

Reassessing the substrate specificities of the major *Staphylococcus aureus* peptidoglycan hydrolases lysostaphin and LytM

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Abstract

Orchestrated action of peptidoglycan (PG) synthetases and hydrolases is vital for bacterial growth and viability. Although the function of several PG synthetases e.g., penicillin binding proteins is well-understood, the function, regulation, and mechanism of action of the majority of PG hydrolases have remained elusive. Lysostaphin-like zinc-dependent metalloendopeptidases specifically hydrolyse the glycyl-glycine peptide bond in the notorious pathogen *Staphylococcus aureus*. In this work, we have employed NMR spectroscopy to study the substrate specificity of the well-established bactericide lysostaphin as well as pre-designated *S. aureus* autolysin LytM. Our results show that the substrate specificities of these highly homologous enzymes are divergent and formerly also inaccurately defined. Yet, we provide substrate-level evidence for the functional role of these enzymes. Indeed, we show that LytM and anti-staphylococcal bactericidin lysostaphin target the D-Ala-Gly cross-linked part of mature peptidoglycan.

eLife assessment

This manuscript describes a **valuable** study aimed at identifying the substrate specificity of two cell wall hydrolases LSS and LytM in *S. aureus*. The authors show that LytM has a novel function of cleaving D-Ala-Gly instead of only Gly-Gly by using synthetic substrates and **convincing** NMR-based real-time kinetics measurements. The biological relevance of the reported results will have to be investigated in future in vivo experiments.

Introduction

In the age of antibiotic resistance, multi-resistant bacteria pose a serious threat to global health. This calls for novel strategies to fight the infections¹. Contemporary means to treat bacterial infections rely on antibiotics. One of the most common mechanisms of action of antibiotics is inhibition of the peptidoglycan (PG) synthesis, a major macromolecular structure in the bacterial cell wall^{2,3}. Alarming, the Gram-positive bacterium *Staphylococcus aureus* (*S. aureus*) is notorious in developing resistance towards β -lactam based antibiotics e.g., penicillin and their derivatives, which target penicillin binding proteins (PBPs) that are vital for PG synthesis⁴. These methicillin-resistant strains of *S. aureus* (MRSA) can cause life-threatening infections which are very difficult to eradicate⁵. Moreover, although still rarely occurring, outbreaks of infections caused by vancomycin intermediate-level and fully resistant *S. aureus* (VISA/VRSA) are lurking on the horizon⁶. Development of alternative means to treat multi-resistant bacterial infections is therefore needed.

Cell division, cell shape determination, PG remodelling and recycling is administrated and executed by peptidoglycan hydrolases (PGHs), enzymes produced to function as (auto)lysins in the regulation of the cell wall during growth and division^{7,8}. On the other hand, PGHs may also function as defensive weapons against other bacterial species as in the case of lysostaphin, an exolysin secreted by *S. simulans* biovar staphylolyticus, which displays bacteriocidal action against competing *S. aureus*⁹. The potential chemotherapeutic role of PGHs is based on the targeted destruction of the protecting PG by hydrolysis, which leads to growing turgor pressure and thus lysis of the bacterial cells^{7,9}. Given that PGHs are promising bacteriocins as well as druggable targets for the treatment of multidrug-resistant *S. aureus* infections, profound knowledge of their structure, function as well as substrate specificity is instrumental to harness their full potential as a new breed of antibiotics¹⁰.

S. aureus and other Gram-positive bacteria are protected by a thick PG layer that is composed of repeating β -1,4 linked *N*-acetylmuramic acid (MurNAc) and *N*-acetylglucosamine (GlcNAc) disaccharide units, forming the conserved glycan backbone of murein^{7,11} (**Fig. 1A-B**). Each MurNAc carboxyl group is linked to a stem peptide (L-Ala-D-iso-Gln-L-Lys-D-Ala-D-Ala) and two stem peptides are connected via a cross-bridge structure, the exact composition and length of which depends on the bacterial species in question. In *S. aureus* the cross-bridge is characteristically composed of five glycine residues⁷. Cross-bridging provides an integral structural support for the entire PG wall and allows PG to reach a thickness of over 40 layers (20–80 nm) in Gram-positive bacterial species^{7,12}.

While cell wall composition and biosynthesis of PG are relatively well understood, the perception of PG maintenance and hydrolysis is vague¹⁰. One prominent PGH family are the lysostaphin-like endopeptidases, which specifically target the cross-bridge peptide bonds of *S. aureus* PG^{13,14}. Here we compared LytM and lysostaphin (LSS), which both belong to the zinc-dependent M23 family of metalloendopeptidases and are designated as glycyl-glycine hydrolases. They have been shown to cleave the peptide bonds between glycine residues in the pentaglycine cross-bridge of *S. aureus* PG (**Fig. 1B**)^{9,15–20}.

S. simulans LSS, the founding member of the M23 endopeptidase family, is an exolysin possessing bacteriolytic properties towards staphylococci with a pentaglycine cross-bridge structure (e.g. *S. aureus*, *S. carnosus*, *S. cohnii*) (Schindler & Schuhradt, 1964; Schleifer & Fischer, 1982). LytM is a *S. aureus* autolysin with a catalytic M23 domain structurally very similar to that of LSS (**Fig. S1**). The common fold consists of a characteristic narrow groove formed by a β sheet and four surrounding loops. At one end of the groove resides the catalytic site in which a zinc cation is coordinated by two conserved histidines and an aspartate. The zinc cation, which polarises the peptide bond, and a nucleophilic water molecule activated by two other conserved histidines act in concert to hydrolyse the substrate glycyl-glycine bond²².

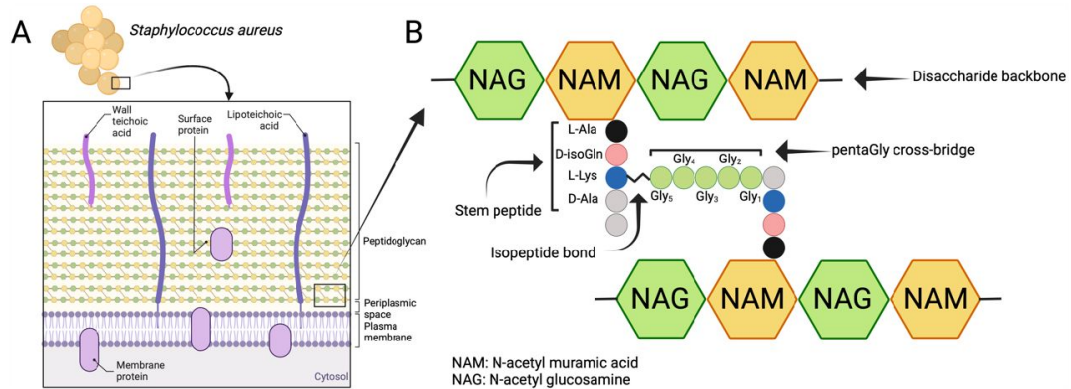


Figure 1.

Structure of the cell wall PG in *S. aureus*. **(A)** Schematic overview of the cell wall in *S. aureus*. **(B)** Structure of the peptidoglycan.

Despite tens of years of effort in studying substrate specificities of LSS-like M23 endopeptidase family members, the exact molecular targets of these enzymes have remained enigmatic, contradictory, and yet imprecise. Interpretation of results is further complicated by diverse conventions used for the numbering of cross-bridge residues. Indeed, the exact cross-bridge bond that LSS targets remains controversial; Browder *et al.* (1965) reported LSS cleavage between glycines 4 and 5 while Sloan *et al.* (1977) observed cleavage of all glycyl-glycine bonds with several substrates of different sizes^{23,24}. Recently, using mass spectrometry (MS), Schneewind *et al.* (1995) observed LSS-mediated cleavage between glycines 3 and 4²⁵. This observation was supported by a recent NMR spectroscopic study highlighting that hydrolysis by LSS produced fragments in which either two or three glycines are interlinked to the lysine sidechain²⁶. On the other hand, Xu *et al.* (1997) reported cleavage at several sites with digested muropeptides: between glycines 1 and 2, 2 and 3 as well as 3 and 4²⁷. Additional studies carried out with FRET peptides reported cleavage between glycines 2 and 3 (~60 %) and glycines 3 and 4 (~40 %)²⁰.

Much less is understood about the functional role of *S. aureus* autolysin LytM. This is partially due to lack of profound knowledge of its substrate specificity. Indeed, based on its high sequence homology with LSS catalytic domain as well as its association with *S. aureus* cell wall maintenance, LytM has implicitly been envisaged to target pGly cross-bridges in the *S. aureus* cell wall. LytM has been shown to hydrolyse pGly into di- and triglycine, and tetraglycine into diglycine²⁸. Understanding the substrate specificity is of utmost importance for deciphering the functional role of endogenous LytM in cell division, PG remodelling, antimicrobial resistance, and PG synthesis/hydrolysis in general.

Thus far studies of PG hydrolase specificity have typically utilised end-point kinetics together with LC/MS analysis of digested PG fragments or turbidity reduction assays to determine the site(s) and efficiency of hydrolysis^{29,30}. However, these approaches have several pitfalls e.g., they do not provide information on reaction kinetics or atomic resolution of reaction products, which severely limits determination of substrate specificity. In seeking to understand the functional role of these enzymes we have deciphered substrate specificity of LSS and LytM catalytic domains by taking a systematic approach by monitoring hydrolysis of various synthesised PG fragments as well as muropeptides from purified sacculus extracted from *S. aureus* cells using solution-state NMR spectroscopy and utilising turbidity reduction assay on living *S. aureus* cells. NMR enables following the hydrolysis reaction in real time as well as identification of hydrolysis products.

Here we show that the substrate specificities as well as catalytic efficiencies of M23 family PGHs targeting *S. aureus* PG are different from what has been earlier anticipated. Moreover, our results reveal that quite unexpectedly LytM substrate specificity extends beyond glycyl-glycine endopeptidase activity, which calls for revision of their classification.

