
Does Similar 3D structures Mean Similar Folding Pathway? Exploring the Conformational Folding Landscape of AVR Effectors from Phytopathogenic Fungi with High-Pressure NMR.

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Résumé

Effectors are virulence factors consisting in sequence-unrelated small proteins secreted by pathogenic microorganisms during infection. The NMR or crystal 3D structures of several effectors from the rice blast fungus *Magnaporthe oryzae* have been recently solved, including those of AVR-Pia and AVR-Pib [1,2]. Despite a lack of sequence similarity, both proteins have very similar β -sandwich structures. Structural convergence of proteins with poor sequence identity is rather common, probably due to the great sequence diversity of proteins, associated to a limited 3D structure accessible repertoire. Is this structural similarity associated to a similar folding pathway? This is the question we tackle in the present study. To this aim, we have analyzed the high-pressure unfolding of AVR-Pia and AVR-Pib with high-pressure NMR. We have designed a new approach to analyze the HP NMR data, based on distance-geometry calculations, that provides a meaningful description of the protein conformational folding landscape. As a result, a comparison of the folding pathways of AVR-Pia and AVR-Pib will be presented.

References :

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