

Amino acid co-evolution: Evolutive restriction of the structure and function of plant profilin.

Lucio Montero Valenzuela, Gabriel Guillén, Federico Sánchez.  
Av. Universidad #2001, Col. Chamilpa, Postal Code 62210, Cuernavaca,  
Morelos, Mexico  
Postal box 510-3, Postal Code 62250. [lucioric@ibt.unam.mx](mailto:lucioric@ibt.unam.mx).

Profilin is a 14 kDa protein family that regulates actin cytoskeleton polymerization. Profilins bind to actin, to phosphatidyl-inositol 4,5-bisphosphate and to proteins with proline rich sequences, such as poly-L-proline and the proline-rich motif of vasodilator-stimulated phosphoprotein (VASP) or the Wiskott-Aldrich syndrome protein (WASP). Profilins share a high structural similarity among the Eukarya domain although their sequence identity ranges only from 5 to 30%. It seems that the low conservation of certain profilin amino acids is not sufficient to explain its structural similarity. Recently, it was shown that besides the individual amino acid conservation among a protein family, some relationships between amino acids need to be conserved in a protein to determine structure and function. These relationships are reflected in the co-evolution of defined amino acid positions. We measured the co-evolution of amino acid positions in the profilin family, using the Statistical Coupling Analysis (SCA) software [1]. The SCA for the plant profilins detected five co-evolving positional groups. Four of them were in profilin interaction sites with its known ligands: proline rich sequences, actin and phosphatidyl-inositol 4,5-bisphosphate.

-----  
This research was partially supported by CONACYT 42562-Q and by Dirección General de Asuntos del Personal Académico IN-215805-2 grants. [1] Suel, G.M., S.W. Lockless, M.A. Wall, R. Ranganathan, "Evolutionarily conserved networks of residues mediate allosteric communication in proteins", Nature Structural Biology. January 2003. 10(1): 59-69