Results

Substrate specificities of Lysostaphin M23 enzyme family

Due to inconsistent nomenclature used in the literature to annotate *S. aureus* PG cross-bridge structure and hence substrates used in the enzymatic assays and specificity studies, we conducted a systematic bottom-up approach to delineate the significance of various PG structural elements for the specific activities of LSS and LytM. We prepared a panoply of synthetic peptides faithfully replicating the chemical structure of the recognised *S. aureus* PG fragments (**Fig. 2J**, Table S1). The common denominator - the scaffold structure - in the PG fragments used in this study, is the pGly cross-bridge as it is uniquely present in *S. aureus* PG (**Fig. 1B**).

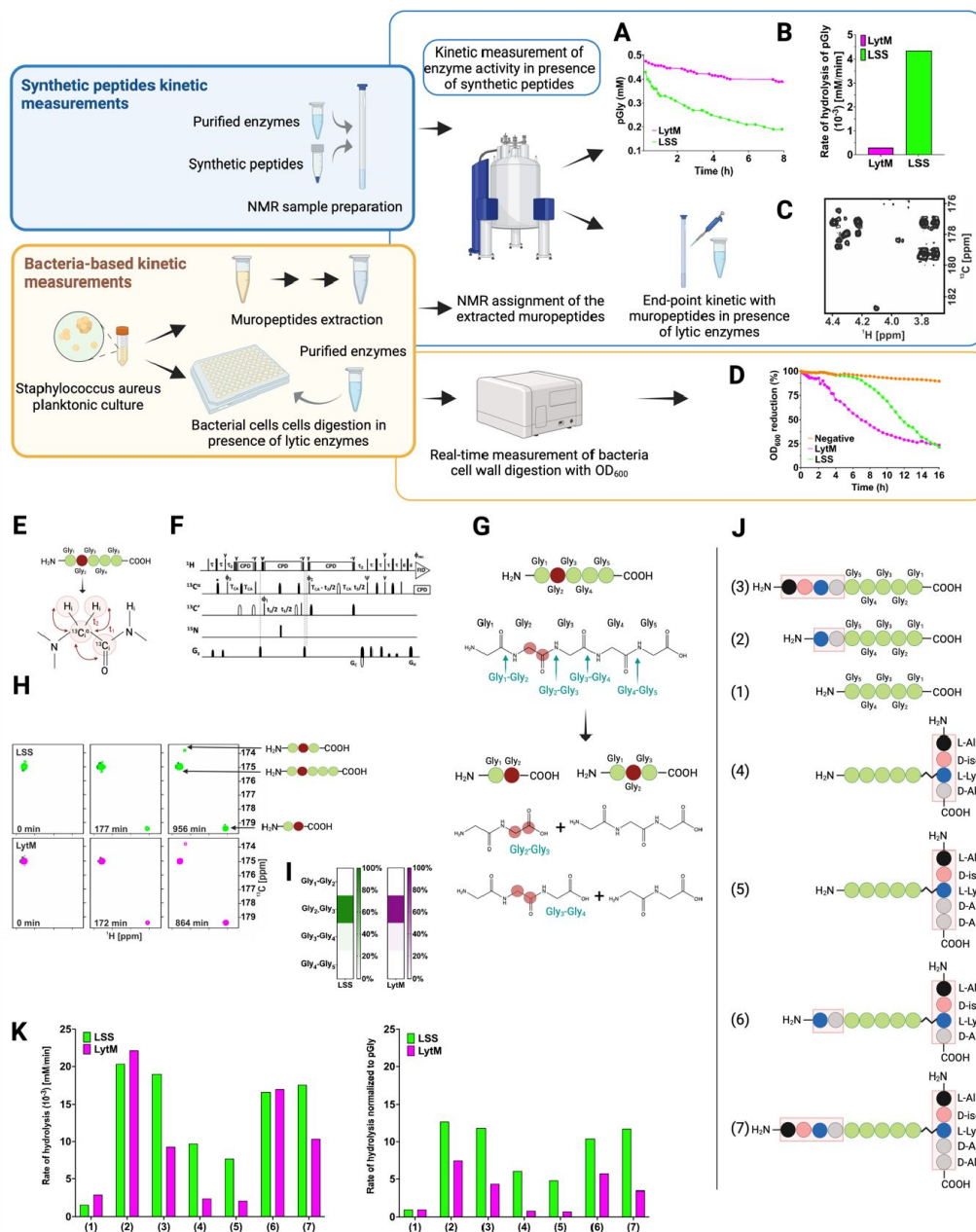


Figure 2.

Workflow to study M23 PGH substrate specificities. **Panels in the upper left corner**, the two main strategies used in the study. Kinetic measurements carried out with PG fragments (synthetic peptides) were supported by bacteria-based kinetic measurements using *S. aureus* USA300 cells. **Panels in the upper right corner**, (A) hydrolysis of synthetic pGly (mM) by LSS (green) and LytM (magenta) monitored by ^1H NMR spectroscopy over time (h). (B) Rate of hydrolysis (mM/min) of pGly derived from A in the first 60 min of the reaction for LSS and LytM. (C) ^{13}C -HMBC NMR experiment showing the end-point kinetic of extracted muropeptides from *S. aureus* USA300 cells. (D) Turbidity assay using *S. aureus* USA 300 cells in the presence of LSS and LytM. The cell lysis is expressed as percentage reduction of the bacteria suspension optical density at 600 nm over time (h). (E) Pentaglycine hydrolysis by LSS and LytM using Gly₂¹³C-labelled substrate. (F) NMR pulse sequence for the acquisition of glycine Ha-detection optimised 2D HA(CA)CO spectra, showing correlations between ^{13}C and ^1H atoms. (G) With a label the otherwise identical products of the two hydrolysis reactions G₂-G₃, G₃-G₄ can now be differentiated. (H) The appearance of the peaks of the labelled products as a function of time. The labelled glycine has a different CO shift when as G₂ in triglycine or G₂ in diglycine. (I) Heatmap summarising the bond preferences for the enzymes. (J) Depiction of peptides used to study target bond specificity of the enzymes. Hydrolysis of peptides 1-7 by LSS (green) and LytM (magenta). (K) Initial rates of substrate hydrolysis (mM/min) and (L) the same rates normalised to that of pGly.

Figure 2 highlights the strategy employed to study substrate specificity and kinetics of LSS and LytM using two different approaches; monitoring hydrolysis of synthetic peptides mimicking PG fragments and mucopeptides extracted from *S. aureus* sacculus using solution-state NMR spectroscopy, and monitoring lysis of bacterial cell wall using turbidity reduction assay. In the turbidity reduction assay lytic efficiencies of externally administered LSS and LytM against *S. aureus* USA300 (MRSA) strain were compared (**Fig. 2D**). These data show that OD₆₀₀ of late stationary cells reduced from 100 % to 25 % in 16 hours for LytM and LSS.

Given that pGly has long been recognised as the common, non-redundant and yet physiological substrate unit for M23 family endopeptidases, we wanted to accurately define substrate specificities, catalytic efficiencies, and the sites of cutting for the catalytic domains of LSS and LytM. To measure the rate of pGly hydrolysis *in vitro*, we added the corresponding enzymes and monitored decaying substrate concentration with respect to reaction time using quantitative ¹H NMR spectroscopy (**Fig. 2A**). Results indicate that LSS hydrolyses pGly 15-fold faster than LytM. *In vitro* hydrolysis rates of pGly (**Fig. 2B**) and reduction in *S. aureus* USA300 cell turbidities (**Fig. 2D**) display consistent differences in catalytic efficiencies of LytM and LSS. However, we see that overall, the lytic efficiency of LSS and LytM against USA300 cells is higher than the rate of pGly hydrolysis *in vitro*. This suggests that *S. aureus* cell wall as a macroscopic substrate or cellular milieu differs significantly from the conditions used for the kinetic assay *in vitro* i.e., pGly as a substrate represents a poor model for describing substrate specificity and functional differences of M23 family endopeptidases. As the next step, we therefore determined the scissile bonds in pGly as well as extended substrate specificity studies of these enzymes beyond the pGly cross-bridge.

LSS and LytM preferentially hydrolyse the Gly₂-Gly₃ bond in pentaglycine

We recently showed using a two-dimensional ¹³C-HMBC NMR experiment that LytU hydrolyses pGly into di- and triglycine¹⁸. Whether this was the result of hydrolysis of the bond between Gly₂ and Gly₃, and/or between Gly₃ and Gly₄ in pGly remained undefined because the products are the same in both reactions. Selective ¹⁵N,¹³C-labelling (**Fig. 2E**) breaks the isotopic symmetry of pGly without introducing *per se* any non-physiological tags to the substrate and enables to define the preferred cleavage sites for LSS and LytM in pGly using ¹H-¹³C NMR spectroscopy. As can be appreciated in **Figure 2G,H**, isotopic labelling of Gly₂ at Cα and CO carbons in pGly allows unambiguous determination of cleavage site, because the characteristic chemical shift of a C-terminal ¹³CO resonance (179.4 ppm) is markedly different from a non-terminal ¹³CO chemical shift (173.8 ppm) at physiological pH. Representative two-dimensional ¹Hα-¹³CO correlation maps, collected with the glycine-optimised 2D HA(CA)CO NMR experiment (**Fig. 2F**) from the selectively Gly₂-¹³C-labeled pGly are highlighted in (**Fig. 2H**). These data clearly show that LytM and LSS are highly specific for the bond between Gly₂ and Gly₃ (> 85-94 %, **Fig. 2H**). However, residual cleavage activity towards the bond between Gly₃ and Gly₄ is also evident (< 15 %).

