Scientific Papers. Series E. Land Reclamation, Earth Observation & Surveying, Environmental Engineering. Vol. XV, 2026
Print ISSN 2285-6064, CD-ROM ISSN 2285-6072, Online ISSN 2393-5138, ISSN-L 2285-6064

INTERRELATIONSHIP BETWEEN SOIL MICROORGANISMS AND AIRBORNE MICROFLORA IN URBAN ENVIRONMENT

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Abstract

The present study aims to establish the potential similarity between airborne microorganisms and soil microorganisms. We analyse the percentage of similarity based on dominant types of soil microorganisms and their frequency of occurrence in ground air, as well as their association with specific fractions of fine dust particles. For the purpose of the study, eight sampling plots were selected, with different anthropogenic pressure. A six-stage cascade impactor was used to collect air samples. Soil samples were taken from a depth of 0-15 cm. The dominant types of microorganisms were determined. DNA identification was performed. The results show that bacteria predominate in the first levels of the cascade impactor. Fungi are concentrated at sieves 4.7-7.0 µm. Actinomycetes are most concentrated at sieves 3.3- 4.7 µm and 2.1-3.3 µm. The most common from Bacilli are B. megaterium and B. cereus. The amount of soil microorganisms, as a percentage similarity to the air microflora, increases with increasing anthropogenic pressure and reach up to 8%. The increased presence of opportunistic soil microorganisms in heavy construction areas in Sofia poses a significant risk to public health, which highlights the need for specific regulations related to minimizing dust generation.

Key words*: airborne microorganisms, DNA, soil microorganisms, urban environment, 16S rRNA.*

INTRODUCTION

Surface air, although long considered only as a transit medium for microorganisms, is now defined as a dynamic and complex microbial habitat that plays a critical role in environmental quality. Airborne microorganisms are often defined as bioaerosols. According to this is important to point out that bioaerosols include not only bacteria, fungi, actinomycetes, viruses and their fragments, but also any type of biological components, such as pollen and other plant fragments, for example. There is evidence that bioaerosols constitute up to 25% of the total mass of atmospheric aerosols (Shammi et al., 2021). This data determines the important role of airborne microorganisms in the analysis of atmospheric air quality.

From this perspective, air pollution is one of the main causes of deterioration of human health, as well as the functioning of ecosystems. Increased levels of pollutants in the air lead to changes in naturally occurring processes in ecosystems. These changes lead to a decrease in the degree of air decontamination, carbon dioxide assimilation, soil acidification, etc. Particulate matter concentrations are indicators of complex mixtures of pollutants (Masselot et al., 2024). It has been found that air quality is worse in urban areas than in rural areas. The main sources of dust pollution are road transport, industry, as well as the use of solid fuels for heating and power generation, and construction and excavation human activities (Ketchman & Bilec, 2013; Khan & Strand, 2018; Sager, 2020). In recent years, several studies have highlighted the potential relationship between the concentration of fine particulate matter, of various origins, and the content of microorganisms in the air (Mansour et al., 2014; Palladino et al., 2021). Concentration of settled microorganisms on fine particulate matters has different significance for ambient air quality. Determining the content and predominant groups of microorganisms can serve as an indicator of air quality.

The main sources of atmospheric microorganisms are land and water surfaces, with soil being the most significant reservoir for airborne microorganisms above land. Soil microorganisms enter the atmosphere through processes of mechanical soil breakdown as a result of various human activities, wind erosion, etc. Research shows that airborne microbial communities often reflect the structure of communities in surrounding surface ecosystems

