



## **An AFLP study of PHA-degrading Black Aspergilli strains.**

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Polycyclic aromatic hydrocarbons (PHA) pollutants result from natural (forest fires) or human activity (automobile exhaust, coal refining processes, oil industry ...). They are widely distributed in the environment and 16 of them have been listed as priority pollutants by the Environmental Protection Agency. While a considerable amount of information is available on the bacterial PAH metabolism, little is known about PAH metabolism by fungi. *Aspergillus niger*, a strain belonging to the nigri group (or Black Aspergilli), is one of the most important taxa of filamentous fungi for industry: several of them are used in the fermentation industry to produce different hydrolytic enzymes such as amylases or lipases and organic acids like citric and gluconic acid. Recently, there are candidates for genetic manipulation in the biotechnological industries since *A. niger* has been granted the GRAS (generally regarded as safe) status by the food and Drug administration. Many strains of *A. niger* are known to efficiently degrade PHA, leading to the possibility of using them in bioremediation. Thus, the identification of efficient PHA-degrading strains and the PHA degrading system are important issues.

Given the use of *A. niger* strains in biotechnology and bioremediation, a ground work in taxonomy is needed for rigorously establish their taxonomic position. This work will simplify the search of improved PHA-degrading strains. The classical systematic of black Aspergilli (based on morphologic characters such as colour, size, form and conidial ornamentation) does not lead to an unambiguous classification. Alternative molecular techniques such as DNA sequencing, RFLP analysis of mitochondrial and chromosomal DNA, and RAPD analysis where also used. In most of the cases they failed to recognize intra- and inter-species variation among the black Aspergilli. The main drawback of these techniques is that they only use a single molecular marker per genome. AFLP (Amplified Fragments Length Polymorphism) is a molecular tech-

nique that allows the simultaneous study of hundreds of molecular site per genome. In this study we report the use of this technique to fine-tune the taxonomy of black *Aspergilli*. Our results show that AFLP better recognize intra- and inter-species variation than the ITS-5.8S rDNA patterns.

Our results show that the AFLP technique has a better discriminatory power than other molecular tools (such as ITS sequencing), for all taxonomic levels, providing a better phylogenetic resolution. This study will be extended to environmental an PHA-degrading strains.