The substrate specificity of LytM and LSS is determined by the D-Ala-Gly cross-link between adjacent PG monomers

In the next phase, we sought to understand the role of plausible auxiliary contacts arising from stem peptides flanking the pGly cross-bridge for the substrate specificity of LSS and LytM. To this end, several larger peptides with PG specific extensions around the pGly scaffold were utilised (**Fig. 2J**). To alleviate complications arising from multiple sites of hydrolysis in pGly, we decided to monitor the rate of substrate hydrolysis rather than the rate of product formation, and to use a similar substrate concentration for all the PG fragments (~0.4 mM) (**Fig. S2**). These data using substrates 1-7 are shown in **Figure 2K**. Normalisation of the absolute rates with respect to the common scaffold structure, pGly, should reveal on the substrate level the preference of LSS and LytM towards different PG fragments (**Fig. 2L**).

Clearly, the overall rate of hydrolysis for LytM and LSS increases with peptides that mimic cross-linked PG fragments (**Fig. 2K**). Indeed, cross-linking L-Lys-D-Ala dipeptide N-terminally to pGly in **2** increased the rate of hydrolysis with respect to **1** by a factor of 12 and 7.3 for LSS and LytM, respectively (**Fig. 2L**). Further elongation towards the N-terminus (ADiQKDA-GGGGG, **3**) had only incremental contribution to the rate of overall substrate hydrolysis, 16.8 and 3.3 for LSS and LytM, respectively.

Next, we inspected the influence of a stem peptide linked to the C-terminus of pGly on the substrate hydrolysis rate. In PG fragment **4** the stem peptide is linked to the pGly via an isopeptide bond between lysine ϵ amino group and the C-terminus of pGly. The PG fragment **5** is similar but corresponds to the peptide moiety in a PG monomer (or pentaglycyl-Lipid II) (**Fig. 2J**). For LSS, the rate of hydrolysis increased by 5- and 4.5-fold for substrates **4** and **5**, respectively. This increase in overall rate of substrate hydrolysis with respect to pGly is roughly two times smaller than for the linear PG fragments **2** and **3** that contain a D-Ala-Gly cross-link. For LytM, the outcome was in stark contrast to the results observed with LSS. Indeed, LytM activity towards PG fragments **4** and **5** dropped to 69 and 49 %, respectively, of that found for **1**.

Next, we studied the significance of capping the pGly moiety from both its termini. PG fragments **6** and **7** both contain an N-terminal D-Ala-Gly cross-linkage in their structure but differ in **6** having a C-terminal tetra- and **7** a pentapeptide stem i.e., the latter has a D-Ala-D-Ala moiety in its structure. For LSS, 10-fold rate enhancements with respect to **1** for substrate hydrolysis were observed, comparable to enhancements with substrates **2** and **3**, indicating that the moiety C-terminal to pGly does not contribute to LSS specificity. Hence, based on these results, it can be deduced that LSS strongly favors substrates that contain a D-Ala-Gly cross-link i.e., **2**, **3**, **6** and **7**. In the case of LytM, rate enhancements of PG fragments **6** and **7** with respect to **1** were 5.5- and 3-fold, respectively, meaning that the branched stem peptide linked to the C-terminal end of pGly has a slight negative effect on LytM specificity. These data indicate that similarly to LSS, LytM is more specific towards substrates **2**, **3**, **6** and **7** i.e., PG fragments that contain a D-Ala-Gly cross-link.

In all, overall rates of substrate hydrolysis using comparative real time kinetics convincingly indicate that LytM as well as LSS prefer mature PG fragments as substrates i.e., PG units that contain a D-Ala-Gly cross-link between two stem peptides. In contrast to the mere end-point kinetics carried out in the past for LytM and LSS, our present results clearly demonstrate the preference of these enzymes for cross-linked PG fragments beyond redundant glycyl-glycine endopeptidase activity. However, the substrate specific real time kinetics assay does not tell anything about the site(s) of hydrolysis in the substrates. To understand substrate specificity and the physiological role of these PGHs, we inspected the outcome of these reaction assays in more detail.

LSS and LytM display different substrate specificities than earlier anticipated

NMR spectroscopy allows identification of atom connectivities within the substrate and products, enabling determination of site(s) of hydrolysis at atomic resolution. **Figure 3A** displays the LSS-catalysed hydrolysis of substrate **2**, the simplest of our PG fragments that contains the cross-link between D-Ala and Gly₁ of pGly synthesised by the transpeptidase. Expansion of the region corresponding to the ¹Hα resonance of D-Ala in the ¹H spectrum of **2** shows that upon hydrolysis of **2**, two products are formed as manifested themselves by increasing concentrations of KDAG₁ and KDAG₁G₂ (**Fig. S3** shows the identification of the product peaks based on ¹³C-HMBC spectra). Owing to their different chemical structures, the products display separate peaks, resolved at 800 MHz ¹H field, which allows determination of individual reaction rates. Given that the ¹H method we used is quantitative the preferred site of hydrolysis in the PG cross-

bridge can be identified based on product concentrations (**Fig. 3C-E**). These data show that in 2 LSS hydrolyses amide bonds between Gly₁-Gly₂ as well as Gly₂-Gly₃ with a clear preference for the first one.

By coupling real time kinetics data with identification of reaction products, we determined the cutting sites and the reaction rates of the corresponding products for a total of seven PG fragments for LSS and the combined results of their analyses are shown in **Figure 3E**. The difference in panels C and E is that for the latter we considered only reactions which dominate for the particular PG fragment whereas in the heatmap representation the relative product concentrations at the end of the hydrolysis reaction are shown. These results are consistent with analyses of substrate hydrolysis rates in that they show that LSS clearly favors PG fragments with a D-Ala-Gly cross-link. Pentaglycine or other PG monomers in which Gly₁ is not cross-linked to the stem peptide of the adjacent PG fragment are hydrolysed at slower rate and the cutting site is shifted by one residue downstream compared to the cross-linked ones. In addition, the bond specificity of the hydrolysis reaction increases with D-Ala-Gly cross-linked PG fragments. In this case, LSS favors cutting the amide bond between Gly₁ and Gly₂ and the hydrolysis rate of this bond is several times higher than that of the Gly₂-Gly₃ bond, or those of Gly₂-Gly₃ and Gly₃-Gly₄ bonds in PG monomers devoid of D-Ala-Gly cross-link.

As we reckoned that D-Ala-Gly cross-link is critical for efficient hydrolysis of LSS substrates, we wanted to study how the length of the glycine containing cross-bridge influences substrate hydrolysis (Figs. S4, S5). Substrate **12**, containing four consecutive glycines attached to Lys-D-Ala was hydrolysed between Gly₁ and Gly₂, as well as Gly₂ and Gly₃, exactly like substrate **2**. However, the hydrolysis rate of the Gly₂-Gly₃ bond was 3-fold faster than in the case of **2**. This is probably due to the absence of tetraglycine as a secondary substrate in the reaction i.e., the reaction products resulting from hydrolysis of **12** do not significantly compete with the primary substrate for binding to the LSS catalytic center. Substrate **13** (KDAGGG) was hydrolysed very slowly and **14** (KDAGG) not at all.

We carried out a similar analysis for LytM using the same set of PG fragments (**Fig. 4B**). The most striking observation is clearly visible in **Figure 3B** showing hydrolysis of **2** by LytM, which results in formation of products KDA and KDAG₁. Indeed, given that LytM is a well-established glycyl-glycine endopeptidase^{17,22,28}, we were taken by surprise to observe that LytM, in addition to Gly₁-Gly₂ bond hydrolysis, is also able to cleave the D-Ala-Gly₁ amide bond in the *S. aureus* PG cross-bridge whenever the cross-linked D-Ala-Gly structure is available.

We verified that the observed D-alanyl-glycine bond hydrolysis, which has not been reported before this study, is stereospecific and linked to LytM activity. We performed an identical kinetic assay using KLAGGGGG as a negative control. It confirmed that the enzyme is indeed D-enantiomer specific as no cleavage between alanine and glycine was observed (Fig. S6). Further, using a protocol identical to that of LytM we engineered, expressed, and purified the well-established inactive H291A mutant of LytM and tested it with substrate **2**. As expected, LytM H291A showed no activity. The results confirm that in addition to being a glycyl-glycine endopeptidase as reported earlier^{17,22,28}, LytM belongs to a small family of endopeptidases which cleave the peptide bond between D-Ala and Gly.

In substrates **2** and **6** LytM cleaves between D-Ala-Gly and Gly₁-Gly₂ with approximately equal rates. Using substrate **2** we did not observe a significant concentration-dependent change in the relative reaction rates of D-Ala-Gly and Gly₁-Gly₂ hydrolysis in the [S]/[E] range tested, from 725:1 to 1:2, when [LytM] = 50 μM. For the N-terminally longer substrates **3** and **7**, the balance is shifted in favor of hydrolysis of Gly₁-Gly₂. Regarding substrates lacking the D-Ala-Gly cross-link, LytM seems to disfavor the stem peptide in the C-terminus of pGly and the overall rate of hydrolysis with respect to pGly is diminished more drastically in comparison to LSS.

