Identification of phytopathogenic fungi and oomycetes from peat substitute substrates

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In the current global concern about climate change, the protection of peatlands is becoming increasingly important, leading to a reduction in the use of peat in substrates for horticulture.

As part of the project "Development and evaluation of peat-reduced production systems in horticulture (ToPGa)", mycological influences associated with peat-reduced culture media are being investigated, with a major focus on preloading fungi and oomycetes on peat substitutes, of which potential plant pathogens are important.

In this research work, the use of fiber nettle (*Urtica dioica* L. convar. *fibra*) as well as digestate (fermentation residue) from biogas generator plants as possible components of peat substitutes is investigated. The possible pre-contamination of the substrate components with fungi and oomycetes is considered in order to classify the isolated species according to their lifestyle and consequently to identify possible phytopathogenic species.

Sample material from digestate and fiber nettle was first prepared for isolation of microorganisms.

For the isolation of fungi, two main methods were used: first, isolation via dilution series (Waksman, 1922) and second, by directly placing material on nutrient media (Warcup, 1950). For the isolation of oomycetes, a bait test with rhododendron leaves was used (Junker et al. 2018). All three methods aim to culture living fungi and oomycetes found in the samples.

After isolation, DNA was extracted from the cultures and PCR of the ITS region was performed. Subsequently, the PCR products were purified and sequenced.

Microorganisms were identified by comparing their sequences (BLAST) with those in NCBI GenBank and by morphological determination of the cultures.

The partial results of the current work show a collection of 144 fungal isolates from the digestate and fiber nettle samples. These isolates were successfully identified at the genus level. To date, no oomycetes have been isolated from the samples.

Processing is ongoing and new samples are currently being processed and additional organisms isolated.

After identification at the species level, classification by lifestyle and thus determination of plant pathogens will proceed.