Bioinformatic Applied in Studies of the Structural Motifs in RGD and ECD Disintegrins

Costa Junior, N.B.[1], Muniz, J.R.C.[1], Selistre-de-Araujo, H.S.[2] and Souza, D.H.F.[1]

[1]Depto de Química, Universidade Federal de São Carlos (UFSCar), São Carlos, Brazil; [2]Depto Ciências Fisiológicas-UFSCar, São Carlos, Brazil.

Snake venom metalloproteases (SVMPs) are divided into four groups (PI-PIV) that differ for the presence of additional domains on the carboxyl side of the metalloproteinase domain. Disintegrins and disintegrin-like domains are released in the venoms by proteolytic processing of PII and PIII metalloproteases, respectively and represent potent inhibitors of integrin–ligand interactions. The disintegrin-like domain shows high sequence identity with disintegrins, however, the disintegrin-like domain does not contain the typical RGD sequence found in disintegrins. We investigated here, using bioinformatic, if the region containing the RGD and ECD motifs in disintegrin and disintegrin-like domains are structurally related. The amino acid sequences of disintegrin and disintegrin-like SVMPs were retrieved from the National Center for Biotechnological Information (www.ncbi.nih.nlm.gov) and aligned using the MULTIALIGN Interface Page. The proteins show, in the region of disintegrin domain, high degree of sequence identity. To identify similarities of proteins folds superimpositions of all crystallographic structures of disintegrin and disintegrin-like were performed (with PYMOL software). The region superimposed contained 10 residues of RGD and ECD loops. The root-mean-square distance (rmsd) values calculated for the 10 Cα is about 1 Å .These data show that the loop containing ECD (in PIII SVMPs) is structurally related to the RGD region of RGD-disintegrins, which are derived from PII SVMPs.

Supported by FAPESP, CNPq and Capes.