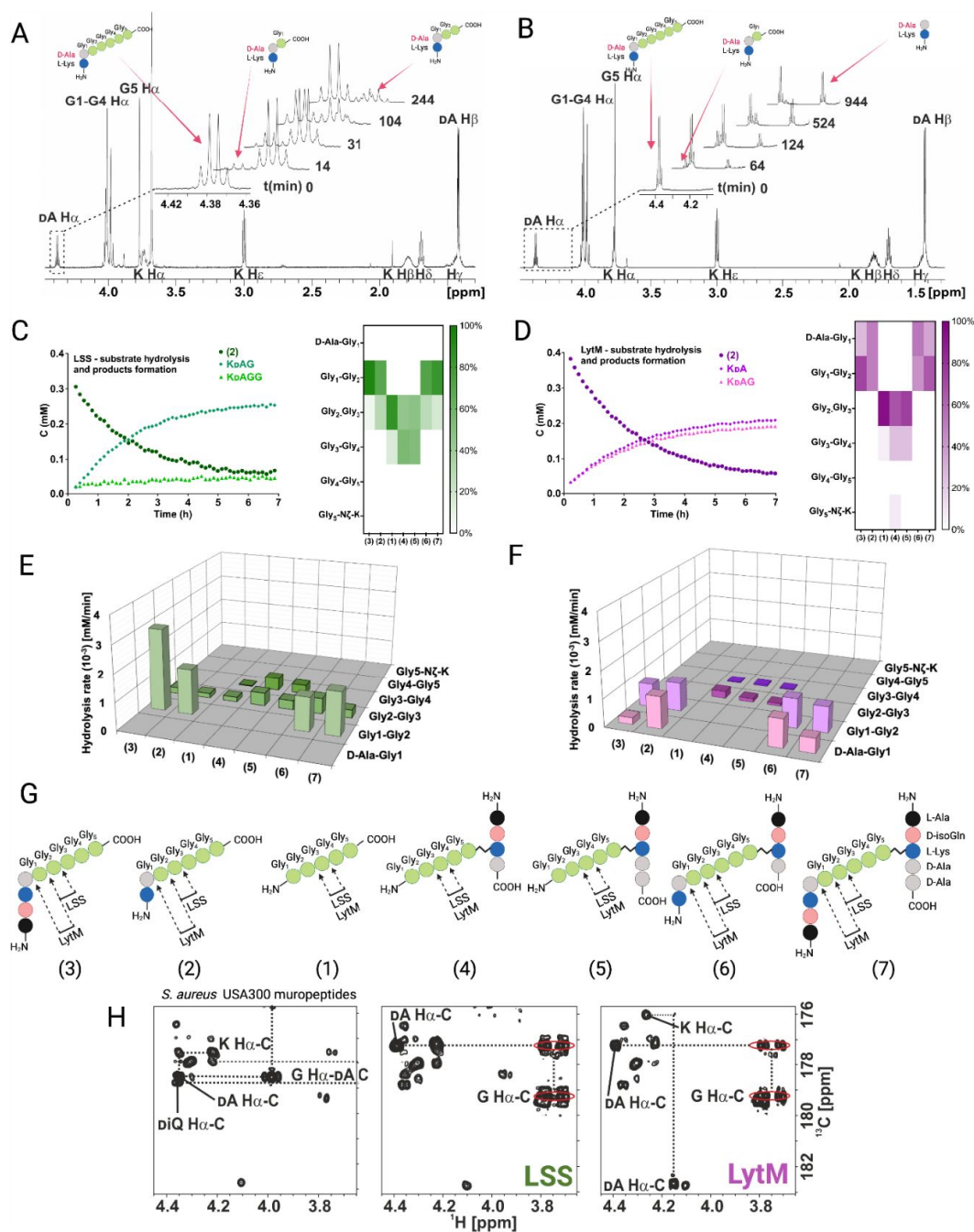


Figure 3.

Hydrolysis of peptides **1-7** by LSS (panels on the left) and LytM (panels on the right). Representative examples of real time NMR monitoring of substrate hydrolysis: Quantitative ^1H spectra at selected time points in the hydrolysis reactions of peptide **2** by LSS (**A**) and LytM (**B**). In hydrolysis by LSS peaks of Ala H α in products K_DAG and K_DAGG gradually appear as a function of time, whereas in LytM reaction K_DA and K_DAG are formed. (**C**, **D**) Concentrations in function of reaction time derived from NMR peak integrals for the representative reactions, and on the right, relative product concentrations at reaction end points for the studied PG fragments. **E**, **F**) Rates of formations of products in hydrolyses by LSS and LytM of the studied PG fragments **1-7**. **G**) Bonds cleaved by LSS and LytM in the different PG fragments. **H**) Hydrolysis of muropeptides extracted from *S. aureus* USA300 sacculus by LSS and LytM. On the left, a section of the carbonyl carbon region of the ^{13}C -HMBSC spectrum before addition of an enzyme. Middle panel, when LSS is added the bond between alanine and glycine is cleaved and a characteristic peak pattern of an Ala-linked C-terminal glycine H α appears, encircled in red. On the right, the latter is present also in the spectrum acquired after hydrolysis by LytM. Additionally, the H α peak of a Lys-linked C-terminal alanine appears.

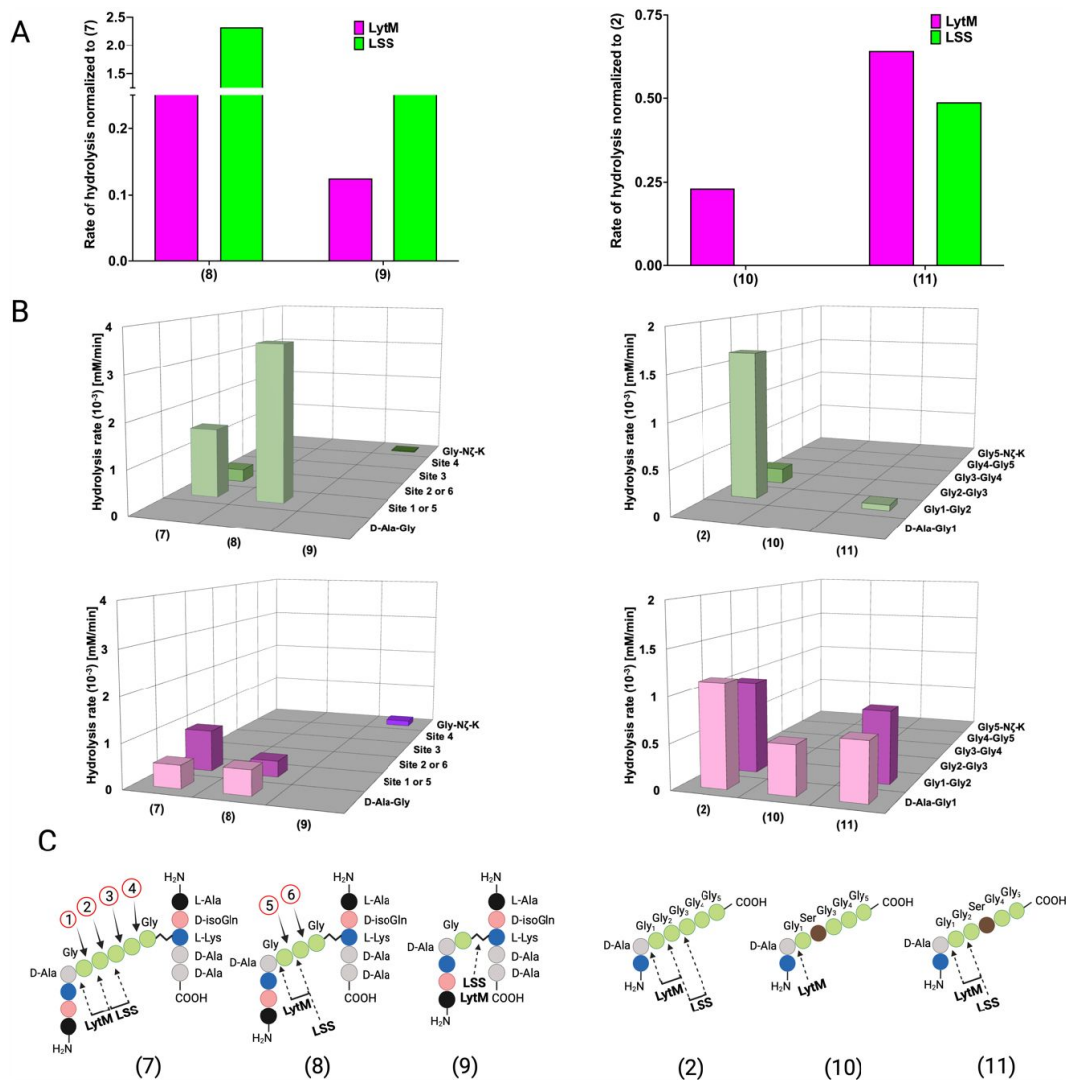


Figure 4.

Hydrolysis of PG fragments with a shorter cross-bridge or with serine in cross-bridge. Rates of substrate hydrolysis (**A**) and formation of product(s) in hydrolysis (**B**) by LSS (green) and LytM (magenta) of fragments **8** and **9** as compared with fragment **7** (panels on the left) and of fragments **10** and **11** as compared with fragment **2** (panels on the right). (**C**) Depictions of structures of used PG fragments.

Analogously to LSS, we compared the rate of hydrolysis of shorter PG fragments with LytM to map the critical length of the glycine-bridge in the substrate needed for the hydrolysis (Figs. S4, S5). Compared to **2**, the rate of hydrolysis did not change drastically when shortening the glycine chain from five glycines to three. However, LytM strongly favored D-Ala-Gly cleavage in **13** (KDAGGG) whereas it preferred Gly₁-Gly₂ cleavage in **12** (KDAGGGG). Unlike LSS, LytM can still hydrolyse **14** (KDAGG). Only the D-alanyl-glycine bond is cleaved, and the reaction is five to ten times slower than hydrolysis of **2**, **12** and **13**. Owing to its D-Ala-Gly cleavage efficiency, we tested whether LytM could also hydrolyse KDAAGGGG and KDAAG type substrates. However, the former was hydrolysed like pGly that is, no D-Ala-L-Ala cleavage occurred, but KDAAGG and KDAAGGG products were observed instead (not shown). *Enterococci* cell wall PG mimicking peptide KDAAG was not cleaved at all. This data further confirms that LytM is not only a glycyglycine endopeptidase but also acts as a D-alanyl-glycine hydrolase.

