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Soil antibiotic resistome-risk for human health

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The soil antibiotic resistome bacteria play an important role in development and spread of antibiotic resistance in humans. There is little known about the natural bacterial resistome in soil. The purpose of this study was to detect the antibiotic resistance soil bacteria in different ecosystems: Natural ecosystem (primeval forest), agroecosystems and urboecosystems. Were isolated 384 dominating bacteria, among them 67 antibiotic resistant bacteria. All isolates were multi-drug resistant, of which greater than 68% were resistant to 9 antibiotics (vancomycin, lincomycin, ampicillin, cefepime, streptomycin, gentamicin, oleandomycin, ofloxacin, ciprofloxacin). A study of soil samples from the primeval forests showed that the microbial community characterized by a low content of antibiotic-resistant microorganisms. Among 78 isolated bacteria only two of them *Bacillus cereus*, and *Pantoea agglomerans* demonstrated high level of resistance to antibiotics. A total 106 strains were isolated from the soil of medicinal plants: *Mentha piperita*, *Inula helenium*, *Thymus serpyllum*, *Rosa odorata* and *Calendula officinalis*, 13 of them were antibiotic-resistant. High level of antibiotic resistance was detected for *Enterococcus faecalis*, *Bacillus cereus*, *Serratia marcescens*, *Yersinia enterocolitica*, *Pantoea agglomerans* and *Serratia odorifera* biogroup 1. Seven bacteria: *Enterococcus faecalis*, *Serratia marcescens*, *Yersinia enterocolitica*, *Enterobacter cloacae*, *Yersinia pestis*, *Hafnia alvei* and *Bacillus cereus* isolated from soil with cultivated winter wheat have displayed the high resistance to most of tested antibiotics. The greatest number of antibiotic-resistant bacteria have been isolated from soil of urboecosystems. Among the 118 tested bacteria, 30 were antibiotic resistant. Multi-resistance were such pathogens as: *Enterococcus faecium*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa* and *Escherichia coli*.

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