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Modelling of *Bacillus amyloliquefaciens* CCMI 1051 cultures using artificial intelligence based tools

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Abstract

It is well known that *Bacillus* species produce a wide variety of metabolites with interesting biological activities, namely antibiotic compounds as iturinic lipopeptides, being the aspartic acid a favourable nitrogen source for iturinic compouns production by *B. subtilis* and by *B. amyloliquefaciens*. The incubation time is another factor to be considered on antibiotic production.

On the other hand, Artificial Neural Networks (ANN) are widely accepted as a tool that offers an alternative way to tackle complex problems. They can learn from examples, are fault tolerant in the sense that they are able to handle noisy and incomplete data, are able to deal with non-linear problems, and once trained can perform prediction and generalization at high speed.

The prediction of Bacillus sporulation (BS) and antifungal activity of compounds (AFA), from incubation time of cultures (IT) and from aspartic acid concentration (AA) is a complex and highly nonlinear problem for which there are no known methods to predict them directly and accurately.

The aim of this study is to optimize the production of antifungal compounds in B. *amyloliquefaciens CCMI 1051 cultures* using ANN. The database to be used contains anti-fungal data of cultures with different IT (1-9 days) using AA (0.4-5.6 g/L) as nitrogen source [1].

In order to obtain the best prediction of the AFA and BS, different network structures and architectures have to be elaborated. The optimum number of hidden layers and the optimum number of nodes in each of these will be found by trial and error. The model being depicted above was in meam time accomplished, and the results obtained with it appointed that the maximum AFA is achieved with 2.6 g/L of aspartic acid on day 9. However, with AA of 4.8 g/L a similar maximum value of activity is obtained for incubação time over 6 days. The model shows a dual behaviour for AFA, depending of the IT. When the IT is higher than 5 days the AFA versus AA shows a pronounced sigmoid profile, converging to a common maximum value of AFA. On the other hand, for IT lower than 5 days mentioned profile is ill-defined and the common converging point isn't observed.

The conclusion is that the use of ANNs show to be a potent computational tool that must be present in any intelligent predictive task applied to Bacillus cultures, evidencing nitrogen source as key factor to be considered in these kind of problems, where the time of incubation plays a role in secondary production of active compounds.

[1] Caldeira A.T., Savluchinske-Feio S., Arteiro Santos J.M., Coelho, A.V., Roseiro J.C (2008) Journal of Applied Microbiology, 104, 808–816.