The data shows that 46.3% of airborne bacteria originating from the immediate ground environment (Zhao et al., 2022). When studying air quality, it is necessary to analyze the microbial load, including the presence of specific microorganisms generally present in soils. Such information can show the influence of anthropogenic activity - construction, excavation activities, maintenance of parks and gardens - on the quantity and specificity of microorganisms present in the air. Given that the main source of airborne microorganisms is soil (Ruiz-Gil et al., 2020), and it contains a number of pathogens (Pales, 2024), it is of key importance to analyze the percentage of major and commonly occurring soil microorganisms in the air, in order to prevent human health and increase environmental hygiene. While the microbiological characteristics of soil, aquatic habitats, etc. have been studied in detail, revealing specific and interconnected ecosystems, air often remains neglected as an independent habitat for microorganisms. The air environment is often considered only as a spreading factor for microorganisms. New analyses show that air is a real and specific ecosystem, inhabited by a microbiome that is vast in both number and diversity (Amato et al., 2023). Airborne microorganisms not only influence climate processes through the formation of ice nuclei and cloud condensation, but also have a direct impact on human health, agriculture, and ecosystem stability. In conditions of increasing urbanization and anthropogenic pressure, understanding the mechanisms by which microorganisms are transferred from land surfaces to the ground air layer becomes fundamental for protecting public health and optimizing urban hygiene (Chen et al., 2020).

The study of the entry and distribution of microorganisms into the air environment will provide important information about the microbiological load of individual ecosystems. This information will predict in the future the microbiological effect of air pollution resulting from the ever-increasing construction activities in urban areas.

The main goal of this study is to establish the degree of similarity between air and soil microflora in urban environments by analyzing the distribution of dominant types of soil microorganisms in individual fractions of fine dust particles under the influence of different anthropogenic pressures.

MATERIALS AND METHODS

The study was conducted in early September 2025, on the territory of the municipality of Sofia, Bulgaria, covering four areas with intense anthropogenic pressure (Sample Plot (SP) 1-4) and four areas in parks and mountain regions with low anthropogenic pressure (Sample Plot (SP) 5-8).

SP1 - Formation of a green park area, flower beds (manually) in Geo Milev Park - with the presence of anthropogenic pressure. Coordinates: 42°41′12.18″N 23°21′50.37″ E.

SP2 - Reconstruction of sidewalks in the residential district of Geo Milev - with the presence of anthropogenic pressure. Coordinates: 42°42′51.73″N 23°21′33.37″ E.

SP3 - Reconstruction of the roadway on Vladimir Vazov Blvd. - with the presence of anthropogenic pressure. Coordinates: 42°42′31.95″N 23°22′17.73″ E.

SP4 - Construction of a residential complex in the residential district of Dragalevtsi - with the presence of anthropogenic pressure. Coordinates: 42°38′13.93″N 23°18′39.35″ E.

SP5 - Western Park, heavily forested inner part - without the presence of anthropogenic pressure, only recreational activity is established. Coordinates: 42°20′09.59″N 23°15′20.53″ E.

SP6 - Hunting Park, heavily forested inner part - without the presence of anthropogenic pressure, only recreational activity is established. Coordinates: 42°39′48.90″N 23°20′17.98″ E.

SP7 - Vitosha Nature Park, tourist trail - without the presence of anthropogenic pressure, only recreational activity is established. Coordinates: 42°36′54.66″N 23°17′35.10″ E.

SP8 - Plana Mountain, tourist trail - without the presence of anthropogenic pressure, only recreational activity is established. Coordinates: 42°30′38.53″N 23°21′39.25″ E.

The present study includes analysis of the quantity of the main microbiological groups of the air microflora and determination of the total microbial number of each sample. Analysis of the main groups of soil microorganisms

