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SELECTION OF FUNGI FOR THE PRODUCTION OF ENZYMES WITH POTENTIAL FOR INDUSTRIAL APPLICATION

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1. INTRODUCTION

Enzymes can be used in different types of textile processing steps, while the alternatives are very aggressive chemicals whose disposal in the environment causes many problems. However, the high cost and lack of long-term stability under storage and process conditions often make their applications difficult. Therefore, the development of low-cost customized enzymatic cocktails, which contain enzymes capable of performing more than one textile treatment simultaneously, constitutes an alternative to reduce the costs of textile enzymatic treatment. In this context, this work aimed to characterize the enzymatic profile of a collection of lignocellulolytic fungi aiming at selecting enzyme-producing strains with potential for application in the processing of cotton fabrics.

2. METHODS

Thirty-five lignocellulolytic fungal strains (wild-type) from the Collection of Microorganisms and Microalgae Applied to Agroenergy and Biorefineries (CMMAABio) were characterized for their ability to produce enzymes with potential for cotton fabrics processing. Total cellulase activity on filter paper (FPase), β-glucosidase (BG), endoglucanase (EG), xylanase (XYL), and polygalacturonase (PG) activities were evaluated to select the most suitable enzyme profile strains for the biostoning process (mainly EG activity in its composition). Each strain was cultivated in its original culture condition (under submerged fermentation conditions). For 33 strains, the culture media used contained sugarcane bagasse pretreated by autohydrolysis, wheat bran, and Mandels' salts as nutrients, supplemented with 0.1% PEG 6000 or Triton X-100 (Sousa, 2017; Peixoto, 2019). In addition, the optimized culture media described by Damaso et al. (2019) and Gomes et al. (2019) were used for two strains. Flasks were inoculated with five mycelial plugs and incubated in a rotary shaker at 28-32°C and 180 rpm (depending on the fungal strain). Aliquots of the supernatant were collected for enzyme and total protein quantification after five days of cultivation. The samples were kept at 4°C for 15 days, and the enzymatic activities and total protein content were reassessed to test their stability. The experiments were performed in quadruplicate. One unit of enzymatic activity was defined as the amount of enzyme capable of releasing one µmol of sugar per minute per milliliter of reaction (IU/mL). The statistical analysis was carried out with Excel software to detect the means and standard deviation values.

3. RESULTS AND DISCUSSION

After evaluating 35 pre-selected fungal strains (**Table 1**), the supernatants of the *Talaromyces* sp. BRM058818, *Trichoderma* sp. BRM065713 and *Neofusicoccum* sp. BRM063874 showed the highest values of EG (0.374±0.006 IU/mL), XYL (137.652±18.205 IU/mL), and FPase (2.155±0.217 IU/mL), respectively. Polygalacturonase (pectinase) activity was not detected in any of the supernatants evaluated. The supernatants of the *Talaromyces* sp. BRM058818, *Trichoderma* sp. BRM065713 and *Neofusicoccum* sp. BRM063874 maintained 47.05% (EG), 4.34% (XYL), and 10.62% (FPase) of the original activities after 15 days at 4°C.

Table 1. Enzyme profile of 35 fungal strains pre-selected from the CMMAABio culture collection. The indicated values are the means of four repetitions followed by the standard deviations.

