CONSTRUCTION OF A SECONDARY METABOLITE DEFICIENT PENICILLIUM CHRYSOGENUM STRAIN AS A GENERIC PRODUCTION HOST FOR SECONDARY METABOLITES

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Secondary metabolism of the filamentous fungus *Penicillium chrysogenum* has been intensively explored to relate specific secondary metabolites to their respective biosynthetic gene clusters. We have removed the three main biosynthetic gene clusters that specify the antibiotic penicillin, the mycotoxin roquefortine and the yellow pigment chrysogine, in order to generate a secondary metabolite deficient strain. This strain produces increased levels of other secondary metabolites some of which have not been detected before. The strain and its biosynthetic potential will now be further investigated for the expression of novel enzymes and biosynthetic pathways to make the synthesis of antibiotics and other secondary metabolites more specific and efficient. Using structure guided protein engineering new enzymes will be further designed and optimized for the construction of a newly designed biosynthetic pathway into a novel platform strain.