Gembloux Agro-Bio Tech
Université de Liège

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Interactions of natural rhamnolipids produced by *Pseudomonas aeruginosa* with plant model membranes

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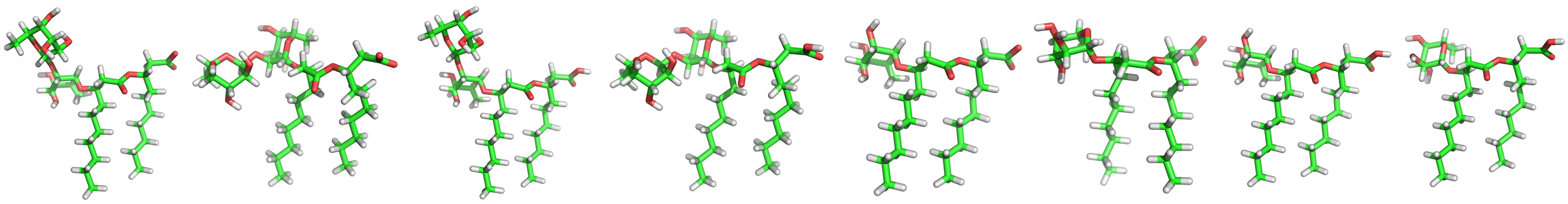
Introduction

It is well known that chemical pesticides have harmful effects on human health and environment. In this context, the interest for alternative products such as biopesticides is increasing. Among them, elicitors act on the plants by inducing systemic resistance against diseases caused by fungal, viral, bacterial agents and insects. Rhamnolipids are surface active molecules produced mainly by various strains of the bacterium *Pseudomonas aeruginosa*. These secondary metabolites are composed of one to three fatty acids with various chain lengths linked through a glycosidic bond to one or two rhamnose moieties. The fatty acids are linked together through an ester bond. These molecules have shown several biological activities including plant defense stimulation. It has been suggested that this elicitor activity could be related to an interaction of rhamnolipids with the lipid bilayer of the plant plasma membrane (PPM) and lead to its destabilization, which can activate the plant defense signaling pathways. In this context, interactions of two rhamnolipids (Rha-C_{10}-C_{10} and Rha-Rha-C_{10}-C_{10}) with biomimetic membranes of PPM such as Langmuir monolayers and multilayers were investigated using biophysical and *in silico* approaches.

Rhamnolipid Structures

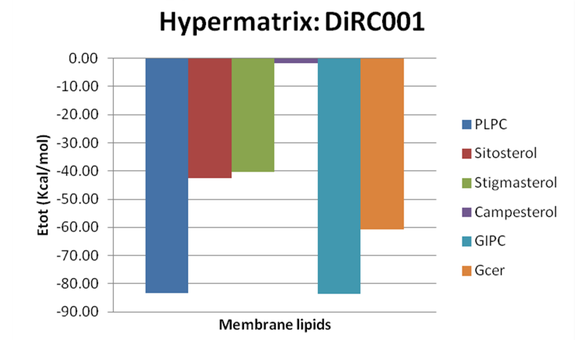


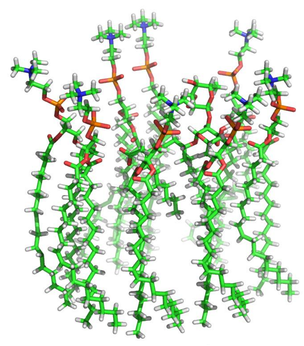
DiRC001 DiRC002 DiRNC001 DiRNC002 MonoRC001 MonoRC004 MonoRNC001 MonoRNC002

Most probable chemical structures of the rhamnolipids were determined using the STRUCTURE TREE procedure according to the molecule potential energy.

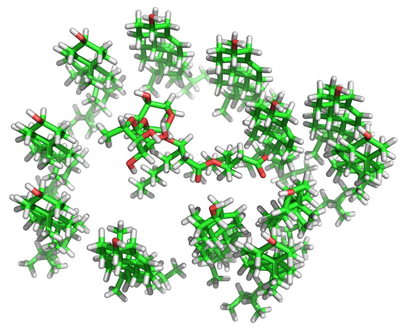
Hypermatrix

The ability of each rhamnolipid structure to form an assembly with several PPM constituents (phospholipid (PLPC), sterols (Sitosterol, Stigmasterol, Campesterol) and sphingolipids (GIPC, Glucosylceramide)) was calculated using the HYPERMATRIX procedure, which calculate and minimize the energies of interaction between all molecules of the complex until the lowest energy structure is reached.

