Molecular Topology for the Search of New Anti-MRSA Compounds

by **Jose I. Bueso-Bordils** [1,*], **Pedro A. Alemán-López** [1], **Rafael Martín-Algarra** [1], **Maria J. Duart** [1], **Antonio Falcó** [2] and **Gerardo M. Antón-Fos** [1]

[1] Departamento de Farmacia, Universidad Cardenal Herrera-CEU, CEU Universities C/Ramón y Cajal s/n, 46115 Alfara del Patriarca, Valencia, Spain

[2] ESI International Chair@CEU-UCH, Departamento de Matemáticas, Física y Ciencias Tecnológicas, Universidad Cardenal Herrera-CEU, CEU Universities San Bartolomé 55, 46115 Alfara del Patriarca, Valencia, Spain

* Author to whom correspondence should be addressed.

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Abstract

The variability of methicillin-resistant *Staphylococcus aureus* (MRSA), its rapid adaptive response against environmental changes, and its continued acquisition of antibiotic resistance determinants have made it commonplace in hospitals, where it causes the problem of multidrug resistance. In this study, we used molecular topology to develop several discriminant equations capable of classifying compounds according to their anti-MRSA activity. Topological indices were used as structural descriptors and their relationship with anti-MRSA activity was determined by applying linear discriminant analysis (LDA) on a group of quinolones and quinolone-like compounds. Four extra equations were constructed, named DF_{MRSA1}, DF_{MRSA2}, DF_{MRSA3} and DF_{MRSA4} (DF_{MRSA} was built in a previous study), all with good statistical parameters, such as Fisher–Snedecor F (>68 in all cases), Wilk's lambda (<0.13 in all cases), and percentage of correct classification (>94% in all cases), which allows a reliable extrapolation prediction of antibacterial activity in any organic compound. The results obtained clearly reveal the high efficiency of combining molecular topology with LDA for the prediction of anti-MRSA activity.

Keywords: **antibacterial**; **antibiotics**; **anti-MRSA**; **computational chemistry**; **linear discriminant analysis**; **molecular topology**; **molecular connectivity**; **topological indices**; **quinolones**; **QSAR**