

# MOLECULAR DOCKING INVESTIGATION OF METHANOLIC EXTRACT COMPOUNDS FROM *Ricinus communis* AGAINST MICROBIAL PATHOGENS

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## Abstract

The present study aims to isolate and identify some constituents of *R. communis* leaves, their analytical characterization, and their in-silico bioactivities against selected bacteria and fungi to establish the QSAR model of the main active compounds [1].

We have evaluated the interaction of Lupeol, Amyrin, and both Ricinine and Quercetin derivatives against twelve protein receptors of six selected pathogens (*S.aureus*, *E.coli*, *P.aeruginosa*, *Bacillus subtilis*, *S.cerevisiae* and *A.niger*); Our results shows that for *S. aureus*, ricinin is more active on the 4URM receptor and for *Saccharomyces cervisea*, Lupeol is more active on the P47026 receptor.

**Key-words:** *Ricinus communis*, Molecular Docking, Antimicrobial activities.

## 1-INTRODUCTION

*Ricinus communis* is a widely studied medicinal plant as source of several active compounds displaying interesting pharmacological activities due namely to Lupeol, Amyrin, and both Ricinine and Quercetin derivatives [2].

## 2-MATERIELS & METHODS

Methanolic extract of *R. communis* leaves was obtained by the conventional maceration process, then, characterized by FTIR-NMR structural elucidation strategy. The identified compounds were *in-silico* tested against twelve protein receptors of six selected pathogens (*S.aureus*, *E.coli*, *P.aeruginosa*, *Bacillus subtilis*, *S.cerevisiae* and *A.niger*). The virtual docking was carried out using SwissDock software after ligand preparation using Chimera. Visualization and quantitative analysis of protein/ligand interactions were performed using Biovia Discovery Studio.

## 3-RESULTS & DISCUSSION

The structural elucidation allows the identification of Ricinine (R), Lupeol (L), alpha-Amyrin(A), Quercetin (Q), Quercetin-3-O-  $\beta$ - D-glucopyranoside (QGP) and Quercetin-3-O-  $\beta$ - rutinoides (QR) in the obtained extract. The binding energies  $\Delta G$  (kcal/mol) of the various Ligand-Protein complexes range from -5.31 for the L-6KZV complex of *E.coli* to -11.22 for the QR-4LXJ complex of *S.cervisea*. For *S.aureus*, ricinin is more active on the 4URM receptor (DS=-6.94), quercetin is more active on the 3FRA receptor (DS=-8.42) and finally QGP is more active on 3FRA (DS=-9.6). For *Saccharomyces cervisea*, Lupeol is more active on the P47026 receptor (DS=-8.53), aAmyrin and Quercetin-3-O- $\beta$ -rutinoides are more active on the 4LXJ receptor with a DS=-8.77 and DS=-11.22 respectively.

## 4-CONCLUSION

The six studied compounds are synergically more active against *Staphylococcus aureus* and *Saccharomyces cerevisiae*; the two QSAR basic models that can be deduced and written as:

**QSAR *R.communis*-*S.aureus* = -6.94 [R-4URM] -8.42 [Q-3FRA] -9.6 [QGP - 3FRA].**

**QSAR *R.communis*-*S.cervisea* = -8.53 [L-P47026] -8.77 [A- 4LXJ] -11.22 [QR - 4LXJ].**



Figure 1: Steps of Methanolic extract of *R. communis* leaves & analytical characterization

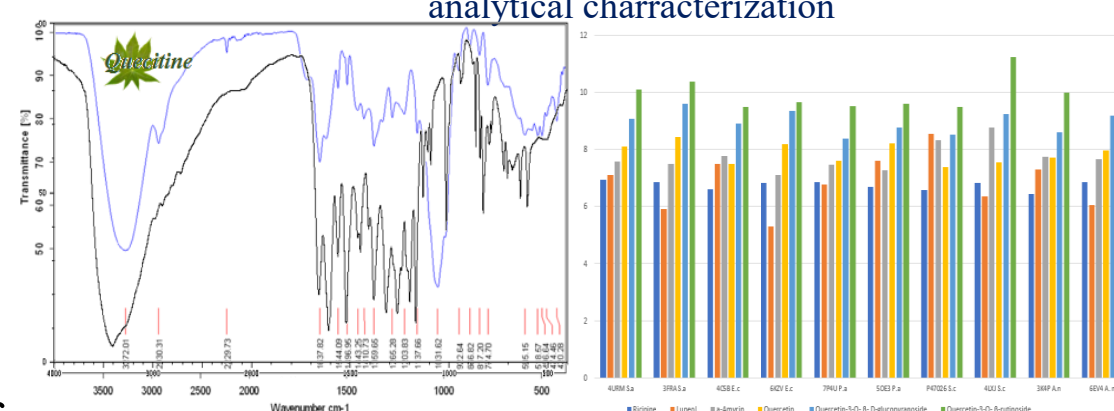


Figure 2: FTIR characterization & Insilico results

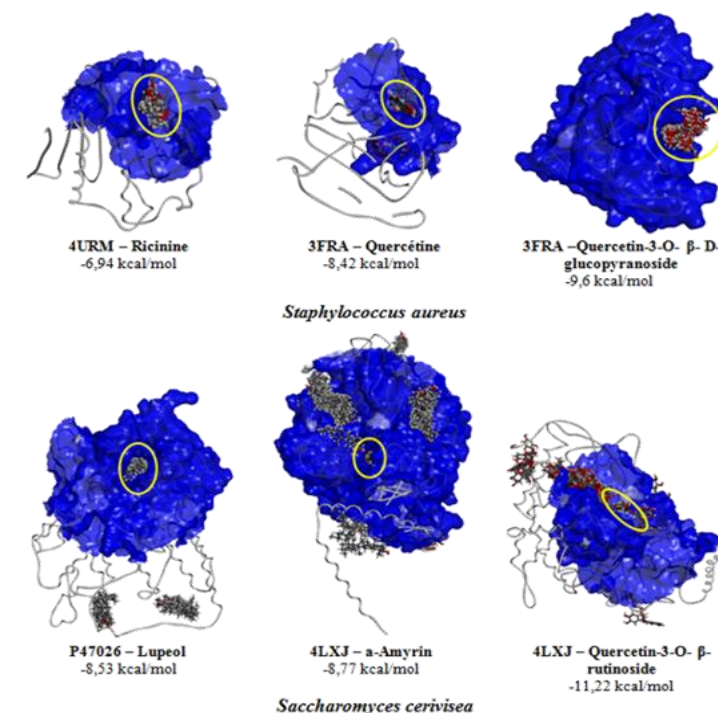


Figure 3: 3 D visualisation of Ligand-Receptor complexes

## References

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