SPECIFIC SOIL MICROORGANISMS EFFECT ON SOIL ORGANIC MATTER STABILIZATION AND QUALITY PARAMETERS UNDER DROUGHT CONDITIONS

A. Jurys, D. Feizienė

Lithuanian Research Centre for Agriculture and Forestry, Institute of Agriculture, Department of Plant Nutrition and Agroecology

arnoldas.jurys@lammc.lt, dalia.feiziene@lammc.lt

Introduction. In order to produce high yield it is necessary to reduce soil degradation, loss of organic carbon and biodiversity. Specific microorganisms degrade substrates and compounds. In this way we can reduce nutrient losses and increase SOM (soil organic matter). The aim of this study was to determine the influence of specific soil microorganisms to decompose plant residues on soil CO_2 and C sources.

Materials and methods. Field experiments carried out on *Endocalcari – Endohypogleyic Cambisol* at the Institute of Agriculture, Lithuanian Research Centre for Agriculture and Forestry. Research scheme involved 2 treatments as control and 4 treatments with different microorganisms (single or mixed). Soil CO_2 emission was determined with IRGA, soil C sources and biodiversity – with Biolog EcoPlate.

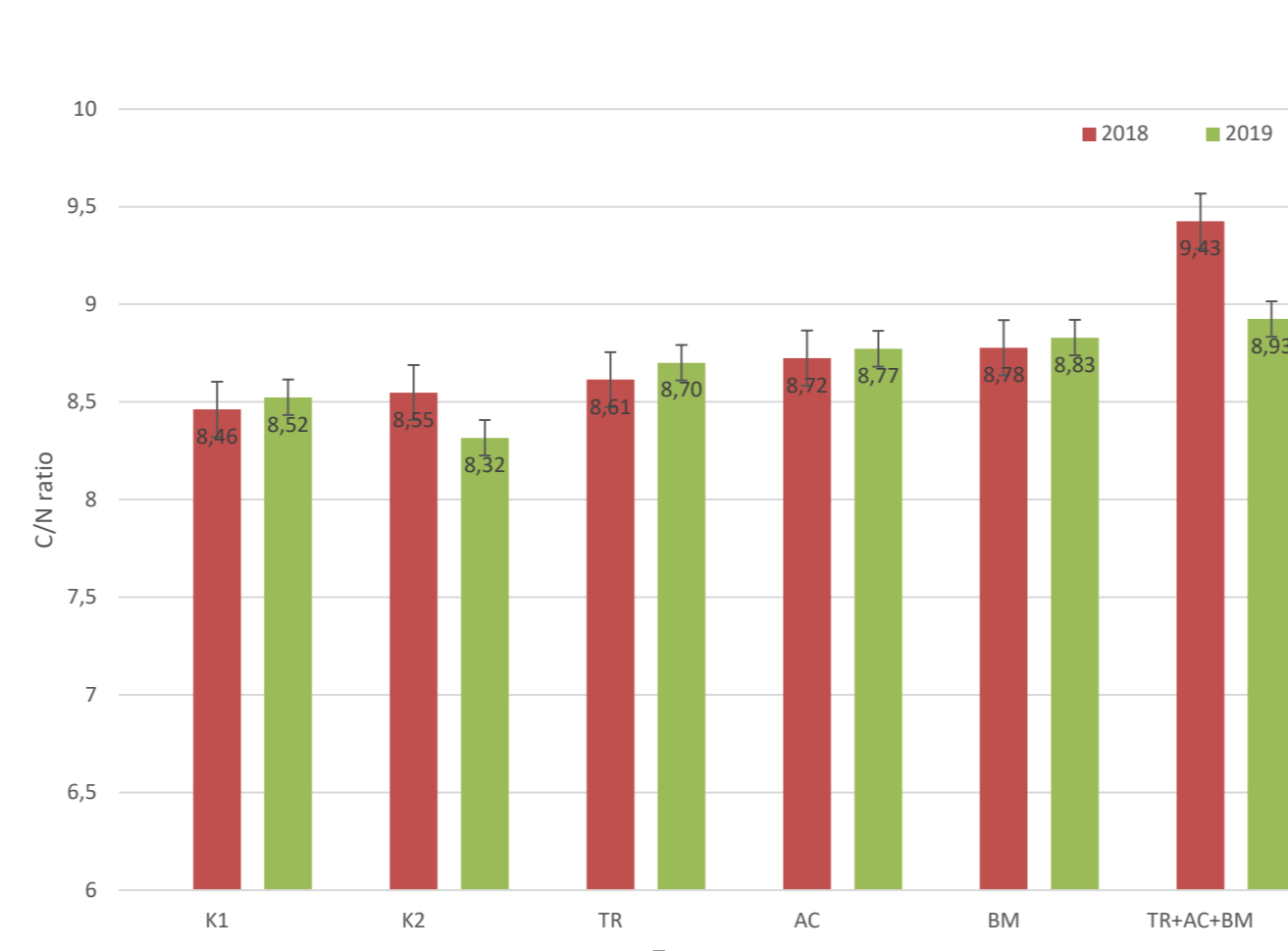**Results and discussion.**

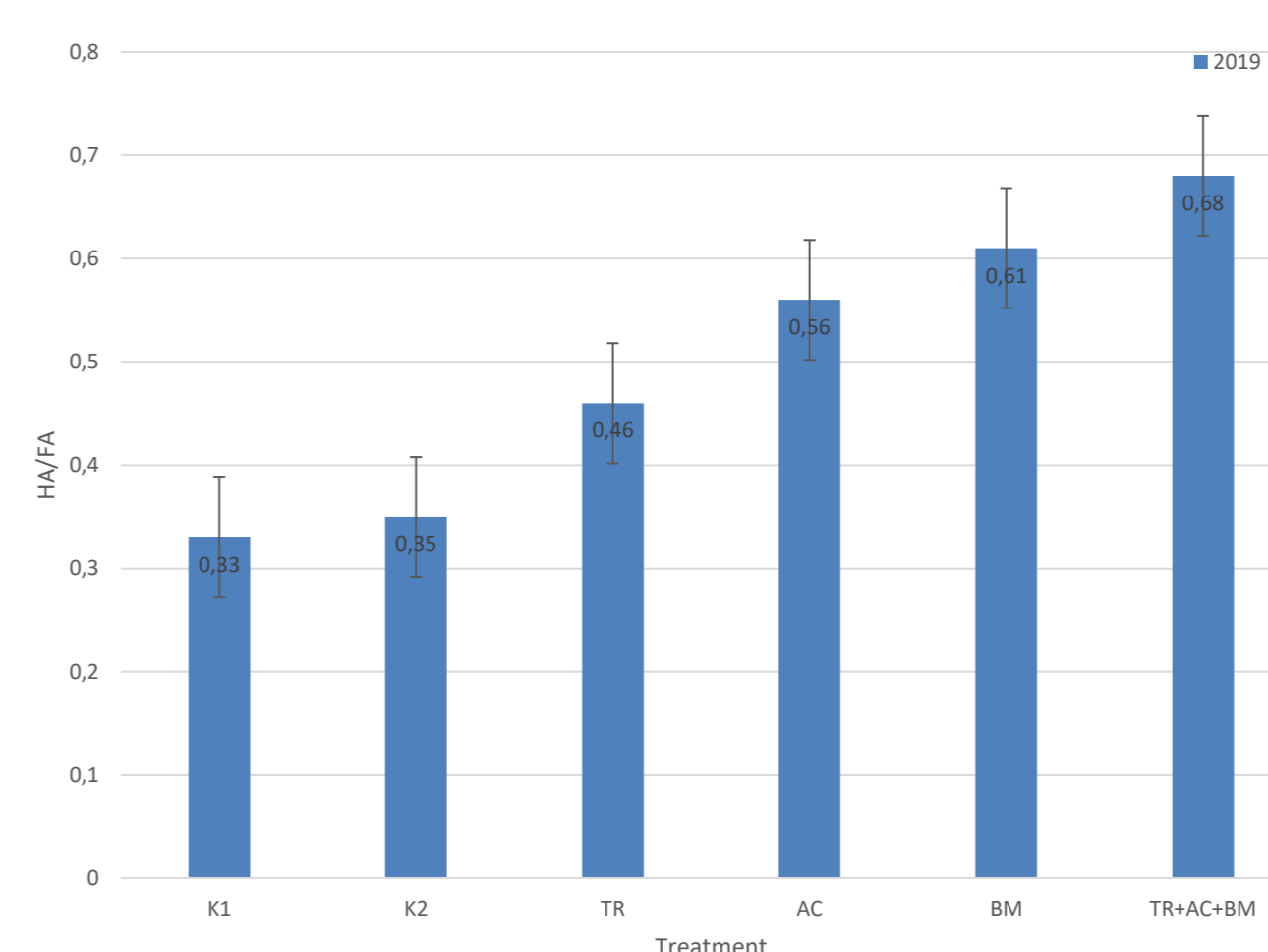**Figure 1.** SOC variation 2018-2019
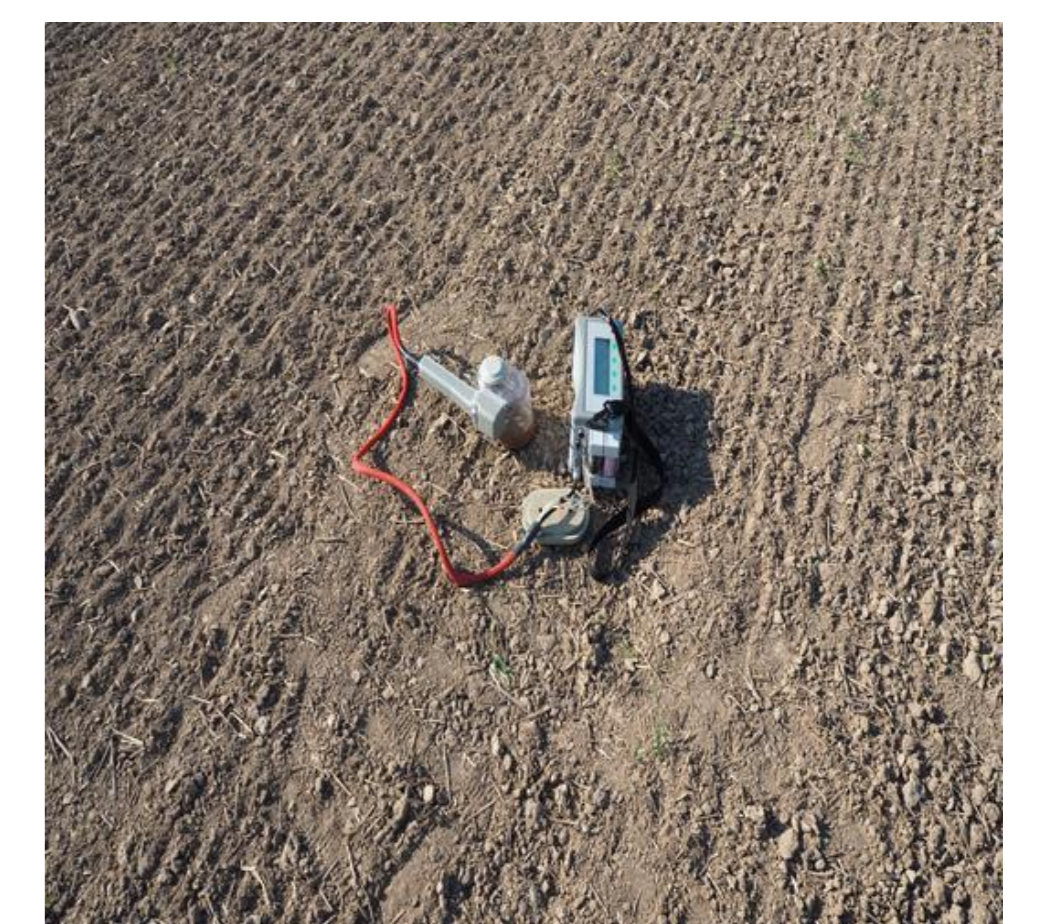