(bacteria, actinomycetes and micromycetes) and determination of the total microbial number. The study also includes determination of the species of the genus *Bacillus: Bacillus cereus, Bacillus subtilis, Bacillus megaterium* and *Bacillus mycoides*. For precise monitoring of ground-level air microflora, a 6-stage cascade impactor was used, operating on the principle of inertial sedimentation. Sampling was performed once from each of the surveyed points, with one cubic meter of air being passed through the impactor at a uniform speed. The device divides the air sample (with a volume of 1 m^3) into six fractions based on the aerodynamic diameter of the particles: 1st stage (> 7.0 μm); 2nd stage (4.7-7.0 μm); 3rd stage (3.3-4.7 μm); 4th stage (2.1-3.3 μm); 5th stage (1.1-2.1 μm); 6th stage (0.65-1.1 μm). A Petri dish with a specific medium was placed at each level of the impactor. Samples were taken at a height of 1.5 m (the breathing zone) at a temperature of 11°C and a humidity of 86%. The incubation process was carried out under the following parameters: total microbial number (bacteria) on meat peptone agar (MPA) - incubation at 28°C for 48 hours in an aerobic environment. Actinomycetes - dense plating on starch ammonia agar (SAA), incubation at 35°C for a period of 10 days. Micromycetes - plating on Capek Dox Agar medium, incubation at 30°C for 7 days. Soil samples were taken once, with a sterile probe from a depth of 10 cm. The samples were placed in sterile bags and analyzed within 24 hours. Each sample was pre-cleaned of impurities and prepared for analysis by serial dilutions. For counting of germinated colonies, dense plating on solid agar media was used. The media and incubation period were identical to those used for the study of air samples. To determine the representatives of the genus *Bacillus: Bacillus cereus, Bacillus subtilis, Bacillus megaterium* HiBacillus Identification Kit (HiMedia Laboratories, India, Mumbai) was used. The study is based on a colorimetric test. The test is based on the principle of pH change. *Bacillus* species show metabolic changes during incubation, for which the color change in the medium is an indicator. To perform the analysis, each of the samples was previously prepared and purified. Incubation was performed at 37°C for 48 hours. The data were read using a color scale based on the color change of the plate. Given the specific colonies that *Bacillus mycoides* forms, it was also reported. After performing the analysis, pure cultures were prepared to confirm the identity of the bacilli by DNA sequencing. Molecular genetic identification of the isolated strains was performed by determining 16S rRNA gene nucleotide sequences using primer pair 27F (5'-AGAGTTTGATCMTGGCTCAG-3') × 1492R (5'-GGTTACCTTGTTACGACTT-3'). PCR amplifications were performed using the MyTaq HS DNA Polymerase 2x Mix (Bioline Ltd., UK). The resulting PCR products were separated by agarose gel electrophoresis, stained with GelRed (Biotium, USA). The amplified DNA fragments were excised and purified from the agarose gel using the GeneJET Gel Extraction Kit (Thermo Scientific, USA). The purified DNA fragments were directly sequenced in both directions (forward and reverse) using the same primers employed for amplification. The evaluation and analysis of the resulting chromatograms and nucleotide sequences were carried out using CHROMAS v2.31 and Vector NTI v.11 software packages. Final taxonomic identification and alignment were performed by comparing the consensus sequences against the NCBI BLAST database (GenBank).

The numerical data were processed with StatSoft Statistica 12 software. For each sample, the mean value of three replicates and the standard deviation SD were calculated, at a statistical significance threshold of $p < 0.05$ (95% confidence interval).

RESULTS AND DISCUSSIONS

In urban areas, anthropogenic activities such as road traffic, construction, and industrial processes significantly accelerate the transport of soil particles and their associated microbes into the ground air. The study by Chen et al. (2020), highlights that the soil environment is one of the main pathways for the emission of microorganisms into the air.

The results for the reported amounts of microorganisms for each of the fractions are shown in Table 1.

Table 1. Microbiological parameters of air samples (CFU*$10^2/m^3$)