Hydrolyses of PG fragments mirror scissions in muropeptides extracted from *S. aureus* USA300 sacculus

To confirm the scissile bond specificity determined for LSS and LytM using synthetic PG fragment mimicking peptides, we extracted and purified muropeptides from *S. aureus* USA300 sacculus using the established protocol³¹. After administering muropeptide samples with LSS and LytM, we observed hydrolysis of the same amide bonds as with corresponding synthetic PG fragments (Fig. 2J). LSS hydrolyses the peptide bond between Gly₁ and Gly₂, recognised as appearance of peak of the C-terminal Gly₁-Hα-¹³C' resonance correlated with the corresponding ¹Hα-¹³C' resonance of D-Ala (Fig. 3H). Identical correlations are observed for LytM, indicating that it also hydrolyses the amide bond between Gly₁ and Gly₂ (Fig. 3H). However, additional resonances stemming from the C-terminal D-Ala that is correlated with the neighboring Lys are also observed. This indicates that LytM is cutting both glycyglycine and D-alanyl-glycine bonds also in muropeptides extracted from *S. aureus* sacculus.

Differences in susceptibilities of *S. aureus* mutants towards Lysostaphin and LytM can be explained by their substrate specificities

Composition of the cell wall PG of Staphylococci, including e.g., *S. aureus*, *S. simulans*, *S. epidermidis*, can be modulated by intracellular enzymes. For instance, gene products of *fem* (factor essential to methicillin resistance) family members, i.e., *femX*, *femA* and *femB* catalyse nonribosomal insertion of mono-(Gly₅), di-(Gly₄-Gly₃) and di-(Gly₂-Gly₁) glycines into the glycine cross-bridge in *S. aureus* PG, respectively³². Reduced susceptibility of *S. aureus* *βfemB* and *βfemAB* mutant strains towards LSS has been observed earlier^{30,33}. We pondered whether the length of the cross-bridge of *S. aureus* could influence the catalytic efficiency or target bond specificity of LSS and LytM. To this end, we studied hydrolysis of PG fragments **8** and **9** mimicking tri- and monoGly cross-bridge composition of PG in *S. aureus* *ΔfemB* and *βfemAB* mutants, respectively (Fig. 4). Interestingly, LSS hydrolyses **8** with an increased rate as compared to **7**. Furthermore, specificity increases i.e., cutting of glycyglycine bond, corresponding to the site “2” in **7** and site “6” in **8**, is not observed. Quite surprisingly, we also observed that LSS is able to hydrolyse substrate **9**, devoid of glycyglycine bond. Instead, LSS hydrolyses the Lys Nζ-monoGly C isopeptide bond. The rate of hydrolysis is, however, drastically lower (1.3%) than that of the amide bond between glycines in **7**. This result is excellent agreement with earlier studies on *S. aureus* *ΔfemB* and *βfemAB* mutants and muropeptides extracted from these strains. Indeed, lytic efficiency of LSS against *ΔfemB* mutant is not drastically reduced while the minimum inhibitory concentration (MIC) is three orders of magnitude higher for the *βfemAB* mutant³². A dramatic reduction of LSS lytic performance against *βfemAB* mutants was likewise observed in a turbidity reduction assay³⁰. However, residual lytic activity of LSS can be explained by its ability to hydrolyse the Lys Nζ-monoGly isopeptide bond existing in the *βfemAB* mutant.

Similar results were obtained with LytM except for the scissile bond specificity. Even if the number of glycines in the cross-bridge is reduced from five to three, LytM is still able to hydrolyse both D-Ala-Gly and glycyl-glycine bonds (sites “1” or “5”) (**Fig. 4**). This is in accordance with results on shortened linear peptides (Fig. S5) as well as with previous turbidity reduction assay data on *ΔfemB* mutant³⁰. However, if stem peptides are crosslinked with only a single glycine in the cross-bridge (9), LytM displays diminished activity by 8-fold in comparison to 7. Yet somewhat surprisingly, considering the cleavage of D-Ala-Gly bond in substrate **14** (KDAGG, Fig. S5), LytM hydrolysed the Lys N ϵ -monoGly C isopeptide bond. This again provides rationale for non-negligible lytic activity observed for LytM on *βfemAB* mutants although devoid of glycyl-glycine peptide bonds in their cross-bridge³⁰.

Next we tested the activity of LSS and LytM on PG fragments originating from so-called lysostaphin immunity factor (Lif/epr)-containing strains of *S. aureus*, that is the significance of serine substitutions in the PG cross-bridge on substrate hydrolysis^{34–36}. Of the two PG fragments, **10** and **11**, having Gly₂ or Gly₃ replaced by a serine, only **11** was hydrolysed by LSS. LSS cleaved the bond between Gly₁ and Gly₂ in **11** although with a rate 30-fold slower than that for substrate **2**. The results with LSS correlate well with earlier observations that show only fractional lytic activity of LSS towards *Staphylococcal* strains with serine in the cross-bridge³⁰. LytM was able to hydrolyse both PG fragments. **11** was cleaved similarly to the PG fragment **2**, whereas LytM specifically cleaved the D-Ala-Gly amide bond in **10** as it contains serine in the second position. The rates of substrate hydrolysis were not drastically lower i.e., by a factor of 4.3 (**10**) and 1.5 (**11**) in comparison to **2**. These data provide rationale to the observed differences in lytic efficiencies of LSS and LytM on *S. aureus* cells having serine substitutions in the cross-bridge³⁰. Hence, given that LytM exhibits significant catalytic activity towards D-Ala-Gly cleavage, it is less susceptible to serine substitutions in the cell wall PG. LytU hydrolysed only the amide bond between Gly₃-Gly₄ in **10** and no activity was detected with **11** as serine substitution for Gly₃ results in non-scissile bonds Gly₂-Ser₃ and Ser₃-Gly₄ in **11**. The effect of serine in a fragment containing an isopeptide bond was not tested in this study.

Structural level perspective on deviating substrate specificities for LSS and LytM

We combined the detailed substrate-level information in terms of real time reaction kinetics and scissile bond specificities together with the existing structural models available for LSS and LytM to glean structural-level understanding of enzyme specificities. Based on these data and using the nomenclature formulated by Schechter and Berger³⁷, we delineated substrate specificities for LSS and LytM (**Fig. 5**). It is clear that LSS is a glycyl-glycine endopeptidase as P1 and P1' positions are invariably occupied by Gly residues. However, the rate of hydrolysis increases when D-Ala occupies the P2 position, that is when LSS recognises a D-Ala-Gly cross-link in the cell wall. LytM is flexible regarding the P1 site, it can be accommodated either by D-Ala or Gly, whereas the P1' position is invariably occupied by Gly.

Why does LytM hydrolyse a D-Ala-Gly bond but LSS does not? To address this intriguing question, we utilised the existing structure of LytM in complex with the transition state analog tetraglycine-phosphinate²² and used molecular modelling approach to dock PG fragment **2** into the active sites of LSS and LytM. As has been proposed earlier, the Zn²⁺ at the active site polarises the scissile bond by coordinating the carbonyl oxygen of a residue in the P1 position. For LytM this is either D-Ala or Gly, and for LSS it is Gly (**Fig. 5**). D-Ala in the P1/S1 position in the LSS active site results in a steric clash with loop 1, most notably its residues L272-I274, thus preventing hydrolysis of a D-alanyl-glycine peptide bond. In LytM the corresponding loop is shorter allowing accommodation of D-Ala in the P1/S1 position and hence cleavage of D-alanyl-glycine cross-bridge or alternatively, if the substrate has a Gly in the P1 position, the peptide bond between Gly₁ and Gly₂.

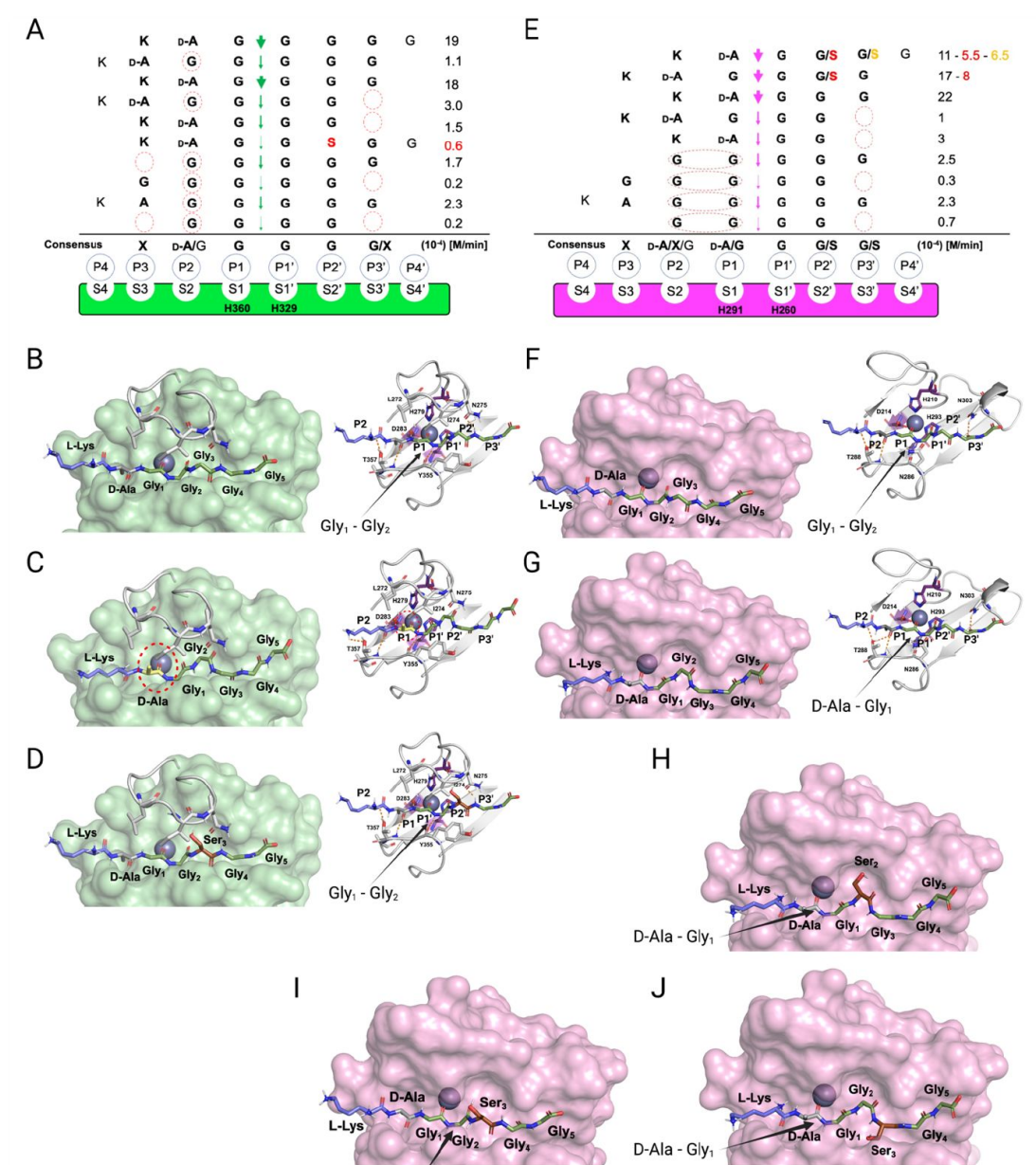


Figure 5.