Figure 2. C/N ratio 2018-2019

Figure 3. HA/FA ratio 2019

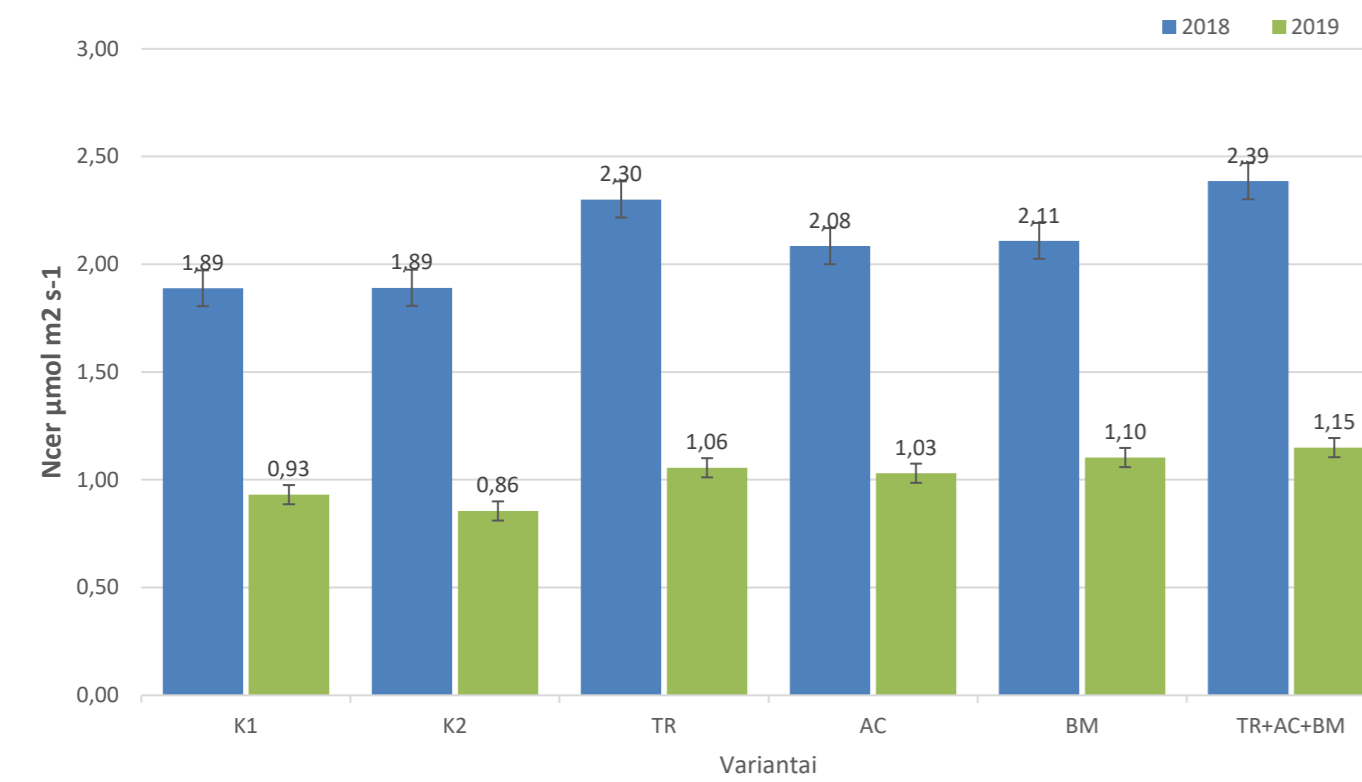**Figure 10.