Homology modelling strategy for prediction of the 3-D structure of a wheat protein inhibitor

A. Facchiano*, G. Colonna*, S. Di Gennaro**, F. Farisei** and E. Poerio**.

*Centro di Ricerca Interdipartimentale di Scienze Computazionali e Biotecnologiche (CRISCEB), II Università di Napoli - via Costantinopoli 16, 80138 Napoli. E-mail: angelo@crisceb.area.na.cnr.it
**Dip. di Agrobiologia e Agrochimica, Università degli Studi della Tuscia - via S. C. de Lellis, 01100 Viterbo.

In order to investigate structural/functional relationships of a wheat subtilisin-chymotrypsin inhibitor (WSCI) (1), we decided to explore its secondary and tertiary structures by applying an homology modelling procedure (using the Modeller program as part of the Quanta package) (2). The barley chymotrypsin inhibitor CI-2A (3), which exhibits 89% sequence similarity with the wheat inhibitor, has been chosen as reference structure. The best model structure obtained for WSCI, shows that 50% of its amino acid sequence (72 residues) are involved in motifs of secondary structure; particularly, 11 amino acid residues give rise to an helix, 12 residues form a long loop connecting two parallel strands, each made up of 6 residues. In the spatial model, the relative positions of such motifs are in agreement with the experimental data obtained upon interaction between WSCI and subtilisin; in fact, the bacterial proteinase cleaves, specifically, the inhibitor peptide bond Met48-Glu49 located in the middle of the above connecting loop. The weak interactions observed (H-bonds and salt bridges) in WSCI model are in perfect agreement with those found in the reference structure of CI-2A. Investigations regarding the modality of interaction between WSCI and susceptible proteinases are in progress.

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