

An Applied Identification Scheme for *Penicillium*

Paterson, R.R.M., Venâncio, A., Lima, N.

The goal is to provide an objective and practical identification scheme for *Penicillium* by using patulin as an example. The taxonomy of penicillia is unstable particularly in the important antibiotic and mycotoxin-producing subgenus *Penicillium*. Non-specialists especially encounter difficulty with assigning names. 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, etc. Patulin is an important mycotoxin which has strict limits in the USA, European Union and elsewhere.

Patulin and/or the isoeipoxydon dehydrogenase (IDH) gene of the metabolic pathway have been analysed in 318 strains of *Penicillium*. The procedures involved predominately TLC and the PCR. These data were used to classify the isolates, although the applied aspects of the scheme are emphasised.

Subgenus *Penicillium* contained most of the IDH and patulin positives. Many of the taxa were represented by positive and negative IDH and patulin detection included within each species. Numerous species were included in each category of patulin detection, IDH detection, etc.

The species and varieties in subgenus *Penicillium* which are associated with patulin production can be reduced to one name, viz. *Penicillium Penicillium* patulin positive. This can be abbreviated to, *Penicillium* Penpat⁺. Other examples are *Penicillium* PenIDH⁺; *Penicillium* PenIDH⁺pat⁺. The occurrence of positive and negative detection within species demonstrates that identifications based on morphology do not necessarily indicate patulin production. The classification will lead naturally to the number of taxa being reduced dramatically. In addition, more meaningful results are obtained in terms of the potential for patulin production. The identification can accommodate quantitative data, and the concept could be extended usefully to other fungi. Identifications will be useful particularly to those attempting to identify weak spots in food commodity systems.

Paterson, R.R.M., Venâncio, A. and Lima, N. 2004. *Research in Microbiology* 155: 507-513.