** CO2 gass detection in treatments.

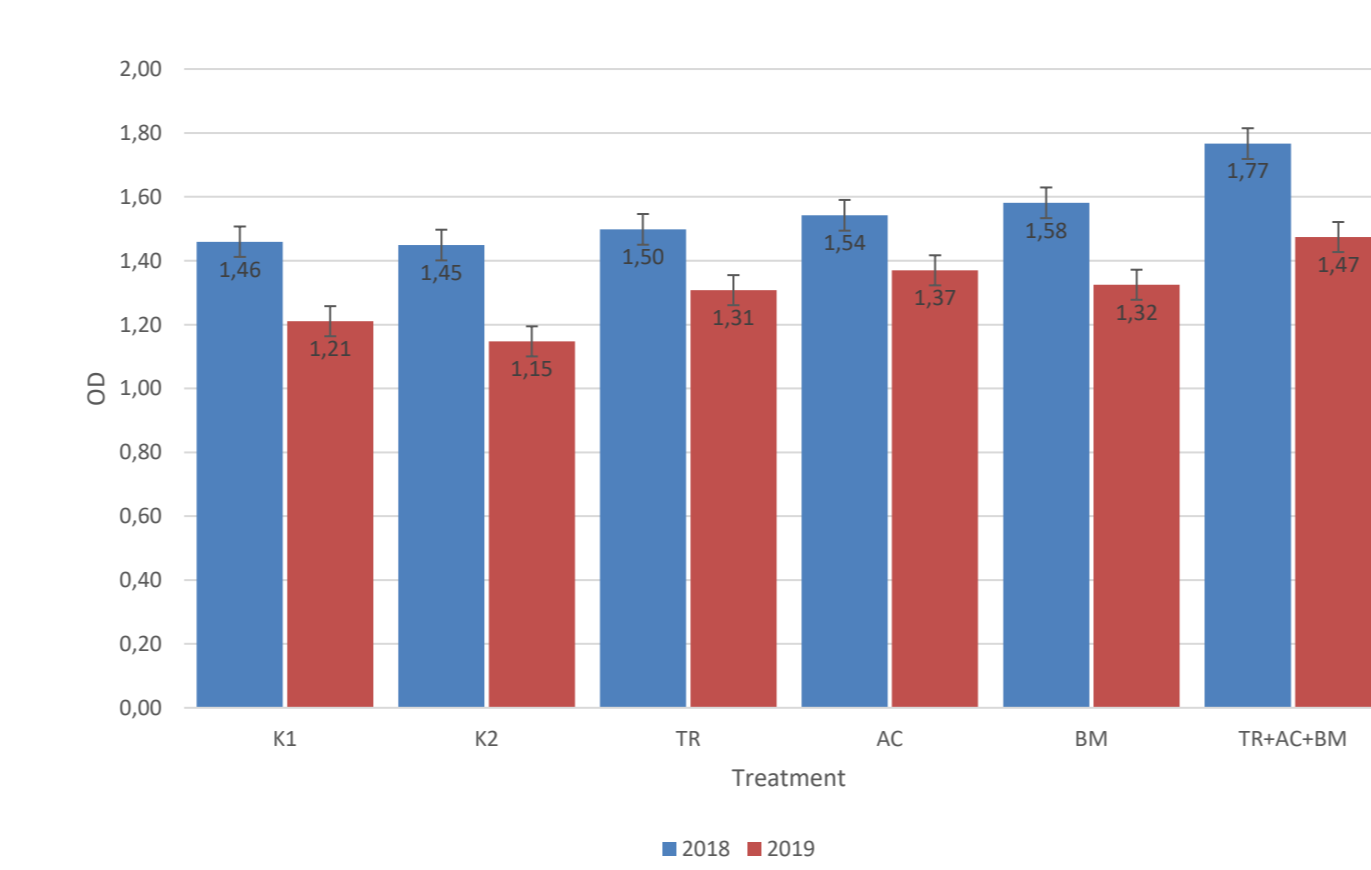**Figure 4.** Average soil CO_2 emission 2018-2019

