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REMOVAL OF TEXTILE DYE (RBBR) FROM WATER

ENVIRONMENT BY FUNGI FROM LIGNOCELLULOSIC COMPOSTS

Justyna Bohacz, Teresa Kornilowicz-Kowalska, Michał Możejko

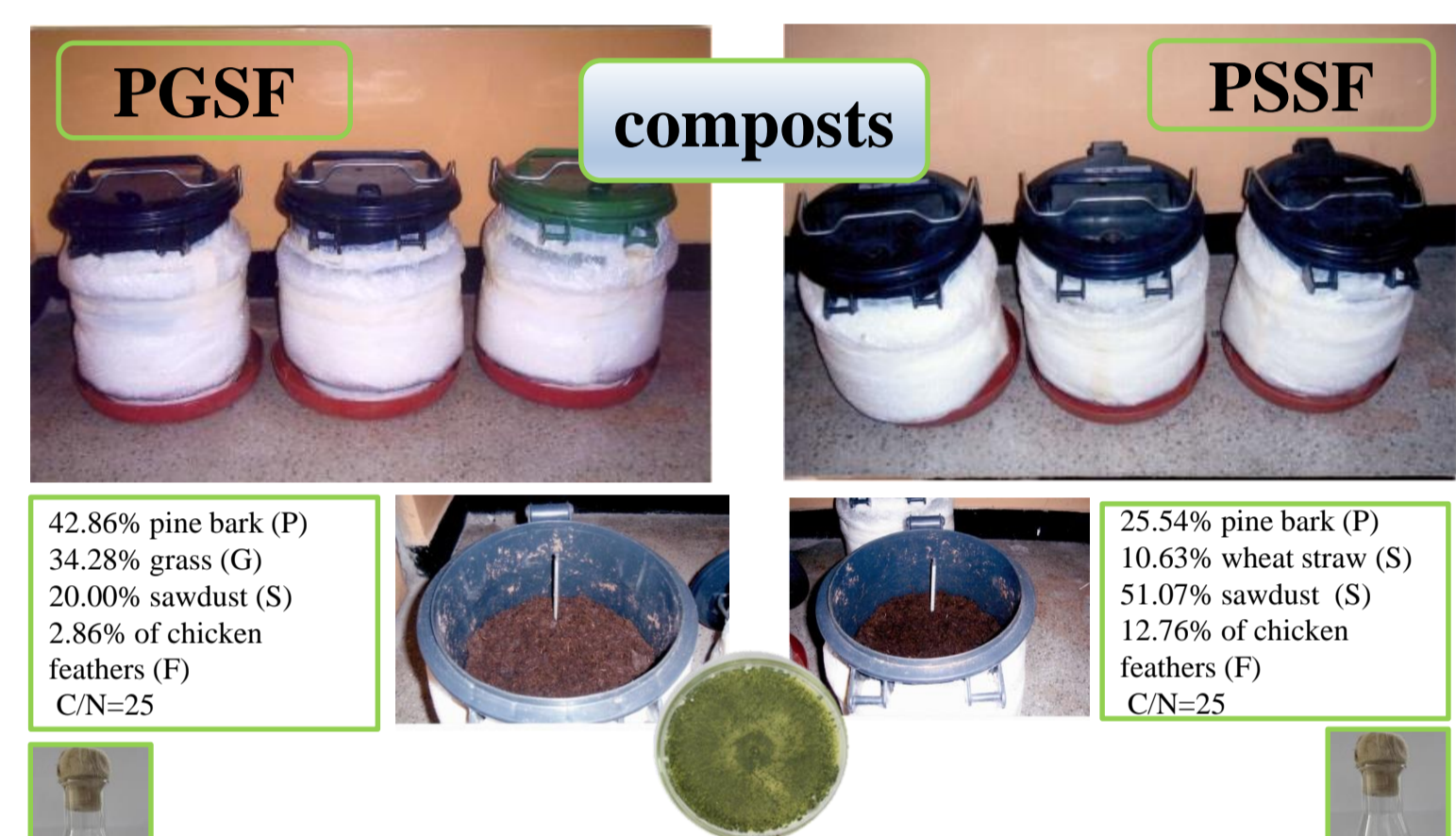
University of Life Sciences in Lublin, Faculty of Agrobiotechnology, Department of Environmental Microbiology, Laboratory of Mycology, Leszczyńskiego 7 Street, 20-069 Lublin, Poland

