PEPTOID SEQUENCING BY MASS SPECTROMETRY

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A new class of peptidomimetics have been emerging as an excellent alternative for the limitations of peptides as therapeutical agents. This group of substances, called peptoids, are oligomers of N-substituted glycines which have its lateral chains connected to the nitrogen atom, differently of peptides where they are attached to the carbon α. This difference confers to peptoids some advantages as high metabolic stability and high cellular absorption. In the case of cyclic peptoids, it has been demonstrated that, among other applications, some of them can inhibit the Tat/TAR complex of HIV-1 virus. The objective of this work is to study the fragmentation behavior of peptoids at the mass spectrometer, and thus defining a standard that can be used for the characterization and sequencing of this class of molecule. The results demonstrated that the traditional series of peptide sequencing do not applied in the case of cyclic peptoids, and also that the Gly-NAsn bond was easily cleaved, but the Gly-NAsp bond was difficult to cleave. A cyclic pentapeptoid, an intermediate compound in the synthesis of a probable inhibitor of the Tat/TAR complex of HIV-1 virus, was completely sequenced by ESI-MS/MS. The future efforts include the study of peptoid fragmentation at a MALDI-TOF-TOF equipment.