Figure 5. AWCD 2018-2019 after 96 h
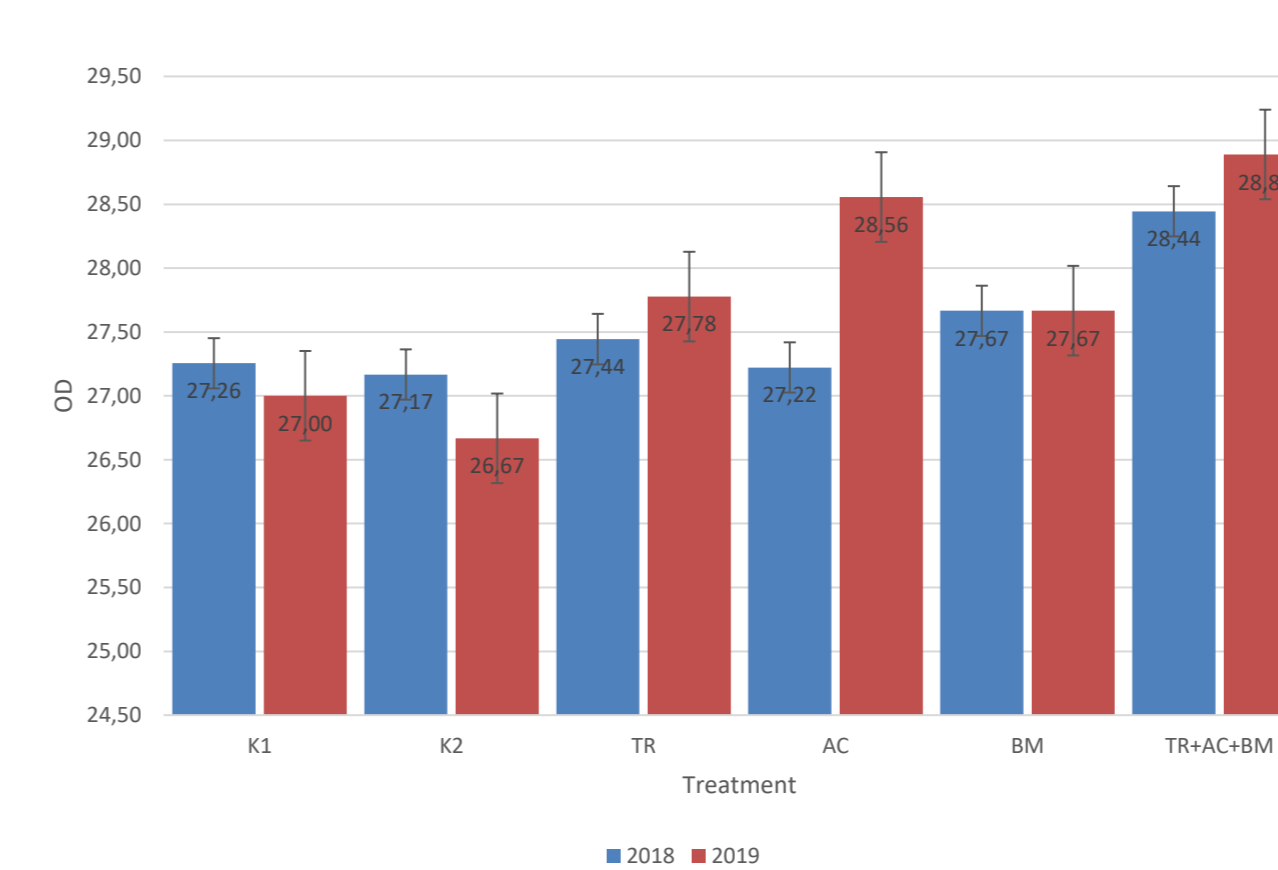

