29,89	27,94

	3_1	3_2	3_3	3_4	3_5	BIP_ 2_1	BIP_ 2_2	BIP_ 2_3	BIP_ 2_4	BIP_ 2_5
pH (H_2O)	7,43	7,86	8,05	8,08	8,18	7,25	7,49	7,70	8,09	8,25
pH (KCl)	7,17	7,35	7,59	7,64	7,71	6,96	7,21	7,46	7,62	7,66
$CaCO_3$ [%]	5,43	2,51	5,86	12,14	27,21	2,96	8,46	8,67	14,02	16,04

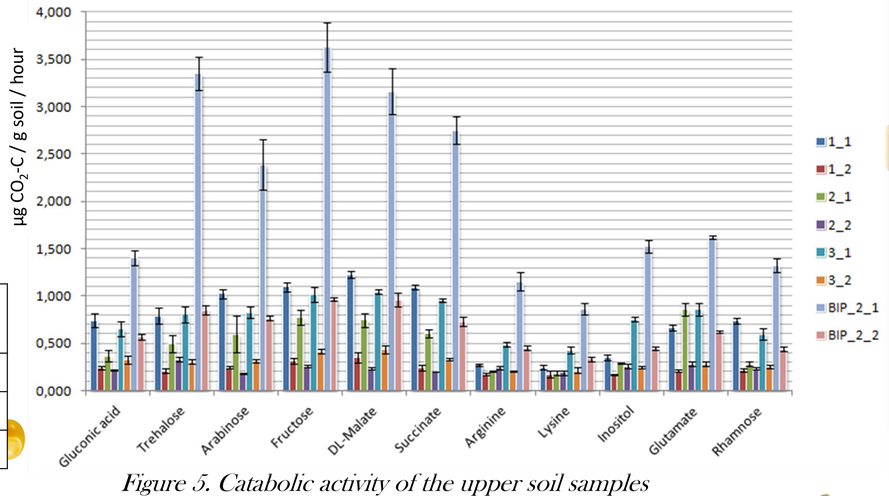

Figure 5. Catabolic activity of the upper soil samples

Materials and methods

The soil was characterized as a chernozem on loessy bedrock *(Fig. 2)*; samples originate from A, AC and C horizons (depth varied because of soil heterogeneity).

Sampling

- Samples were taken in spring, 2017
- **Arable maize fields (Martonvásár):**
- Maize field 1:

  1_1: A1 horizon; 1_2: A2 h.; 1_3: AC1 h.; 1_4: AC2 h.; 1_5: loessy C h.
- Maize field 2 :

  2_1: A horizon; 2_2: AC h.; 2_3: loessy 1C h.; 2_4: sandy 2C h.
- **Fallow field (Martonvásár):**

  3_1: A horizon; 3_2: AC1 h.; 3_3: AC2 h.; 3_4: loessy 1C h.; 3_5: sandy 2C h.
- **Natural grassland (Bicske):**

  BIP_2_1: A horizon; BIP_2_2: AC1 h.; BIP_2_3: AC2 h.; BIP_2_4: loessy 1C h.; BIP_2_5: sandy 2C h.

Bacterial diversity measurements

- Community DNA extraction with MO BIO PowerSoil DNA Extraction Kit
- PCR amplification of 16S rRNA gene with 27F and 1401R primers
- Semi-nested PCR amplification of the products with 27F-GC and 519R primers
- DGGE analysis with INGENYphorU 2 device; dentauring gradient: 40-60%
- Processing the gele with TotalLab v. 2006 software

Catabolic activity measurements

- MicroResp™, using 23 substrates
- Principal Component Analysis (PCA)

Supplementary information about the soil can be found in *Table 1.*

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