

**Antibiotics and antibiotic resistance of soil bacteria in ecosystems**

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Antibiotics are extensively used for animal farming and for agricultural purposes. Residues from human activity and from farms may contain antibiotics and antibiotic resistance genes that can contaminate natural environments. The purpose of this study was to detect the antibiotic resistance soil bacteria in different ecosystems: Natural ecosystem (primeval forest) and agro-ecosystems. A total of 184 isolates from soil of primeval forest and rhizosphere of medicinal plants: *Mentha piperita*, *Inula helenium*, *Thymus serpyllum*, *Rosa odorata* and *Calendula officinalis* were examined for resistance to nine antibiotics. Among bacteria isolated from soil with cultivated *Thymus serpyllum* two of them: *Serratia marcescens* strain 428 and *Yersinia enterocolitica* strain 1020 were moderately resistant to majority of tested antibiotics. From the rhizosphere of *Inula helenium* was isolated one of the most antibiotics resistant bacteria among the others which were tested-*Pantoea agglomerans*. From agro-ecosystem of *Mentha piperita* was isolated and tested *Serratia odorifera* biogroup 1. This strain was resistant to vancomycin, lincomycin, and ampicillin, and moderately resistant to cefepime. From agro-ecosystems of *Calendula officinalis* and *Rosa odorata*, where used organic manure, high level of antibiotic resistance was detected for *Enterococcus faecalis* strains 321, 324 and *Bacillus cereus* (370). A study of soil samples from the primeval forests showed that the microbial community was characterized with low content antibiotic-resistant microorganisms. Among 78 isolated bacteria only two of them *Bacillus cereus*, strain 510 and *Pantoea agglomerans* (434) demonstrated high level of resistance to antibiotics. From this study it is concluded that there were marked differences between the levels of antibiotic resistance in soil microbial community of natural ecosystems and agro-ecosystems. The populations of soil microorganisms in agro-ecosystems were more antibiotic resistance. Two species of antibiotic-resistant bacteria *Bacillus cereus* and *Pantoea agglomerans* were common to both ecosystems. The effect of antibiotics on the biosphere is wide and can impact the structure and activity of environmental microbiota.

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