Total microbial number						
	>7 μm	4.7-7 μm	3.3-4.7 μm	2.1-3.3 μm	1.1-2.1 μm	0.65-1.1 μm
SP1	1.5 ± 0.74	0.6 ± 0.43	0.8 ± 0.24	0.4 ± 0.14	0.5 ± 0.09	0.5 ± 0.15
SP2	2.9 ± 0.74	1.1 ± 0.43	0.9 ± 0.24	0.5 ± 0.14	0.4 ± 0.09	0.2 ± 0.15
SP3	2.9 ± 0.74	1.5 ± 0.43	1.3 ± 0.24	0.4 ± 0.14	0.3 ± 0.09	0.2 ± 0.15
SP4	3.1 ± 0.74	1.5 ± 0.43	0.8 ± 0.24	0.7 ± 0.14	0.3 ± 0.09	0.2 ± 0.15
SP5	0.6 ± 0.09	0.5 ± 0.19	0.7 ± 0.24	0.9 ± 0.38	0.8 ± 0.06	0.5 ± 0.05
SP6	0.4 ± 0.09	0.2 ± 0.19	0.5 ± 0.24	0.9 ± 0.38	0.8 ± 0.06	0.4 ± 0.05
SP7	0.5 ± 0.09	0.1 ± 0.19	0.2 ± 0.24	1.5 ± 0.38	0.9 ± 0.06	0.4 ± 0.05
SP8	0.4 ± 0.09	0.1 ± 0.19	0.2 ± 0.24	1.6 ± 0.38	0.9 ± 0.06	0.4 ± 0.05
Bacteria						
	>7 μm	4.7-7 μm	3.3-4.7 μm	2.1-3.3 μm	1.1-2.1 μm	0.65-1.1 μm
SP1	0.7 ± 0.79	0.3 ± 0.38	0.4 ± 0.13	0.1 ± 0.06	0.3 ± 0.10	0.4 ± 0.15
SP2	1.9 ± 0.79	0.7 ± 0.38	0.6 ± 0.13	0.2 ± 0.06	0.1 ± 0.10	0.1 ± 0.15
SP3	2.6 ± 0.79	1.1 ± 0.38	0.5 ± 0.13	0.1 ± 0.06	0.1 ± 0.10	0.1 ± 0.15
SP4	1.6 ± 0.79	1.1 ± 0.38	0.3 ± 0.13	0.2 ± 0.06	0.1 ± 0.10	0.1 ± 0.15
SP5	0.1 ± 0.09	0.4 ± 0.05	0.3 ± 0.15	0.1 ± 0.30	0.5 ± 0.17	0.1 ± 0.05
SP6	0.3 ± 0.09	0.6 ± 0.05	0.2 ± 0.15	0.0 ± 0.30	0.2 ± 0.17	0.2 ± 0.05
SP7	0.2 ± 0.09	1.0 ± 0.05	0.0 ± 0.15	0.1 ± 0.30	0.2 ± 0.17	0.2 ± 0.05
SP8	0.1 ± 0.09	1.0 ± 0.05	0.0 ± 0.15	0.1 ± 0.30	0.1 ± 0.17	0.2 ± 0.05
Fungi (molds)						
	>7 μm	4.7-7 μm	3.3-4.7 μm	2.1-3.3 μm	1.1-2.1 μm	0.65-1.1 μm
SP1	0.4 ± 0.42	0.1 ± 0.05	0.2 ± 0.27	0.1 ± 0.10	0.1 ± 0.05	0.1 ± 0.00
SP2	0.9 ± 0.42	0.1 ± 0.05	0.2 ± 0.27	0.1 ± 0.10	0.2 ± 0.05	0.1 ± 0.00
SP3	0.2 ± 0.42	0.2 ± 0.05	0.7 ± 0.27	0.1 ± 0.10	0.1 ± 0.05	0.1 ± 0.00
SP4	1.1 ± 0.42	0.1 ± 0.05	0.1 ± 0.27	0.3 ± 0.10	0.1 ± 0.05	0.1 ± 0.00
SP5	0.1 ± 0.11	0.3 ± 0.15	0.2 ± 0.05	0.2 ± 0.13	0.2 ± 0.08	0.4 ± 0.15
SP6	0.1 ± 0.11	0.0 ± 0.15	0.1 ± 0.05	0.1 ± 0.13	0.1 ± 0.08	0.1 ± 0.15
SP7	0.3 ± 0.11	0.0 ± 0.15	0.1 ± 0.05	0.3 ± 0.13	0.2 ± 0.08	0.1 ± 0.15
SP8	0.3 ± 0.11	0.0 ± 0.15	0.1 ± 0.05	0.4 ± 0.13	0.3 ± 0.08	0.1 ± 0.15
Actinomycetes						
	>7 μm	4.7-7 μm	3.3-4.7 μm	2.1-3.3 μm	1.1-2.1 μm	0.65-1.1 μm
SP1	0.4 ± 0.17	0.20 ± 0.06	0.20 ± 0.14	0.20 ± 0.00	0.10 ± 0.00	0.00 ± 0.00
SP2	0.1 ± 0.17	0.30 ± 0.06	0.10 ± 0.14	0.20 ± 0.00	0.10 ± 0.00	0.00 ± 0.00
SP3	0.1 ± 0.17	0.20 ± 0.06	0.10 ± 0.14	0.20 ± 0.00	0.10 ± 0.00	0.00 ± 0.00
SP4	0.4 ± 0.17	0.30 ± 0.06	0.40 ± 0.14	0.20 ± 0.00	0.10 ± 0.00	0.00 ± 0.00
SP5	0.4 ± 0.20	0.10 ± 0.05	0.20 ± 0.15	0.30 ± 0.05	0.10 ± 0.00	0.00 ± 0.05
SP6	0.0 ± 0.20	0.00 ± 0.05	0.50 ± 0.15	0.20 ± 0.05	0.10 ± 0.00	0.10 ± 0.05
SP7	0.0 ± 0.20	0.00 ± 0.05	0.50 ± 0.15	0.20 ± 0.05	0.10 ± 0.00	0.10 ± 0.05
SP8	0.0 ± 0.20	0.00 ± 0.05	0.50 ± 0.15	0.20 ± 0.05	0.10 ± 0.00	0.10 ± 0.05