Figure 6. Substrate richness (R) 2018-2019
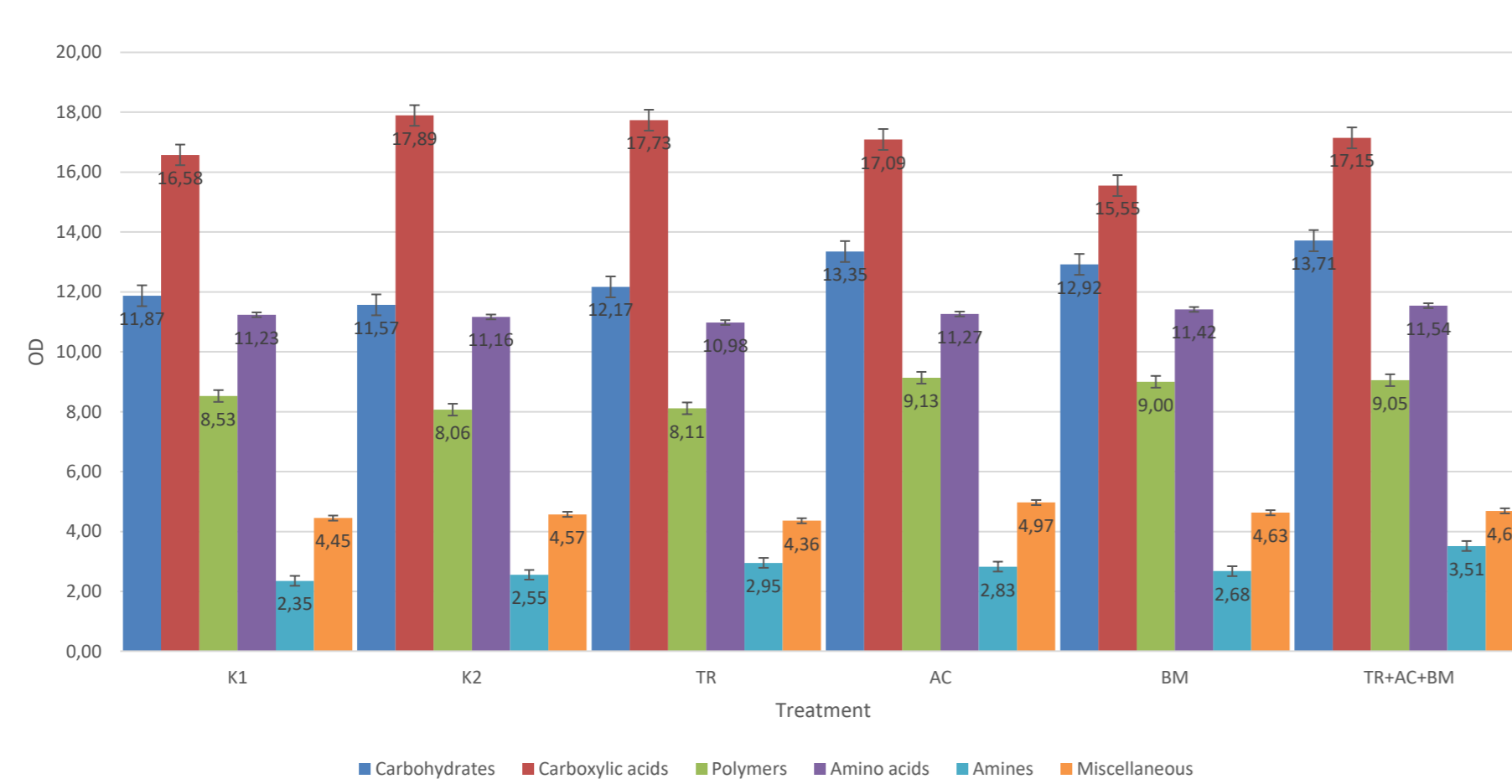

