QSAR STUDY FOR ANTIBACTERIAL ACTIVITY FROM MOLECULAR STRUCTURES OF BENZAMIDE AND OXAZOLIDINONE DERIVATIVES

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ABSTRACT

QSAR STUDY FOR ANTIBACTERIAL ACTIVITY FROM MOLECULAR STRUCTURES OF BENZAMIDE AND OXAZOLIDINONE DERIVATIVES

Quantitative Structure-Activity Relationship (QSAR) approach is one of fields in computational chemistry. There are many successful predictive models developed for various activity predictions. Due to the emergence of new patterns of resistance of bacteria to antibacterial agents, new antibacterial agents are needed. Data of benzamide and oxazolidinone derivatives from previous studies were reanalyzed for their antibacterial activities by using different descriptors generated by DRAGON 5. Two methods of variables selection were used, which are stepwise regression and forward selection procedures available in MINITAB 14 statistical software. Multiple linear regressions (MLR) analysis was used in developing QSAR models to determine whether the descriptors used can give good QSAR model. The QSAR models have been evaluated and validated to determine their stabilities and prediction capabilities. Six QSAR models have been developed and their statistical results were compared with data from the previous studies. Four QSAR models developed have higher correlation coefficient, R^2 and cross-validation R^2_{cv} values, showing higher stabilities and prediction capabilities. The best QSAR model has R^2= 0.93 and R^2_{cv}= 0.91 and three descriptors were included in this QSAR model. The R^2_{cv} for –log MIC of *B. subtilis* is 0.912, *S. aureus* is 0.710, *E. coli* is 0.766, MIC of *A. ficcum* is 0.272, *A. paraciticus* is 0.789, and log (1/C) of *S. aureus* is 0.692.

CHAPTER 1

INTRODUCTION

1.1 Computational chemistry

Computational chemistry is a discipline using mathematical methods for the calculation of molecular properties or for the simulation of molecular behaviour assisted by computers. Computational chemistry is used to model molecular system before synthesizing that molecule in the laboratory. This information is very useful because synthesizing a single molecule could require a long period of time and raw materials, and also generate toxic waste. Thus, problem in research can be solved by using computer as an instrument. Computational models may not be perfect but they are often good enough to exclude 90% of possible compounds as being inappropriate for their proposed use (Young, 2001).

Other use of computational chemistry is to understand the problem completely. There are some properties such as structure of a molecule that can be obtained computationally more easily than by experimental means. There are also insights into molecular bonding, which can be obtained from the result of computations, and cannot be obtained from any experimental method. So that, many researchers now are using computational modelling to