According to air analysis data, sample areas with construction activities have microbial abundance about twice as high as green areas. The results show that bacteria predominate in

the first levels of the cascade impactor, where larger particles settle. Fungi are also most concentrated in the upper levels of the impactor, with the main percentage of them in the second stage of sedimentation (4.7-7.0 µm). In the case of actinomycetes, we again observe a greater number of CFU/m^3 in the petri dishes of the larger sieves 3.3-4.7 µm and 2.1-3.3 µm. These data are very intriguing considering that these are the sieves that capture the main soil particles (Padoan et al., 2021). The results of the soil analyses are provided in Table 2.

Table 2. Microbiological parameters of soil samples (CFU*10^4/g soil)

	TMN	Bacteria	Actinomycetes	Micromycetes
SP1	12.6 ± 2.63	7.6 ± 1.76	3.4 ± 1.04	1.6 ± 1.18
SP2	10.14±2.63	5.9 ± 1.76	3.2 ± 1.04	1.04 ± 1.18
SP3	6.2 ± 2.63	3.6 ± 1.76	1.4 ± 1.04	1.2 ± 1.18
SP4	9.6 ± 2.63	4.4 ± 1.76	1.6 ± 1.04	3.6 ± 1.18
SP5	12.78 ± 3.7	9.02 ± 2.5	2.73 ± 0.64	1.03 ± 1.45
SP6	17.24 ± 3.7	12.18 ± 2.5	1.95 ± 0.64	3.11 ± 1.45
SP7	20.73 ± 3.7	13.94 ± 2.5	2.27 ± 0.64	4.52 ± 1.45
SP8	20.45 ± 3.7	14.63 ± 2.5	3.42 ± 0.64	2.4 ± 1.45

As expected, the data on the quantities of individual groups of microorganisms, as well as the total microbial number in the soil, are hundreds of times higher than the results for air samples. This is completely understandable, given that soil is one of the richest environments in microorganisms (Llado et al., 2017). However, in undisturbed green areas, the reported total microbial count is higher compared to anthropogenically loaded soils. The results for the percentage distribution of the individual microbiological groups without taking into account the individual level of the separator are presented in Figure 1. Respectively, the percentage ratio of the studied soil samples is presented in Figure 2.