Figure 11. Phosphorus solubilizing bacteria
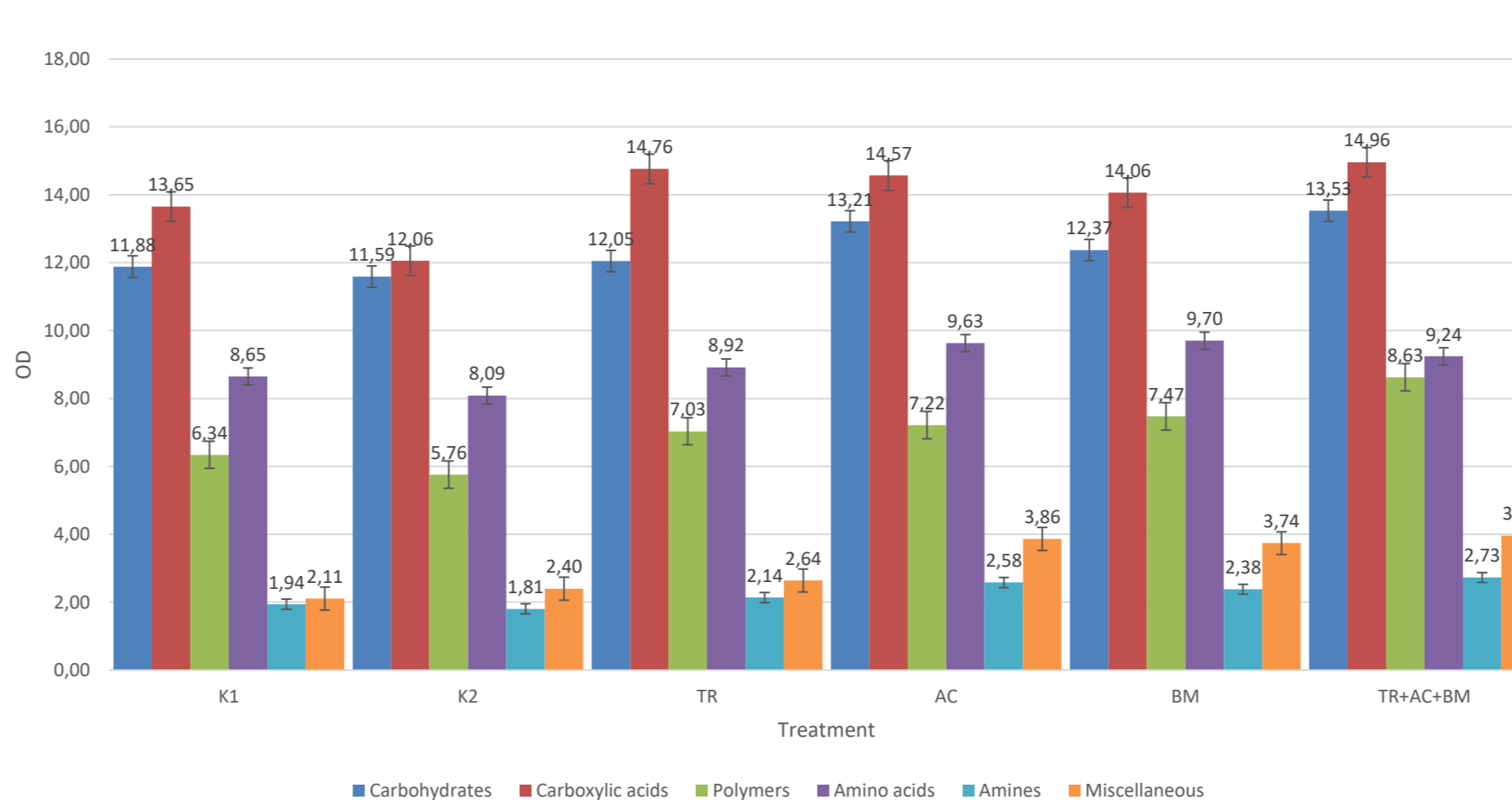