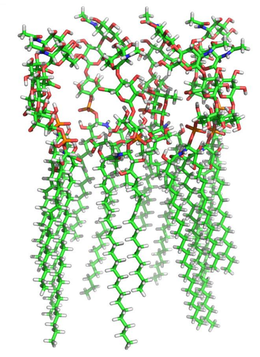




DiRC001/PLPC



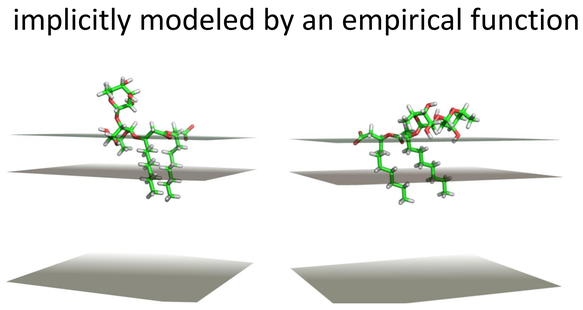
DiRC001/Campesterol



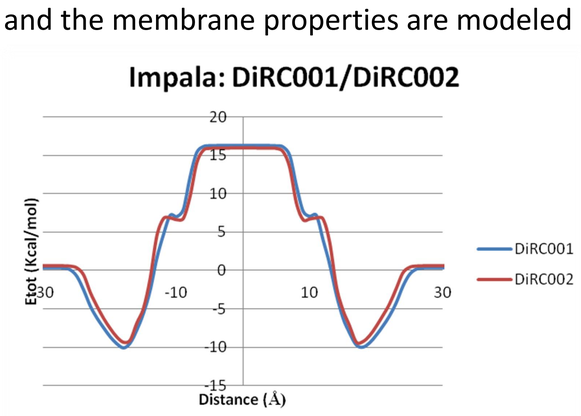
DiRC001/GIPC

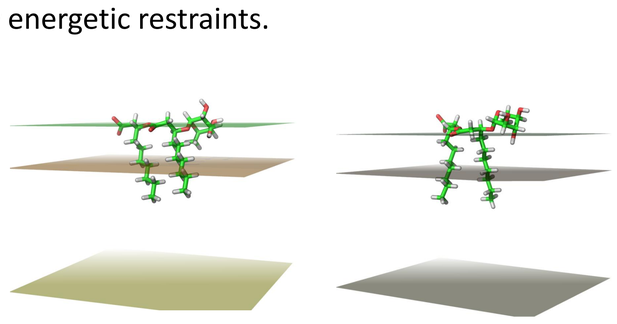
Impala

The ability of the rhamnolipid structures to insert within the PPM was assessed using IMPALA simulations. IMPALA uses a membrane model in which phospholipids molecules are implicitly modeled by an empirical function and the membrane properties are modeled by energetic restraints.

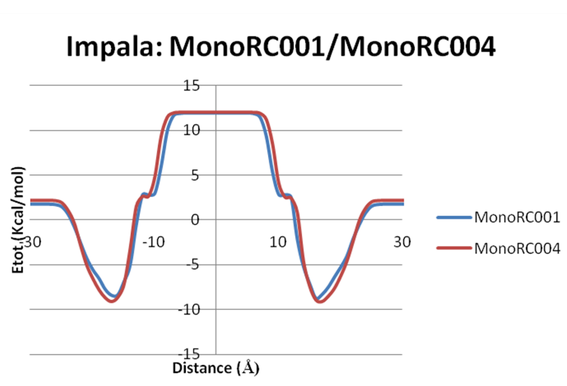


DiRC001 DiRC002



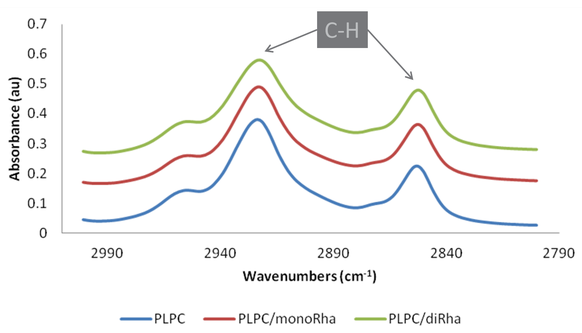


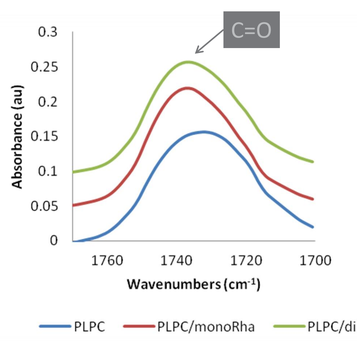
MonoRC001 MonoRC004

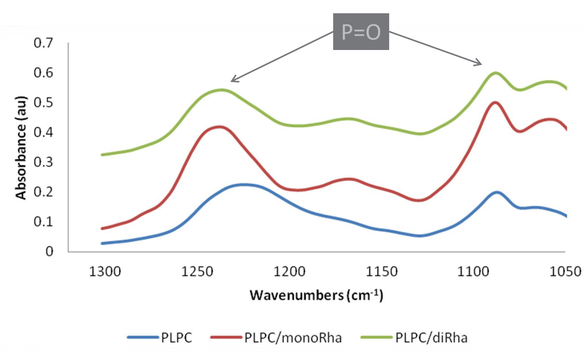


FTIR Spectroscopy

Alkyl chains, phosphate and carbonyl groups are involved in the interactions of both rhamnolipids with the PLPC, the main membrane lipid.







Acknowledgments

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FIELD Finding Interesting Elicitor Lipids