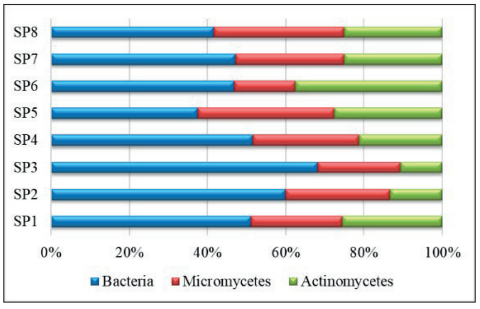


Figure 1. Percentage of the main microbiological groups in relation to the total microbial number of airborne microorganisms

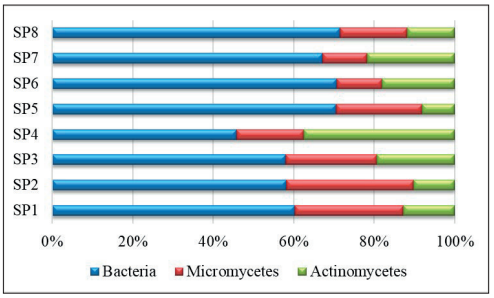


Figure 2. Percentage of the main microbiological groups in relation to the total microbial number of soil microorganisms

In both types of air and soil samples, a dominant presence of the group of bacteria is observed. However, there are certain specifics. Thus, in air samples, the participation of the groups of actinomycetes and fungi is noticeably greater compared to the percentage distribution in soil samples. These data once again prove that the air environment is not just a carrier of microorganisms, but a specific ecosystem, with specific characteristics and environmental conditions for the development of air microorganisms (Amato et al., 2023). The higher percentage of actinomycetes is probably related to the specificity of their spores and the way they spread, given their size and severity (Reponen et al., 1998).

The studied typical soil representatives of the genus *Bacillus: Bacillus cereus, Bacillus subtilis* and *Bacillus megaterium, Bacillus mycoides* were recorded both in all soil samples and in all air samples. When analyzing the data, over 69% of all CFU/m^3 of the studied bacilli developed in the petri dishes from the upper stages of the impactor, i.e. those that capture larger fractions. These data confirm the data that the soil particles fall mainly in the impactor range from 7 to 3.3 μm bacilli were also found in the remaining fractions, but in much smaller quantities.

The analysis revealed that soil samples were generally dominated by *Bacillus megaterium* and *Bacillus cereus*. In air samples, sequencing studies revealed that *Micrococcus luteus* and *Kocuria rosea* were dominant. Other studies also indicated that *Micrococcus luteus* and *Kocuria rosea* were common in the air (Fang et al., 2007; Turnbull et al., 2019). Other studies have found that the genus *Bacillus* constitutes a very large percentage of the microflora of outdoor air, while *Micrococcus* is part of the dominant airborne microorganisms in indoor spaces. Such data require in-depth studies on the mode of entry into the air and the distribution of airborne microorganisms (Fang et al., 2014).

The percentage of the studied bacilli (total) in the soil and air samples is presented in the Figure 3.

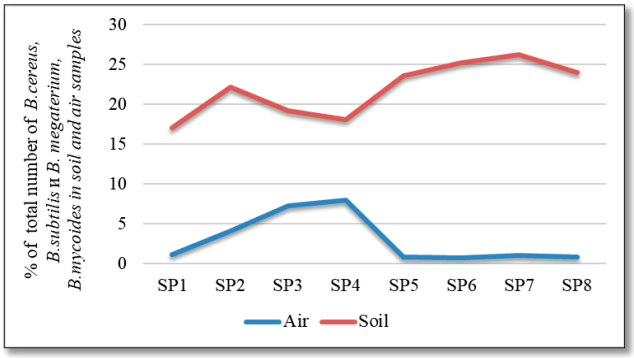


Figure 3. The percentage of the studied bacilli (total) in the soil and air samples