Figure 7. C sources 2018, after 96 h

Figure 8. C sources 2019, after 96 h
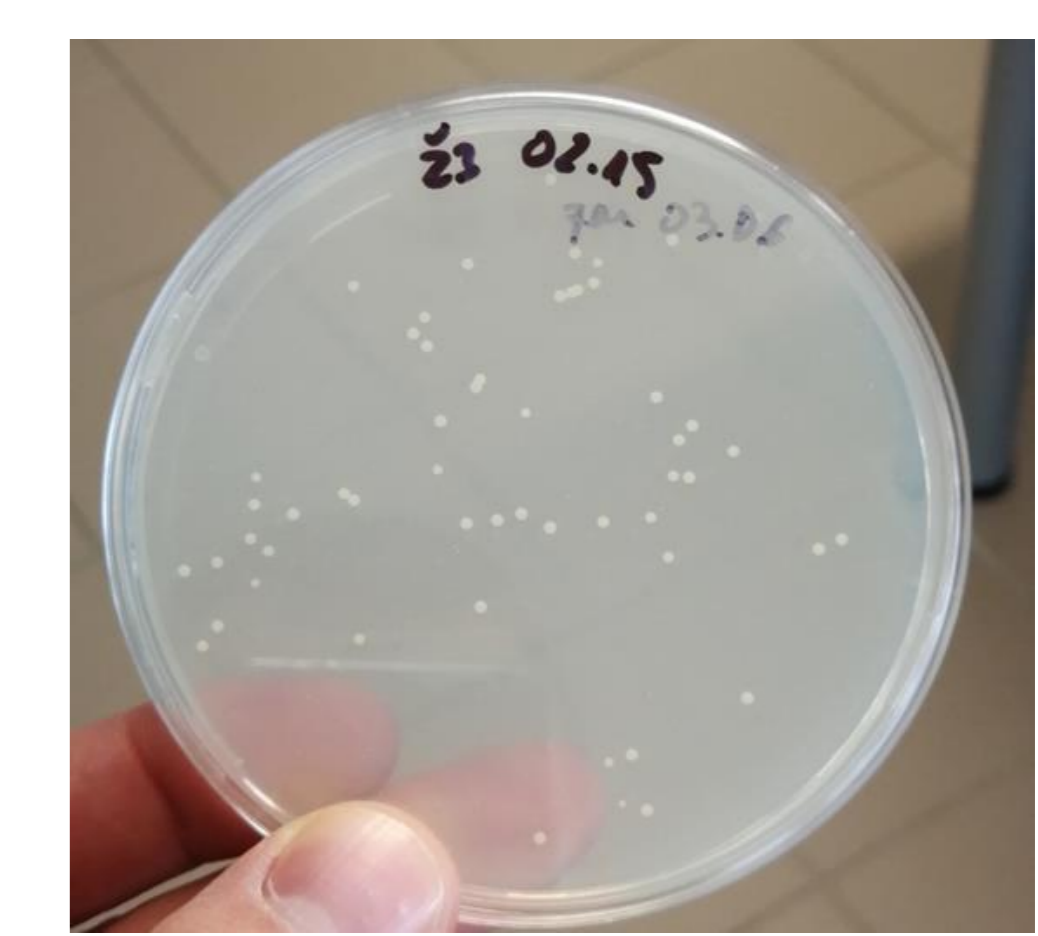

Figure 12. Nitrogen fixing bacteria

Conclusions:

In 2018: **SOC** (Fig. 1) in treatment No. 3 (*Trichoderma reesei*) was 9,1% higher than in control 1 and 6,7% than in control 2. **C/N ratio** (Fig. 2) was 10,2% higher in treatment with *Trichoderma reesei, Acinetobacter calcoaceticus, Bacillus megaterium* (treatment 6) compared to K1 and 9,3% than K2. Average **soil CO_2 flux** (Fig. 4) was highest in treatment No. 6 (*Trichoderma reesei + Acinetobacter calcoaceticus + Bacillus megaterium*) 20,8% compared to K1 and K2.

C sources detection (Fig. 7) were higher than in both controls respectively: Carbohydrates in treatment No. 6 by 13,6% and 15,6%, Carboxylic acids in treatment No. 5 (*Bacillus megaterium*) by 36.5%, Polymers in treatment No. 4 (*Acinetobacter calcoaceticus*) by 6.7 and 11.7%, amino acid by 2,7% and 3.3%, amines in treatment No. 6 by 33,1% and 27,3%, miscellaneous compounds in treatment 4 by 10,4% and 8%. **AWCD** (Fig. 5) in treatment 6 was 17,4% and 18% **R** (Fig. 6) was 4,2% and 4,5% higher than in both controls.

In 2019: highest **SOC** (Fig. 1) was in treatment No. 5 (*Bacillus megaterium*) 7% higher compared with K1, and 5,8% compared to K2. **C/N** ratio (Fig.2) in treatment 6 was 4,5% higher than K1 and 6,8% than K2. Highest **HA/FA** (Fig. 3) ratio was in treatment 6 – 51,5% higher than K1 and 48,5 % than K2. Mean soil **CO_2 flux** (Fig. 4) was highest in treatment No. 6. 19% compared to K1 and 25,5% than K2. The highest OD values after 96 h for **C sources** (Fig. 8) detection were as follows: Carbohydrates in treatment 6 was 12,2% and 14,4% higher than K1 and K2. Carboxylic acids in treatment 6 was 8,7% higher than K1 and 19,4%. Polymers in treatment 6 was 26,5% and 33,3% higher than controls. In treatment 5 amino acid meanings was 10,9% and 16,7% higher than controls. In treatment 6 amines was 28,8% and 33,8% higher than controls. In treatment 6 miscellaneous was 46,8% and 39,4% higher than controls. In treatment 6 **AWCD** (Fig. 5) 17,9% and 22,2% higher than controls, **R** (Fig. 6) was 6,5% and 7,7 % higher than controls.