Substrate specificity of LSS and LytM.

Schechter and Berger nomenclature is employed to describe the differences in substrate specificity between LSS (panel **A**) and LytM (panel **E**). Scissile bond in the substrate is between the P1 and P1' positions, indicated by green (LSS) and purple arrows (LytM), and hence residues towards the N-terminus from the scissile bond are P1-P4, whereas those towards the C-terminus are designated as P1'-P4'. PG fragments devoid of stem peptide linked to the C-terminal glycine are shown aligned with respect to their cleavage sites together with the rate of hydrolysis of the particular scissile bond. Consensus sequence displays preferable amino acid(s) that are accepted in the specific position (...P2, P1, P1', P2'...) with respect to the cleavage site. Red circles/ovals indicate missing or less than optimal amino acid accommodation in the particular P site, which translates into reduced catalytic efficiency. Serine substitutions in the glycine bridge and associated rates of hydrolysis are indicated by red and orange colors. Panels **B-D** show the docking results for fragments **2** and **11** into the catalytic site of LSS and panels **F-J** show the docking results for fragments **2**, **10**, and **11** into the catalytic site of LytM. LSS and LytM are capable of cleaving the Gly₁-Gly₂ bond in **2** (Panels **B**, **F**). LytM is also able to cleave the D-Ala-Gly₁ bond (Panel **G**), however, in LSS this would result in a steric clash between the D-Ala side chain and the residues in loop 1 (Panel **C**).

The same loop 1 gates the LSS active site and establishes the structural basis for Lif function. Serine in the P2' position severely hinders accommodation of the substrate to the LSS active site, which results in a drastic drop in the rate of hydrolysis (**Fig. 5**). In LytM the three residues shorter loop renders the active site more voluminous, which permits the short polar sidechain of Ser to fit in to the P2' or P3' positions. Consequently, substrates **10** (KDAGSGGG) and **11** (KDAGGSGG) can still be hydrolysed with relatively high efficiency (ca. 50%) in comparison to PG fragment **2** which contains a pGly bridge. Interestingly, as the P1' position only allows Gly, **10** cannot be hydrolysed between Gly₁ and Ser₂. However, LytM is able to hydrolyse the D-alanyl-glycine bond due to the positioning of the Ser into the P2' position. LSS cannot hydrolyse **10** as it would require the disallowed P1' position to accommodate Ser or alternatively P1 to be occupied by D-Ala, both of which are prevented by the extended loop 1 structure in LSS.

Interestingly, when the D-Ala-Gly cross-link is missing e.g., in pGly or PG fragments **4** and **5**, the latter mimicking a non-cross-linked PG monomer, the cleavage site is shifted within the glycine cross-bridge that is, cutting occurs between Gly₂ and Gly₃ since in minimum a substrate with four residues occupying P2, P1, P1' and P2' sites is required for both LSS and LytM. Owing to this limitation in substrate size and distinct difference in the substrate specificity of LSS and LytM, we observe that while both enzymes can hydrolyse tetraglycine, only LytM can cleave **14** (KDAGG) since it accepts D-Ala in the P1 position. We observed significant reduction in rate of hydrolysis for both LSS and LytM when the substrate is too short i.e., it cannot fill the P3'/S3' position. This is probably due to the stabilising hydrogen bonds that are formed between the longer glycine chain and a key asparagine residue in loop 4, Asn372 and Asn303 for LSS and LytM, respectively (**Fig. 5B, F**).

Discussion

To gain novel insight into lysostaphin enzyme family specificities, we employed NMR spectroscopy to determine the substrate specificities using real-time kinetics at atomic resolution on substrates mimicking PG fragments. In addition, we verified the sites of hydrolysis on mucopeptides purified from *S. aureus* USA300 sacculus and confirmed lytic efficiencies of LSS and LytM with turbidity reduction assays on bacterial *S. aureus* USA300 cells.

Previous research on substrate specificity is largely based on testing several bacterial strains with varying PG composition^{17,30} either with lysis assays or purified PG. Thus, determination of the site of hydrolysis often relies on applying abductive reasoning to either include or exclude different PG structures according to the assay results. Because this type of experimental set up often does not reveal the direct cleavage site, nor if there are several cleavage sites it should be supplemented with methods allowing direct observation – such as NMR. Yet, the end-point kinetics type of enzymatic assays e.g., administering chromatographically purified mucopeptides with a lytic catalyst and quenching the reaction after overnight incubation, followed by mass spectrometric analysis of reaction products, do not necessarily reflect substrate specificity accurately because they only detect reaction products at the end and do not consider plausible secondary reactions.

Our method is superior to the previous approaches because real-time kinetics data combined with a precise determination of the bond cut-off point reveal the true substrate specificity of LSS. Our data also explain the inconsistencies between results of previous studies, that is, our extensive set of PG fragments allowed a more comprehensive interpretation than previous studies with fewer substrates^{15,20,23–27,30,32,38,39}. LSS recognises the D-Ala-Gly cross-link. In such a substrate, D-Ala occupies the P2 position, which increases the rate of hydrolysis by 10-fold in comparison to substrates which position glycine into P2 (**Fig. 5**). As mature PG in *S. aureus* cell wall is highly (D-Ala-Gly) cross-linked, our results are in excellent agreement with the observed efficiency of LSS towards *S. aureus* cells in numerous studies in the literature^{30,40}. We also showed that LSS

can hydrolyse cell wall in the *S. aureus* $\Delta femB$ mutants³³, having three glycines in the cross-bridge, as they contain cross-linked D-Ala-Gly which occupy the P2-P1 positions and two glycines accommodated in the P1'-P2' positions (**Fig. 5A**). However, our data also demonstrate that LSS is capable of efficiently hydrolysing glycyl-glycine bonds in PG fragments with different levels of cross-linking, including also non-cross-linked PG monomers. In such a case, Gly₁ and Gly₂ house the P2 and P1 positions and the scissile bond is shifted from the preferable Gly₁-Gly₂ bond one residue forward to the Gly₂-Gly₃ amide bond. This confirms the findings made by Maya-Martinez and colleagues with non-cross-linked PG fragments i.e., LSS leaves two or three glycines connected to Lys sidechain²⁶.

Hence, our results provide rationale to the previous observations which show discrepancy regarding the LSS site of hydrolysis. To summarise, LSS prefers cutting between Gly₁ and Gly₂, whenever Gly₁ is cross-linked to D-Ala of neighboring stem, whereas it hydrolyses the amide bond between Gly₂ and Gly₃ in non-cross-linked (devoid of D-Ala-Gly bond) PG fragments.

LytM was originally categorised as a glycyl-glycine endopeptidase based on lytic experiments performed using purified cell walls, which showed that it is active against *S. aureus* and *S. carnosus* but not against *Micrococcus luteus*.¹⁷ *M. luteus* PG has the following structure: Ala-(D-γGlu-Gly)-Lys[D-Ala-Lys-D-Glu(-Gly)-Ala-D-Ala-Lys-D-γGlu(-Gly)-Ala]-D-Ala and thus contains neither Gly-Gly nor D-Ala-Gly bonds¹⁴. As was suggested by Ramadurai et al. (1999)¹⁷ *M. luteus* lacked the bond necessary for LytM cleavage, and here we have identified that bond to be D-Ala-Gly in addition to the known specificity towards glycyl-glycine bonds.

The only other recognised D-Ala-Gly hydrolase in *S. aureus* is LytN. Contrary to LytM, it contains a catalytic CHAP domain, which cleaves both D-Ala-Gly and MurNAc-L-Ala bonds, in other words is a D-alanyl-glycine endopeptidase as well as an N-acetylmuramoyl-L-alanine amidase domain²⁹. D-Ala-Gly cleavage activity has also been found from a CHAP domain of a *S. aureus* Phage $\phi 11$ murein hydrolase. In this hydrolase amidase activity is contained in another domain of the modular protein³⁹. Recently also *Enterococcus faecalis* EnpA, which belongs to the M23 metalloendopeptidase family, has been shown to cleave D-Ala-Ala bond in *E. faecalis*. D-Ala-Gly cleaving activity was also reported, although without quantitative information regarding catalytic efficiency. Given that the P1 site in EnpA can accommodate D-Ala, it exhibits substrate specificity similar to that of LytM, which allows occupation of the P1 position by D-Ala (and Gly). In this way, LytM and EnpA deviate from LSS which requires invariably glycine in the P1 position. On the other hand, similar to LSS, LytM allows only glycine at the P1' site, whereas EnpA is more promiscuous and can accommodate Gly, L-Ala and L-Ser in this position^{30,38}.

