

Biodiversity informatics: how to reveal epigenetic imprints on secondary metabolism.

In contrast to yeasts, filamentous fungi can express an impressive array of secondary metabolites and enzymes, even in pure culture. However, bioinformatics on genome sequenced fungi has shown that the potential of producing even more secondary metabolites is huge. The exometabolome, exoproteome, exoglycome and exolipidome of fungi are still being explored, and one would expect many new chemical compounds being discovered via epigenetic manipulations on these fungi. Artificial genetic modifiers have been used with success for expressing secondary metabolites that hitherto were unknown for the particular species. However the use of different production media and organismal interactions has occasionally been sufficient to have the filamentous fungi express their cryptic secondary metabolites. Here I introduce a new way of discovering unexpected secondary metabolites: by exploring the diversity within a given species, it seems that “epigenetic priming” results in some of the isolates expressing one or more of the “cryptic” secondary metabolites.