Effect of glycosylation over the structure and flexibility of proteins

Pol-Fachin, L.[1] and Verli, H.[1,2]
[1]Programa de Pós-Graduação em Biologia Celular e Molecular, Centro de Biotecnologia, Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil
[2]Faculdade de Farmácia, Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil

It is known that almost half of the proteins with identified amino acid sequences have potential *N*-glycosylation sites. As a general feature, to be *N*-glycosylated a given protein must contain a specific consensus signature, exposed in the protein surface. The so derived *N*-linked glycans may interfere with several properties of polypeptide chains, whereas few information is available concerning its molecular basis. In this context, considering the lack of information on the effect of glycosylation over the dynamics of polypeptides, this work intends to characterize the influence of *N*-glycans over the structure and flexibility of a series of proteins through molecular dynamics (MD) simulations. The calculations employed the GROMACS simulation suite and GROMOS96 force field for 50ns, added by Löwdin HF/6-31G** derived atomic charges for the carbohydrate residues. The simulated proteins include the human chorionic gonadotrophin, CD2 adhesion domain and complement regulatory protein CD59, all in its glycosylated and non-glycosylated forms. The so obtained results indicate that glycosylation may have implications over the folding and dynamics of polypeptidic chains, for example, by shielding hydrophobic residues in its surface or exposing specific regions to the environment, in good agreement with previous NMR and biochemical data. Therefore, these data point to MD simulations as a potential tool for describing glycans influence over polypeptide chains, as well as for describing the glycoprotein structure and conformation itself.

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