Galectins, β-galactoside-binding proteins, are characterized by having one or two conserved carbohydrate recognition domains (CRDs). Members of this family have been shown to participate in diverse biological functions, such as cell adhesion, cell growth regulation, and apoptosis via their interactions with β-galactoside-containing structures on cell surface, e.g., N-,O-linked glycoproteins, proteoglycans or glycolipids. More importantly, human galectins act as regulatory factors in many types of cancers by either inhibiting or promoting tumor growth. Therefore, to identify selective ligands for human galectins provides not only a useful tool for dissecting how each galectin member interacts with specific glycan structures in correlation with cancer progression, but also a possible solution for the development of clinical therapeutics. Therefore, we focused on different members belonging to this family, obtaining the recombinant proteins and studying not only the interaction with different molecules by means of ITC, thermophoresis or by X-ray crystallography but also characterizing the potential biological activity of selected ligands by cellular biology techniques such as anti-proliferative activity, migration and invasion assays. The importance of this family is furtherly enhanced by the presence of a galectin-fold in the N-terminal domain of the SARS-CoV-2 spike protein suggesting that ligands modulating the interaction with a sugar through the galectin-domain, could represent a suitable COVID-19 therapeutic application.


Keywords: galectin-fold; galectin-inhibitor; anti-tumoral agents; Spike protein

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