The pivotal findings in this paper are the discovery of the D-Ala-Gly hydrolysis activity of LytM, previously designated solely as a glycyl-glycine endopeptidase. Yet, we show for the first time that the substrate specificity of LSS is defined by the D-Ala-Gly cross-link, which increases catalytic efficiency 10-fold with respect to pentaglycine.

Methods and materials

Reagents

Peptides were synthesised by CASLO as Trifluoroacetic acid (TFA) salts. *Escherichia coli* BL21 (DE3)pLysS cells were obtained from Novagen (Novagen). *Staphylococcus aureus* USA300 and Newman D2C RN4220 cells were purchased from American Type Culture Collection (ATCC). The *S. aureus* Newman conditional overexpressing LytU RH7781 mutant was previously described¹⁸.

Protein expression and purification

The catalytic domain of LSS (LSS_{cat} residues 248-384) was produced as a His-tagged GB1-fusion protein. LSS_{cat}GB1 was cloned in pET15b vector (Novagen) and heat-shock transformed into *E. coli* BL21(DE3) pLysS (Novagen). The cells were grown at 37 °C with 250 rpm orbital shaking in Luria-Bertani broth supplemented with 100 µg/ml ampicillin until the OD₆₀₀ reached 0.55-0.6. Then the temperature was lowered to 20 °C and protein expression was induced by adding 0.4 mM isopropyl β-D-1-thiogalactopyranoside (IPTG). The overexpression of the proteins occurred at 20 °C for 20 hours. The cells were harvested by centrifugation at 6000 g for 20 min at 20 °C followed by cell resuspension in 1x PBS buffer and stored in -80 °C until purification. Complete lysis of the cells was achieved using Emulsiflex-C3 homogeniser (Avestin) and lysates were cleared by centrifugation at 35,000g for 30 min at 4 °C. The 6x-His-tagged proteins were captured using Ni-NTA Superflow (QIAGEN) and the His-tag was cleaved at 4 °C for 16-18 hours by human thrombin (Biopharm laboratories). HiLoad 26/60 Superdex 75 pg column (GE Healthcare) was utilised in the size exclusion chromatography of the desired fragments in 20 mM Sodium-phosphate buffer pH 6.5, 50 mM NaCl using an ÄKTA pure system (GE Healthcare).

LytM catalytic subunits (LytM_{cat} residues 185-316) were cloned into pGEX-2T vector and heat-shock transformed into *E. coli* BL21(DE3)pLysS (Novagen). The GST fusion LytM_{cat} protein was produced the same way as LSS_{cat}GB1. The GST fusion proteins were purified with Protino Glutathione Agarose 4B (Macherey-Nagel) and GST was cleaved by human thrombin (Biopharm laboratories) at 4 °C for 16 h. The protein was further purified by size exclusion chromatography (SEC) with a HiLoad 26/60 Superdex 75 pg column (GE Healthcare) in SEC buffer (20 mM Sodium-phosphate buffer pH 6.5, 50 mM NaCl) using an ÄKTA pure chromatography system (GE Healthcare). Eluted fractions were concentrated using Amicon® Ultra to 1 mM final concentration.

The inactive mutant of LytMcat (LytMcat_H291A) was generated using QuikChange II Site-Directed Mutagenesis kit (Agilent Technologies) and the mutation was verified by sequencing. The recombinant proteins were produced and purified same as the wildtype.

The ¹⁵N-labelled LytM_{cat} and LytM_{cat}-H291A were expressed in *E. coli* BL21(DE3)pLysS cells in standard M9 minimal medium using 1 g/l ¹⁵N NH₄Cl (Cambridge Isotope Laboratories) as a sole nitrogen source. The proteins were purified in 50 mM NaH₂PO₄, pH 6.5, 50 mM NaCl using the same protocol as described above for the unlabelled proteins.

Muropeptide extraction

Muropeptides were extracted as before described with modifications³¹. 2 mL of overnight bacteria culture were centrifuged at 10,000 rpm in table microcentrifuge, supernatant was discarded, and bacteria were resuspended in 4 mL of 100 mM Tris HCl pH 6.8, 0.25% Sodium dodecyl sulfate (SDS) to reach OD₆₀₀ equal to 10. After boiling SDS was removed with extensive washes. Cells were then solubilised with 1 mL of dH₂O and incubated for 30 min at room temperature in sonifier waterbath. 500 µL of 15 µg/mL DNase in 0.1 M Tris HCl pH 6.8 solution was added and sample was incubated 1 hour at 37 °C, 150 rpm. 500 µL of 4 mg/mL Pronase (Sigma) were added and sample was incubated overnight at 37 °C, 150 rpm. After enzymes inactivation, the pellet was resuspended with 500 µL of 1 M HCl solution and incubated for 4 hours at 37 °C, 150 rpm to release the teichoic acid. The sample was then washed with dH₂O until pH was between 5 and 6. Finally, the pellet was resuspended with 12.5 mM sodium dihydrogen-phosphate, pH 5.5 or 20 mM sodium phosphate buffer pH 6.5 and adjusted to OD₅₇₈ equal to 3; Mutanolysin (Sigma) solution 5000 U/mL was added and incubated for 16 hours at 37 °C, 150 rpm. After mutanolysin inactivation, sample was centrifuged at 10,000 rpm in table microcentrifuge for 10 min, pellet was discarded and muropeptides were in the supernatant. Muropeptides were dried using Savant SC110A SpeedVac (Thermo Fisher Scientific), resuspended with D₂O and pH was adjusted to 7.5 using deuterated sodium hydroxide. NMR sample was prepared by diluting the muropeptides stock solution in 50 mM dTRIS 7.5, and 0.1 mM DSS as reference compound.

Sample preparation for NMR kinetics

The synthetic peptides were purchased from CASLO. The peptides were resuspended in D₂O at the concentration of 20-40 mM, except for Gly₂ position ¹³C-labeled pGly which was 6.5 mM. For all peptides the pH was adjusted to 7.5 using deuterated sodium hydroxide. Peptides were diluted to a desired concentration in presence of 50 mM deuterated TRIS pH 7.5. For each sample, prepared to 3 mm OD round bottom NMR tube, 0.1 mM Sodium trimethylsilylpropanesulfonate (DSS, Chenomx Internal standard, 5 mM 99,9 % D, lot PS20190624) was added as a reference compound. Reactions were initiated by adding the enzyme to a final concentration of 2 μM or 50 μM.

NMR-based kinetics and resonance assignment of synthetic PG fragments and muropeptides from *S. aureus* sacculus

All NMR experiments were carried out at 25 °C, and at the field strength of 800 MHz of ¹H frequency on a Bruker Avance III HD NMR spectrometer, equipped with cryogenically cooled ¹H, ¹³C, ¹⁵N triple-resonance TCI probehead. NMR data collection for kinetics measurements employed a standard ¹H pulse program (zgpr) having a selective radiofrequency field for residual HDO signal presaturation during the recycle delay. To ensure quantitative detection of substrate and product concentrations, a 20 second long recycle delay was used between the transients used for the signal averaging. 0.1 mM DSS was used as a reference compound both for the peak integration, chemical shift referencing as well as lineshape optimisation. For each time point, experiment was accumulated with 24 transients, yielding an experimental time of 8 minutes per time point.

First, a reference ¹H spectrum was acquired. The sample was then removed from the magnet, and the enzyme was added. The time of enzyme addition was recorded as $t=0$. After the enzyme addition the sample was placed back into the magnet, and the shim was manually readjusted before the start of acquisition of consecutive ¹H spectra to follow the hydrolysis. This preparatory work resulted in a delay of about 5-10 minutes between enzyme addition ($t=0$) and the end of the acquisition of the first spectrum. This delay was accounted for in the data analysis for each experiment.

For the resonance assignment of NMR ¹H_α, ¹³C_α and ¹³C_{CO} chemical shifts in selectively ¹³C-labeled Gly₂ position in pentaglycine (1), a glycine H_α-detection optimised HCACO -type NMR experiment was devised (Fig. S7). The spectrum was collected as a 2D H(CA)CO ¹H-¹³C correlation experiment to establish connectivities between ¹H_α and ¹³C' resonances in Gly₂. The experiment was measured using 2 transients per FID and the overall experimental time was 200 seconds per time point.

Assignment of chemical shift resonances in different synthetic PG substrates and products as well as muropeptides from *S. aureus* USA300 sacculus was based on the measurement of ¹H as well as 2D ¹H-¹³C HSQC, ¹H-¹³C HMBC, and ¹H-¹³C' selective HMBC spectra. Typically, ¹H-¹³C HMBC experiments were measured overnight and at the end of the reaction to warrant the highest sensitivity for product chemical shift assignment.

Data analysis of NMR kinetics

To obtain substrate and product concentrations at each time point, NMR resonances were integrated together with reference compound using Topspin 3.6.5 software package (Bruker). Rates of reactions were calculated using linear regression of the first 40-60 min of the reaction. Goodness of fitting was evaluated by using the R^2 value. All the data fitting had $R^2 \geq 0.9$. Rates of the reaction *versus* substrate concentrations were plotted and Michaelis-Menten fitting was performed using GraphPad Prism software version 9.5.1 (GraphPad Software Inc.).

Staphylococcus aureus cell growth conditions

Staphylococcus aureus USA 300 cells were grown overnight in Tryptic Soy Broth (TSB) and Newman RN4220 and RH7781 were grown in Lysogeny Broth (LB) at 37 °C, 200 rpm by inoculating one single colony in 3 mL of medium. Bacteria were then diluted 1:100 in prewarmed TSB and grown until desired OD₆₀₀.