Fungal strain	EG (IU/mL)	FPase (IU/mL)	XYL (IU/mL)	PG (IU/mL)	BG (IU/mL)	Total protein (mg/mL)
Talaromyces sp. BRM058818	**0.374±0.006**	1.170±0.086	32.359±8.086	0.000±0.000	0.585±0.029	4.282±0.501
Talaromyces sp. BRM063883	0.352±0.045	0.499±0.083	5.587±0.550	0.000±0.000	0.265±0.075	3.094±0.724
Not identified BRM051259	0.300±0.019	0.898±0.024	42.457±8.595	0.000±0.000	0.218±0.033	3.596±0.560
Talaromyces sp. BRM058502	0.295±0.036	0.380±0.106	112.875±2.163	0.000±0.000	0.657±0.026	2.947±0.604
Penicillium sp. BRM052264	0.292±0.029	0.732±0.039	6.252±0.749	0.000±0.000	0.232±0.016	12.839±0.659
Trichoderma sp. BRM063885	0.277±0.143	0.398±0.088	94.768±22.169	0.000±0.000	0.142±0.071	3.421±0.991
Aspergillus sp. BRM058564	0.276±0.022	0.615±0.014	33.485±5.706	0.000±0.000	0.104±0.068	2.110±0.436
Trichoderma sp. BRM057311	0.273±0.060	0.087±0.002	0.000±0.000	0.000±0.000	0.000±0.000	7.963±1.503
Trichoderma sp. BRM058752	0.260±0.016	0.159±0.022	0.000±0.000	0.000±0.000	0.298±0.008	4.676±0.087
Penicillium sp. BRM057056	0.230±0.025	0.718±0.046	4.748±0.961	0.000±0.000	0.141±0.033	8.432±0.699
Epicoccum sp. BRM058216	0.218±0.018	0.201±0.020	5.974±0.275	0.000±0.000	0.288±0.029	2.947±0.193
Diaporthe sp. BRM058724	0.217±0.045	0.281±0.015	7.618±2.132	0.000±0.000	0.152±0.023	2.369±0.027
Trichoderma sp. BRM065713	0.214±0.008	0.168±0.031	**137.652±18.205**	0.000±0.000	0.208±0.024	2.506±0.337
Trichoderma sp. BRM058797	0.206±0.014	0.315±0.021	4.415±0.745	0.000±0.000	0.044±0.022	7.800±0.853
Trichoderma sp. BRM 064739	0.197±0.002	0.235±0.025	0.524±1.650	0.000±0.000	0.000±0.000	2.370±0.360
Diaporthe sp. BRM058797	0.197±0.024	0.085±0.006	0.000±0.000	0.000±0.000	0.000±0.000	7.126±0.488
Aspergillus sp. BRM058619	0.193±0.030	0.158±0.019	50.492±7.345	0.000±0.000	0.000±0.000	1.973±0.442
Trichoderma sp. BRM065715	0.182±0.016	0.212±0.041	1.040±1.232	0.000±0.000	0.000±0.000	2.305±0.315
Trichoderma sp. BRM057347	0.160±0.007	0.089±0.010	0.000±0.000	0.000±0.000	0.000±0.000	3.988±0.502
Talaromyces sp. BRM058850	0.158±0.061	0.112±0.024	0.000±0.000	0.000±0.000	0.000±0.000	4.111±0.589
Not identified BRM063880	0.142±0.010	0.957±0.203	32.309±5.487	0.000±0.000	0.067±0.026	1.791±0.494
Talaromyces sp. BRM052263	0.134±0.006	0.218±0.010	2.257±0.367	0.000±0.000	0.217±0.020	3.592±0.076
Aspergillus sp. BRM058815	0.130±0.010	0.172±0.006	2.736±0.300	0.000±0.000	0.000±0.000	1.824±0.150
Diaporthe sp. BRM052995	0.121±0.008	0.139±0.008	7.404±0.811	0.000±0.000	0.143±0.044	0.332±0.146
Diaporthe sp. BRM 065720	0.111±0.010	0.312±0.037	0.073±0.112	0.000±0.000	0.023±0.016	2.394±0.194
Diaporthe sp. BRM 065719	0.110±0.006	0.580±0.049	0.347±0.095	0.000±0.000	0.139±0.021	2.460±0.049
Diaporthe sp. BRM 065718	0.107±0.009	0.635±0.097	0.325±0.080	0.000±0.000	0.163±0.042	2.098±0.218
Fusarium sp. BRM063875	0.102±0.008	0.877±0.060	0.088±0.124	0.000±0.000	0.015±0.009	2.614±0.214
Not identified BRM058477	0.099±0.007	0.124±0.037	10.127±3.106	0.000±0.000	0.000±0.000	2.905±0.139
Talaromyces sp. BRM058539	0.096±0.004	0.106±0.014	0.100±0.129	0.000±0.000	0.000±0.000	2.768±0.170
Trichoderma sp. BRM063884	0.090±0.006	0.091±0.002	86.434±0.401	0.000±0.000	0.000±0.000	2.187±0.276
Trichoderma sp. BRM065716	0.088±0.011	0.091±0.007	1.211±3.374	0.000±0.000	0.000±0.000	0.899±0.364
Trichoderma sp. BRM065717	0.081±0.006	0.099±0.007	61.597±1.518	0.000±0.000	0.000±0.000	1.936±0.937
Neofusicoccum sp. BRM063874	0.080±0.007	**2.155±0.217**	0.408±0.079	0.000±0.000	0.229±0.029	3.494±0.190
Omnidemptus sp. BRM057051	0.065±0.003	0.066±0.004	0.000±0.000	0.000±0.000	0.000±0.000	2.436±0.264

4. CONCLUSIONS

The fungal strains *Talaromyces* sp. BRM058818, *Trichoderma* sp. BRM065713, and *Neofusicoccum* sp. BRM063874 could be candidates to optimization of their cultivation to increase enzyme production and develop enzymatic processes for the processing of cotton fabrics.

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