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Microbial analysis of “bio-guss” compost tea

The “bio-guss” compost tea, produced by GARTENleben GmbH, is a plant fertilizer with beneficial effects on plants. It is a mixture containing worm-compost, organic herbs, stone dust and other ingredients. The product is supplied in bags intended for preparation of a water extract, which is used for watering of plants.

A microbial analysis of the “bio-guss” compost tea, performed in the frame of this project, was conducted for better understanding the mode of action of the water extract and how it causes the beneficial effects on plants. The aim was to analyze the bacterial composition of the “bio-guss” compost tea. Total counts of cultivable bacteria under different cultivation conditions were determined. Dominant bacterial species present in the analyzed samples were isolated and identified.

Results:

Water extracts of the “bio-guss” compost tea (prepared according to the manufacturer’s instruction) were well colonized by microorganisms. Total counts of the cultivated bacteria ranged from 10^9 to 10^{11} colony forming units (CFU) per teabag, on average. In the frame of this project, we identified only dominant cultivable bacteria growing on basic common media, which comprise only a small proportion of the total microbiota occurring in the environment. It is most likely that the “bio-guss” compost tea contains also cells and/or spores of microorganisms, which do not grow under laboratory conditions or require special growth conditions. Those microbes in general cannot be detected with the methods used in our laboratory.

The “bio-guss” extract contained quite a high number of facultative anaerobic bacteria (on average 1.8×10^{11} CFU per teabag), which grew in aerobic as well as in anaerobic conditions. Thermotolerant species, capable to grow at up to 50°C, were also quite abundant in the extract (1.2×10^{11} CFU per teabag).

The most abundant species were isolated and identified by microscopy and colony morphology description, followed by an extensive biotyping.

In total, we isolated more than 40 bacterial strains. Gram-positive spore-forming and nonspore-forming rods were the most abundant bacterial groups followed by Gram-negative fermenting rods. Moreover, four isolates of streptomyces were isolated.



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According to the identification results, Gram-positive spore-forming rods were represented by *Bacillus* spp. (species *B.adius*, *B. coagulans*, *B. lentus*, *B. megaterium* and *B. subtilis*) and *Paenibacillus* sp. From the Gram-negative fermenting rods, *Enterobacter cancerogenus*, *Enterobacter cloacae*, *Escherichia coli* and *Buttiauxella* sp. were most often identified in the extract. Further isolates were identified as *Microbacterium* sp., *Curtobacterium albidum*, *Exiguobacterium acetylicum* and *Acinetobacter* sp.

According to the results of biochemical tests, **isolated bacteria showed rich enzymatic activities**. They were able to utilize a wide spectrum of carbohydrates and hydrolyse peptides, lipids, large polysaccharides and DNA. Some of the isolates also reduced nitrate and nitrite which indicates possible denitrification activity. These characteristics revealed that the isolated **microorganisms are well adapted to decompose various organic substrates and thus contribute to organic matter and nutrient cycling in soil**.

In general, **we isolated bacterial species that are commonly represented in the environment** - in soil, water, plants and organic matter. Gram-positive spore-forming bacilli are an important group of bacteria. They colonize various habitats, however, they are considered to be autochthonous soil organisms. **Bacilli** are saprophytes and **represent an important part of the rhizospheric microflora**. Due to the spore formation they are able to survive adverse conditions such as lack of nutrients in soil. Since they can degrade various substrates (e.g. proteins, starch) they play a significant role in the biological cycling of carbon and nitrogen and hence **contribute to soil fertility**. Moreover, certain bacilli strains produce various antimicrobial substances. The genus *Enterobacter* is widespread in the environment; it originally inhabits the gastrointestinal tract of warm-blooded animals from where it reaches soil, water, sewage plants, etc. **Streptomyces play an important role in degradation of cellulose. Therefore they are important in decomposition of organic matter and make it available for plants and other organisms.**

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