ABSTRACT

To assess the effects of soil contamination with fluorine compounds on plants, aqueous extracts of soil collected near a broiler farm where ciprofloxacin – a fluoroquinolone antibiotic – had been used. These extracts were used as a growth medium for model plants – common duckweed (*Lemna minor* L.). To exclude the influence of other potential contaminants, parallel cultures of *L. minor* were grown on Murashige and Skoog (MS) media containing fluoride concentrations corresponding to those measured in the soil extracts. Morphological traits, chlorophyll content, and the activity of enzymes involved in its metabolism were analyzed. Additionally, an *in vitro* experiment was conducted in which commercial chlorophyll *a* was incubated with NaF to identify potential chemical interactions between chlorophyll and fluoride ions.

No significant morphological changes were observed either in plants grown in soil extracts or under control conditions. However, in both variants a clear decrease in chlorophyll content and disturbances in the activity of enzymes involved in its metabolism were detected, including δ-aminolevulinic acid dehydratase (an enzyme of chlorophyll biosynthesis) and chlorophyllase (responsible for its degradation). *In vitro* incubation of chlorophyll *a* with NaF resulted in a shift of absorbance maxima in Soret and Qy bands. The observed spectral changes are similar to those described in the literature for fluorine substitution at the carbon atom 3^2 of chlorophyll molecule.

Arugula (*Eruca sativa* L.) is a commonly consumed raw plant and thus represents a model useful in epidemiological context for studying microbiome changes under environmental contamination. To compare the effects of fluoride ions and a fluoroquinolone (pefloxacin) on the plant microbiome, a four-week cultivation of *E. sativa* was carried out on soils enriched with NaF or pefloxacin. NaF concentrations corresponding to environmental levels of F^- and equimolar concentrations of the antibiotic were used. 16S rDNA metabarcoding was performed to analyze changes in the composition of rhizosphere and phyllosphere microbiomes.

Neither NaF nor pefloxacin caused significant morphological changes in *E. sativa*. However, both substances significantly affected microbiome structure in both rhizosphere and phyllosphere. The changes were more pronounced in the phyllosphere, particularly for NaF, where greater fluctuations in the abundance of individual taxa were observed. In both variants, bacterial taxa associated with plant growth and nitrogen assimilation greatly reduced their abundance. In NaF-treated samples, a significant increase in representatives of the order Burkholderiales was observed in the phyllosphere, while in all experimental variants the genus *Pedobacter* disappeared. Both taxa include microorganisms with pathogenic potential and the ability to transfer antibiotic resistance genes.

Additionally, functional profiling of the microbiome was performed using the PICRUSt2 (Phylogenetic Investigation of Communities by Reconstruction of Unobserved States) tool. The most significant changes concerned the abundance of genes associated with metabolic pathways, particularly those involved in carbon metabolism, indicating substantial disruption of central metabolic processes.

Based on the results obtained, it can be concluded that the storage of poultry manure from animals subjected to antibiotic therapy leads to the release of fluorine compounds in amounts harmful to plants. The negative effects of these compounds are manifested mainly at the physiological and biochemical levels, indicating that morphological assessment of bioindicator plants is insufficient for a full evaluation of their toxicity. The results also suggest the possibility of direct chemical interactions between fluoride ions and chlorophyll. Both pefloxacin and fluoride ions exert strong selective pressure on the plant microbiome, leading to the elimination of beneficial microorganisms and the selection of potentially pathogenic and antibiotic-resistant taxa. The observed changes in microbiome functional profiles, particularly in carbon metabolism, indicate a profound impact of these contaminants on the functioning of plant ecosystems.