justyna.bohacz@up.lublin.pl

Introduction

The textile industry, apart from processing raw materials into fibers, fabrics or knits, produces colored wastewater as by-products containing various pollutants, *inter alia*, dyes among which, anthraquinone dyes such as remazol blue are one of the most important. Remazol Brilliant Blue R (RBBR) belongs to these harmful textile dyes, which, after getting into the waters, destroy living organisms. Existing physico-chemical methods of removing these pollutants are not environmentally friendly because they contribute to the formation of secondary toxic colorless products. Biological methods are the environmentally friendly, alternative methods of decolorization of post-dye wastewater. Currently, many scientific centers are searching for effective strains of microorganisms that can be used in the decolorization and detoxification of post-industrial wastewater.

Materials and Methods



The biodegradation abilities of the tested *Trichoderma* strains were evaluated in aqueous solutions obtained after cultures containing 0.02% Remazol Brilliant Blue R (RBBR) as a substrate. Periodically, the percentage of RBBR decolorization was determined as a reliable indicator of detoxification of anthraquinone dyes and the activity of horseradish peroxidase, superoxide dismutase and xylanase was also determined. The concentration of phenolic compounds and the pH of the post-culture liquid were also measured. In order to show significant differences between strains at the significance level of $p < 0.05$ the Tukey's HSD test was used.

Table 1 Results of molecular identification of *Trichoderma* strains

Time of isolation (weeks)	Number of strain	Compost I (PGSF)			Accession number GenBank
		strains	Similarity %	Sequence similarity %	
10	VII	<i>Trichoderma harzianum</i>	100	100	MH571704.1
20	XII	<i>Trichoderma lixii</i>	100	100	MH 602297.1
30	XIX	<i>Trichoderma asperellum</i>	100	100	MH 602236.1
Compost II (PSSF)					
10	VI	<i>Trichoderma citrinoviride</i>	100	100	MH 602423.1
20	VIII	<i>Trichoderma citrinoviride</i>	100	100	MH 602287.1
30	XXV	<i>Trichoderma citrinoviridae</i>	100	100	MH 602289.1

Conclusions

The highest RBBR decolorization abilities showed *Trichoderma asperellum* and *T. harzianum* strains. Darkening of the medium was observed in *Trichoderma citrinoviride* strain cultures. The dynamics of changes in horseradish peroxidase activity, superoxide dismutase and xylanase in aqueous post-culture solutions of the tested fungal strains depended significantly on culture duration as well as on the strains themselves. It was found that peroxidase activity in cultures of *Trichoderma asperellum* strains was highest for the first 14 days of the experiment; in cultures of three *T. citrinoviridae* strains on week 16 and 20 and in *T. lixii* and *T. harzianum* cultures at the end of the experiment, *i.e.* on day 28 and 32 of the culture. Superoxide dismutase in *T. lixii* and *T. citrinoviride* cultures reached the highest level up to the 16th day of culture. The activity of xylanase in cultures of all fungal strains was high till day 12 of the culture. Fungi of the genus *Trichoderma*, in particular *Trichoderma asperellum*, through the high percentage of Remazol Brilliant Blue R decolorization, release of redox enzymes and low-molecular phenolic compounds, can catalyze the biodegradation and detoxification of colored anthropogenic pollutants of aromatic structure. In addition, the high ability of *Trichoderma* adaptation to the aquatic environment, including sewage, provides them an advantage over other fungi in the bioremediation of aquatic environments.

The aim of the work

The aim of the work was to evaluate the abilities of six strains of the genus *Trichoderma*, selected from lignocellulosic composts, to remove anthraquinone dyes from the aquatic environment. Selected strains: *T. asperellum* Samuels, Lieckf. & Nirenberg, *T. lixii* (Pat.) P. Chaverri, *T. harzianum* Rifai and 3 *T. citrinoviride* Bissett strains were identified to the species using molecular methods (nucleotide sequences) and traditional methods (phenotypic traits). The nucleotide sequences of the identified strains were submitted to GenBank.

Results

