Lipid specificity of the interaction of Remorin protein with plant plasma membrane: role of phosphoinositides

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The function of Remorins, a diverse family of plant-specific proteins (1) is far to be fully elucidated. One of them, StREM1.3 (for Solanum tuberosum Remorin from group 1, homolog 3) has been reported to regulate cell-to-cell propagation of the potato virus X (2). It was also shown to be localized to the inner leaflet of plasma membranes (PMs) in raft domains and along plasmodesmata, bridges connecting neighbor cells essential for cell-to-cell communication in plants (3). The mechanisms driving StREM1.3 association with PM is still an open question. It was shown recently that a domain of 28 residues at the C-terminus of the potato (RemCA) is required and sufficient for anchoring to the PM (4).

Here we combined experimental and *in silico* biophysics to unravel the molecular bases of RemCA membrane binding with a special emphasis on lipid specificity. Biomimetic membrane models of plant PM such as monolayers and liposomes were used with various biophysical techniques (Langmuir monolayer technique, Fourier-transformed infrared spectroscopy, circular dichroïsm) and modeling tools (home-made methods and molecular dynamics) (5) to answer to three questions: (i) What is the conformation adopted by RemCA within a membrane?, (ii) Is there any membrane lipid specificity in the RemCA-membrane binding? (iii) What is the role of the two different RemCA domains in the interaction?

Results show that RemCA displays a preference for plant phosphoinositide-enriched inner leaflet plasma membrane rafts. Within the membrane, the C-terminal and the N-terminal domains of RemCA adopt a random coil and a α-helical conformation respectively. The C-terminal domain acts as a driver to bind RemCA to the membrane while the N-terminal domain stabilizes the peptide at the membrane. Lysine residues have a crucial importance in this interaction.

References

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