Development of fluorescent peptide substrates for improved monitoring of SARS-CoV-2 main protease 3CLpro activity based on active site specificity by degradomics approach

Hugo Cesar Ramos de Jesus¹, Peter A. Bell¹, Reinhild Kappelhoff¹, Peter M. Grin¹, Georgina S. Butler¹, Carlos Arterio Sorgi^{1,2}, Christopher M. Overall¹

^{1.} UBC, University of British Columbia, Vancouver, British Columbia, Canada;

SARS-CoV-2 main protease (3CLpro) is crucial for processing the viral polyprotein. While drug development targeting 3CLpro often focuses on the catalytic non-prime (P) side for specificity and potency, the significance of the prime (P\') side in substrate specificity and drug development is often overlooked. We analyzed the P6-P6\' specificity of 3CLpro by identifying over 800 cleavage sites using Proteomic Identification of Cleavage site Specificity (PICS). Cleavage typically occurred after the canonical P1-Gln and non-canonical P1-His and P1-Met residues, with a preference for Arg/Lys at P3 and His at P3\'. Critical hydrogen bonds between the N-terminal Ser1 of protomer-B in 3CLpro dimers form with P1-His but not with P1-Met. However, cleavage at P1-Met456 in native MAP4K5 still occurs. Elevated reactive oxygen species during SARS-CoV-2 infection oxidize methionines. Molecular simulations showed that oxidized P1-Met (P1-MetOX) forms a hydrogen bond with Ser1, and strong positive cooperativity between P1-Met and P3\'-His enhances peptide cleavage rates. The adaptable S3\' subsite accommodates P3\'-His, which stabilizes through backbone hydrogen bonds with Thr25, central to a \"threonine trio\" (Thr24-Thr25-Thr26) in the P\'-binding domain I. Molecular docking simulations highlighted structure-activity relationships affecting 3CLpro-substrate interactions. These determinants were confirmed by MALDI-TOF-MS cleavage assays of P1\'- and P3\'-positional scanning peptide libraries with an internal positive control. These insights guided the design of two new, highly soluble 3CLpro quenched-fluorescent peptide substrates, resulting in a 15-fold improvement in sensitivity for FRET monitoring of 3CLpro activity compared to current assays. These findings should inform medicinal and chemical improvement of new small-molecule inhibitor compounds potent against SARS-CoV-2 3CL^{pro}.

Agradecimentos: Funding was secured through a Canadian Institutes of Health Research Foundation (Grant# 148408), Canada Research Chair in Protease Proteomics and Systems Biology (CMO) and São Paulo Research Foundation - FAPESP (Grant#2022/14928-4, #2024/03414-5).

² FFCLRP - USP, Faculty of Philosophy, Sciences and Letters at Ribeirão Preto, University of São Paulo, Ribeirão Preto, São Paulo, Brazil;