

プロナーゼから得たN-サクシニル-L-
トリアニンp-ニトロアニリド水解酵素の
ウマ α_2 マクログロブリンによる阻害

植木 寛, 元島 愛一郎, 世良 美佐紀, 十時 晨爾*,
船越 崇行*, 庄司 省三*, 久保田 幸穂*

Chemical & Pharmaceutical Bulletin, 34(10) 4207-4214 (1986).

**Inhibition by Equine α_2 -Macroglobulin of an N-Succinyl-L-Trialanine
p-Nitroanilide-Hydrolyzing Protease Purified from Pronase**

Hiroshi UEKI, Aiichiro MOTOSHIMA, Misaki SERA, Shinji TOTOKI*,
Takayuki FUNAKOSHI*, Shozo SHOJI*, and Yukiho KUBOTA*

ABSTRACT: The binding of an N-succinyl-L-trialanine p-nitroanilide-hydrolyzing protease (STA-protease) purified from pronase to equine α_2 -macroglobulin (α_2 M) was investigated in comparison with that of trypsin. The α_2 M subunits (about 90000 daltons), which were electrophoretically detected in the reaction mixture of α_2 M and trypsin, were undetectable in that of α_2 M and STA-protease. The binding molar ratios of enzyme to α_2 M were estimated from the inhibition curves of caseinolytic activity to be 1.5:1 for native and acetylated STA-protease and 2:1 for native and acetylated trypsin. The finding of greater incorporation of monodansylcadaverine into α_2 M reacted with acetylated enzymes than into that reacted with the native enzymes suggests that free amino groups in the enzymes are involved at least partly in the formation of the α_2 M-proteinase complexes. The numbers of thiol groups generated in α_2 M bound to STA-protease and in α_2 M bound to trypsin were both estimated to be approximately 4 mol per mol of α_2 M by the use of thiol-directed fluorescent probes, though there were slight differences in the microenvironments of thiol groups generated in the two α_2 M-proteinase complexes. The values of K_{cat}/K_m were one-half (α_2 M-STA-protease complex) and one-sixth (α_2 M-trypsin complex) of those of the uninhibited enzymes. These results suggest that STA-protease binds to α_2 M both covalently and noncovalently, as does trypsin, and its hydrolytic activities towards casein and low-molecular-weight substrates

are inhibited to various extents.

抄録 プロナーゼから得たN-サクシニル-L-トリアラニン p-ニトロアニリド水解酵素 (STA-protease) とウマ α_2 マクログロブリン (α_2 M) との結合についてトリプシンの場合と比較検討した。電気泳動分析によってSTA-proteaseと α_2 Mの複合体はトリプシンのそれと異なる泳動パターンを示したが、チオール基の生成、複合体形成へのアミノ基の関与、動力的定数の変化など両酵素に著明な差は認められなかった。

* Faculty of Pharmaceutical Sciences, Kumamoto University. 熊本大学薬学部