Penicillium arizonense, a new, genome sequenced fungal species, reveals a high chemical diversity in secreted metabolites

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A new soil-borne species belonging to the Penicillium section Canescentia is described, Penicillium arizonense sp. nov. (type strain CBS 141311T = IBT 12289T). The genome was sequenced and assembled into 33.7 Mb containing 12,502 predicted genes. A phylogenetic assessment based on marker genes confirmed the grouping of P. arizonense within section Canescentia. Compared to related species, P. arizonense proved to encode a high number of proteins involved in carbohydrate metabolism, in particular hemicellulases. Mining the genome for genes involved in secondary metabolite biosynthesis resulted in the identification of 62 putative biosynthetic gene clusters. Extracts of P. arizonense were analysed for secondary metabolites and astalides, pyripyropenes, tryptoquivalines, fumagillin, pseurotin A, curvulinic acid and xanthoepocin were detected. A comparative analysis against known pathways enabled the proposal of biosynthetic gene clusters in P. arizonense responsible for the synthesis of all detected compounds except curvulinic acid. The capacity to produce biomass degrading enzymes and the identification of a high chemical diversity in secreted bioactive secondary metabolites, offers a broad range of potential industrial applications for the new species P. arizonense. The description and availability of the genome sequence of P. arizonense, further provides the basis for biotechnological exploitation of this species.

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