A NOVEL APPROACH FOR MYCOTOXIGENIC FUNGI IDENTIFICATIONS BASED ON UNCOMPLICATED MICROSCOPY AND MYCOTOXIN CHARACTERS

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Species concepts within fungi are (a) subject to frequent revision and (b) unusually protean. However, this allows novel schemes some scope to be considered. The taxonomy of the penicillia is unstable particularly in the important antibiotic and mycotoxin-producing subgenus *Penicillium*. Non-specialists in particular encounter difficulty with assigning names to taxa. Name changes of important fungi have occurred frequently and recently. There are difficulties relating identifications to mycotoxin production. This is necessary for controlling mycotoxin contamination in food, drink, homes, etc. Patulin is an important mycotoxin produced by various fungi and has strict limits in the European Union and elsewhere. Also, it is a useful model mycotoxin per se. The mycotoxin and/or the isoepoxydon dehydrogenase (IDH) gene of the metabolic pathway have been assessed in 318 strains predominately of subgenus *Penicillium*. These data were used to classify the isolates, although the applied aspects of the scheme are emphasised over the purely taxonomic. Of course, the issue of whether to apply a dual nomenclature to different states of pleomorphic fungi is relevant. Subgenus Penicillium contained most of the IDH and patulin positives. Many of species contained positive and negative members, which demonstrates that identifications based on morphology do not indicate patulin production. The species and varieties in subgenus *Penicillium* which have been associated with patulin production can be reduced to one name, viz. Penicillium Pen p+, where p is the abbreviation of patulin. This basic concept has been extended to other mycotoxin producing fungi within the subgenus using published data to indicate the utility of the scheme. The classification will lead naturally to the number of taxa being reduced. In addition, more meaningful results are obtained in terms of assessing the potential for patulin production. The possibilities of direct analysis of environmental samples are also discussed. The scheme could be used with advantage for other fungi.

Acknowledgements:

R.R.M. Paterson is grateful for grant SFRH/BPD/14923/2004 from Fundação para a Ciência e a Tecnologia (FCT), Portugal.