The results of the comparison of the distribution of typical soil microbial species in the air clearly show the influence of human activity. In samples from green areas, where there are no other anthropogenic activities except recreational ones, the percentage of the considered soil microorganisms is lower, compared to areas with some construction activities. Thus, the studied species of bacilli in these areas constitute only about one percent of the total microflora (SP5 - 0.83%; SP6 - 0.71%; SP7 - 1.1% and SP8 - 0.9%). In samples with different types of anthropogenic impact, the percentage of participation of typical soil microflora, represented by the four species of the genus Bacillus, increases. However, it is clearly seen that each of the considered above activities has a different impact on the distribution of typical soil microorganisms in the air environment. We conclude that with increasing anthropogenic load and the area of soil cover disturbance, the amount of typical soil microorganisms in the air increases. Thus, human activities with the most destructive nature of the soil layer (SP3 and SP4) show a much higher percentage of soil bacilli. In SP3, soil bacilli occupy 8.01% of the total microflora, and in SP2, respectively, 7.25%. This is over six times more than in samples without anthropogenic pressure. When we look at the data for SP1, it is impressive that the percentage of soil bacilli is almost similar to that of samples from the fields without anthropogenic pressure - SP1 - 1.2%. The results show that when manually treating the soil, sufficient amounts of soil particles are not generated at high to remain in the ground air and pose a threat to human health. It is important to note, however, that the current study was conducted at a height starting at 1.5 m. Given that garden workers are at a much lower height (around 0.5 m), we recommend that the activity be carried out while wearing protective masks, which minimize the risk of exposure to both fine dust particles and

pathogenic microorganisms. During the reconstruction of the sidewalk areas, given the use of mechanical equipment and the excavation of the peripheral soils, an increase in the percentage of the studied soil microflora in the air samples (4.07%) was observed. The results clearly show that with increasing anthropogenic pressure and increasing construction activities in the city, there is a real danger of increasing the amount of soil microflora in the air. The present study is a clear sign that it is necessary to increase the hygiene requirements during construction activities to minimize dusting. In general, we believe that it is necessary to pay serious attention to the overdevelopment of the city of Sofia, not only from an aesthetic point of view, but also in terms of the quality of the ground air around the construction sites.

CONCLUSIONS

The present study aimed to investigate the similarity of soil and air microbial communities from eight sample areas (four with increased anthropogenic pressure and four without anthropogenic pressure, only with the presence of recreational activity). The present study found that all air samples contained the studied soil-typical microorganisms (Bacillus: *Bacillus cereus*, *Bacillus* subtilis, *Bacillus megaterium*, and *Bacillus mycoides*), but in different quantities. The results of the present study show that in activities with reduced levels of soil destruction and reduced machine activity, the amount of soil bacilli considered as part of the air microflora is lower (SP1 - 1.12%). With the use of equipment that excavates the soil, albeit at a shallow depth, as in the case of the sidewalk reconstruction of SP2, the amount of microorganisms studied in the air increases to 4.07%. These results confirm the strong negative impact of permanent construction activities in the capital of Bulgaria - Sofia. Such data indicate the need to minimize excavation and construction activities on huge areas covering tens of acres, which pose a real risk to the quality of ground air in the surrounding residential areas. The elevated percentage of soil bacilli, particularly potential opportunistic pathogens such as *B. cereus* in areas with heavy construction activities (SP3 and SP4), carries significant public health implications. Inhalation of these bioaerosols bound to fine particulate matter can penetrate deep into the human respiratory tract, potentially causing respiratory diseases, allergies, or systemic infections in immunocompromised individuals residing near construction zones. In terms of urban planning, these findings underscore the urgent need for local authorities to implement stricter regulations on dust management during large-scale construction. Urban planners should integrate compulsory dust-suppression protocols (such as continuous water spraying of disrupted soils) into municipal building permits to maintain ground air quality in rapidly developing urban areas in Sofia. As a pilot study, a key limitation of this research is its specific timeframe (early September). Therefore, future longitudinal and seasonal studies are highly needed to investigate how temporal and meteorological variations, such as humidity, temperature, and precipitation, affect the emission and persistence of soil microorganisms in the urban atmosphere over different seasons.

This pilot study can serve as a basis for in-depth analyses of the possibility of excavation and construction activities to change not only the quantity of airborne microflora, but also to sharply alter its qualitative composition.

ACKNOWLEDGEMENTS

This research work was carried out with the support of Research Fund of Ministry of Education and Science in Bulgaria, project №: КП-06-Н74/5 “Relationships between the amount of fine particulate matter and airborne microorganisms in "hot spots", park areas, urban background areas and control forest areas”.

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