Heparin is a sulfated polysaccharide of animal origin that has an excellent anticoagulant activity. Although it strongly inhibits the coagulation cascade, the interaction with multiple sites results in several side effects. Ideally, an alternative compound should not only present anticoagulant and antithrombotic activities, but also provide a specific binding to components of the coagulation cascade to decrease side effects. In this work, a scan of potential targets of chemically sulfated pectin extracted from Citrus sinensis (SCP), that has an efficient anticoagulant activity, was performed. Plasma aliquots after albumin removal were fractionated by size exclusion, anion exchange and cation exchange chromatographies. The analyses of the interactions between SCP and plasma proteins were performed by fluorescence-based thermal shift assays. The content of subsets that showed positive interaction with SPC was identified by mass spectrometry. For in silico analysis of interactions, SCP structure was drawn with ACD/ChemSketch and docked into its partners structures since all identified SCP interactors have their 3D structure deposited in the Protein Data Bank (PDB). The viability of the complexes generated by the AutoDock Vina were checked with the software PEARLS. The results indicate that SCP interact directly with HClI, probably favoring their interaction with thrombin, and that the SCP interaction with AT probably depends on its association with thrombin or Factor Xa. In addition to the interaction with factors related to homeostasis, SCP may also have activity on the renin-angiotensin and on the complement systems. The knowledge of potential molecular targets of SCP provides clues to understand its mechanism of action in order to guide molecular changes in this compound to increase its specificity.

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Key words: anticoagulant activity, citrus pectin, sulfated polysaccharide