The Structural Characterization of a C1q/TNF-α Domain Containing Lectin OXYL in the Feather Star Anneissia Japonica

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Abstract

The structure of a lectin, OXYL, derived from the feather star, Anneissia japonica (phylum Echinodermata), was analyzed from biochemistry, informatics, and 3D structural prediction. OXYL's primary structure resembled the globular domain of complement C1q in vertebrates. Structural simulations identified OXYL as part of the C1q/TNF superfamily, characterized by a jellyroll β-sandwich fold. The subunits can form monomer to nonamer (9-mer), with trimers being the most stable. However, gel permeation chromatography indicated tetramers as the significant form. In hemagglutination inhibition tests, OXYL bound type-2 N-acetyllactosamine (LacNAc: Galβ1-4GlcNAc) and inhibited agglutination but did not bind lactose (Lac: Galβ1-4Glc). Glycan microarray analysis with 20 immobilized glycans confirmed OXYL's specificity for type-2 LacNAc and its sialic acid α2-3 linkage. The structural simulation showed a suitable molecular docking between type-2 LacNAc and the lectin rather than lactose. OXYL bound to the LacNAc glycan on the microarray was also elucidated to capture human IgG. This finding suggests that the invertebrate C1q/TNF family lectin will mimic vertebrate C1qs, despite lacking evolutionally antibody systems, possess the potential to interact with antibodies.