Turbidity reduction assay

Turbidity assay was performed as previously described with some modifications¹⁸. *S. aureus* USA 300 bacterial cells were incubated at 37 °C, 200 rpm until OD₆₀₀ between 6 to 8 corresponding to late stationary phase. Bacteria were then washed twice using 20 mM Tris HCl pH 7.5, 50 mM NaCl, and resuspended at OD₆₀₀ equal to 5. Bacteria were plated in round-bottom 96-well plate (Thermo Fisher Scientific), and the reaction was started by adding the enzymes at final concentration of 50 µg/mL. The assay was carried out in final volume of 100 µL. Bacteria without any enzyme was used as control sample. Reduction of turbidity of bacteria suspension was followed using BioTek Epoch2 Microplate Spectrophotometer (Agilent Technologies), at 25 °C for 16 hours with continuous shaking at 500 cpm. Data were expressed as normalised reduction of the turbidity over the time. Each reaction was carried out in quadruplicate.

Docking

Substrate 2 for docking was built with Maestro molecular modeling software (Schrödinger, 2021) available in Schrödinger (LLC, New York, NY) and Ligprep ligand preparation tool was used to refine the structure with force field OPLS4. The crystal structures of LytM (PDB code: 4ZYB, (23)) and lysostaphin (PDB code: 4QPB,³⁹) were retrieved from the Protein Data Bank. The protein structures were first prepared with the Protein preparation wizard available in the Schrödinger suite. Protein preparation wizard was used to add missing hydrogen atoms, delete water molecules, and assign correct bond orders with force field OPLS4. Glide^{42–44} was used for docking. The receptor grid was generated with Glide and the Standard Precision (SP) Peptide mode was used for docking. It was noticed that the scoring function favors the strong interaction between the carboxylic acid of the substrate C-terminus and zinc ion, and thus the C-terminus was capped with an N-methylacetamide (NMA) residue. The serine containing peptides were modeled in the binding site by mutating the appropriate residues with Pymol⁴⁵.

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Conflict of Interests

The authors declare that they have no conflict of interest.

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Editors

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Volker Dötsch

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Reviewer #1 (Public Review):**Summary:**

The manuscript aimed at elucidating the substrate specificity of two M23 endopeptidase Lysostaphin (LSS) and LytM in *S. aureus*. Endopeptidases are known to cleave the glycine-bridges of staphylococcal cell wall peptidoglycan (PG). To address this question, various glycine-bridge peptides were synthesized as substrates, the catalytic domain of LSS and LytM were recombinantly expressed and purified, and the reactions were analyzed using solution-state NMR. The major finding is that LytM is not only a Gly-Gly endopeptidase, but also cleaves D-Ala-Gly. Technically, the advantage of using real-time NMR was emphasized in the manuscript. The study explores an interesting aspect of cell wall hydrolases in terms of substrate-level regulation. It potentially identified new enzymatic activity of LytM. However, the biological significance and relevance of the conclusions remain clear, as the results are mostly from synthetic substrates.

Strengths:

The study explores an interesting aspect of cell wall hydrolases in terms of substrate-level regulation. It potentially identified new enzymatic activity of LytM.

Weaknesses:

1. Significance: while the current study provided a detailed analysis of various substrates, the conclusions are mainly based on synthesized peptides. One experiment used purified muropeptides (Fig. 3H); however, the results were unclear from this figure. The results from synthesized peptides may not necessarily correlate with their biological functions *in vivo*. Secondly, the study used only the catalytic domain of both proteins. It is known that the substrate specificity of these enzymes is regulated by their substrate-binding domains. There is no mention of other domains in the manuscript and no justification of why only the catalytic domain was studied. In short, the relevance of the results from the current study to the enzymes' actual physiological functions remains to be addressed, which attenuated the significance of the study.

2. Impact and novelty: (1) the current study provided evidence suggesting the novel function of LytM in cleaving D-Ala-Gly. The impact of this finding is unclear. The manuscript discussed *Enterococcus faecalis* EnpA. But how about other M23 endopeptidases? What is biological relevance? (2) A very similar study published recently showed that the activity of LSS and LytM is regulated by PG cross-linking: LSS cleaves more cross-linked PG and LytM cleaves less cross-linked PG (Razew, A., Laguri, C., Vallet, A., et al. *Staphylococcus aureus* sacculus mediates activities of M23 hydrolases. *Nat Commun* 14, 6706 (2023)). The results of this paper are different from the current study whereby both LSS and LytM prefer cross-linked substrates (Fig. 2JKL). Moreover, no D-Ala-Gly cleavage was observed by LytM using purified PG substrate from Razew A et al. An explanation of inconsistent results is needed here. In my opinion, the knowledge generated from the current study has not been fully settled. If the results can be validated, the contribution to the field is incremental, but not substantial. (3) The authors emphasized a few times in the text that it is superior to use NMR technology. In my opinion, NMR has certain advantages, such as measuring the efficacy of cleavage, but it is not that superior. It should be complementary to other methods such as mass spectrometry. In addition, more relevant solid-state NMR using intact PG or bacterial cells was not discussed in the study. I am of the opinion that the corresponding text should be revised.

3. The conclusions are not fully supported by the data

As mentioned above, the conclusions from synthesized peptide substrates may not necessarily reveal physiological functions. The conclusions need to be validated by more physiological substrates.

4. There are some issues with the presentation of the figures, text, and formatting.

Reviewer #2 (Public Review):

Summary:

This work investigates the enzymatic properties of lysostaphin (LSS) and LytM, two enzymes produced by *Staphylococcus aureus* and previously described as glycyl-glycyl endopeptidases. The authors use synthetic peptide substrates mimicking peptidoglycan fragments to determine the substrate specificity of both enzymes and identify the bonds they cleave.

Strengths:

- This work is addressing a real gap in our knowledge since very little information is available about the substrate specificity of peptidoglycan hydrolases.
- The experimental strategy and its implementation are robust and provide a thorough analysis of LSS and LytM enzymatic activities. The results are very convincing and demonstrate that the enzymatic properties of the model enzymes studied need to be revisited.

Weaknesses:

- The manuscript is difficult to read in places and some figures are not always presented in a way that is easy to follow. This being said, the authors have made a good effort to present their experiments in an engaging manner. Some recommendations have been made to improve the current manuscript but these remain minor issues.

<https://doi.org/10.7554/eLife.93673.1.sa0>

Author Response

Public Reviews:

Reviewer #1 (Public Review):

Summary:

*The manuscript aimed at elucidating the substrate specificity of two M23 endopeptidase Lysostaphin (LSS) and LytM in *S. aureus*. Endopeptidases are known to cleave the glycine-bridges of staphylococcal cell wall peptidoglycan (PG). To address this question, various glycine-bridge peptides were synthesized as substrates, the catalytic domain of LSS and LytM were recombinantly expressed and purified, and the reactions were analyzed using solution-state NMR. The major finding is that LytM is not only a Gly-Gly endopeptidase, but also cleaves D-Ala-Gly. Technically, the advantage of using real-time NMR was emphasized in the manuscript. The study explores an interesting aspect of cell wall hydrolases in terms of substrate-level regulation. It potentially identified new enzymatic activity of LytM. However, the biological significance and relevance of the conclusions remain clear, as the results are mostly from synthetic substrates.*

Strengths:

The study explores an interesting aspect of cell wall hydrolases in terms of substrate-level regulation. It potentially identified new enzymatic activity of LytM.

Weaknesses:

1. *Significance: while the current study provided a detailed analysis of various substrates, the conclusions are mainly based on synthesized peptides. One experiment used purified muropeptides (Fig. 3H); however, the results were unclear from this figure.*

We acknowledge the Reviewer for comments and concerns regarding the potential weaknesses of this study.

Because peptidoglycan is insoluble, as such it is not amenable to solution-state NMR studies. However, soluble peptidoglycan (PG) fragments for NMR analyses can be obtained by digesting bacterial sacculi or via chemical synthesis. Whereas digestion results in mixtures of products, synthesis yields pure molecules. Analysis of NMR spectra of muropeptide-mimicking synthetic peptides before and after enzyme addition provides tools to identify peaks in the much more complex spectra of mutanolysin-treated sacculus.

We will improve data presentation in Figure 3H in the revised version of our manuscript and emphasize the similarity of product peaks in spectra acquired from experiments using either synthetic peptides or mutanolysin-digested sacculus.

The results from synthesized peptides may not necessarily correlate with their biological functions in vivo.

The Reviewer refers several times to the use of synthetic peptides in this study. While it is unclear to us whether the concern is about the synthetic nature of the molecules or because the peptides are devoid of PG disaccharide units, it is true that PG fragments lack the 3D architecture present in intact sacculus, and thus cannot perfectly mimic the *in vivo* milieu. The fragments, as well as purified sacculus, also lack all other components present in an intact bacterial cell wall. Our largest synthetic peptide (7), however, represents a crosslinked muropeptide (stem-pentaGly-stem) which according to the structural model recently presented by Razew et al. (2023) (*Staphylococcus aureus* sacculus mediates activities of M23 hydrolases. *Nat Commun* 14, 6706) is large enough to cover the peptidic interaction interface between substrate and enzyme.

Secondly, the study used only the catalytic domain of both proteins. It is known that the substrate specificity of these enzymes is regulated by their substrate-binding domains. There is no mention of other domains in the manuscript and no justification of why only the catalytic domain was studied. In short, the relevance of the results from the current study to the enzymes' actual physiological functions remains to be addressed, which attenuated the significance of the study.

Lysostaphin catalytic domain was used for experimental simplicity and to allow direct comparison with LytM catalytic domain. Because lysostaphin cell-wall targeting (SH3b) domain interacts with the substrate with variable affinities depending on the substrate structure (Tossavainen et al., Structural and functional insights into lysostaphin-substrate interaction, *Front. Mol. Biosci.* 5, 60 (2018) and Gonzalez-Delgado et al., Two-site recognition of *Staphylococcus aureus* peptidoglycan by lysostaphin SH3b, *Nat. Chem. Biol.* 16, 24-30 (2020)), we would have had skewed results on kinetics because of this interaction.

Catalytic domains were used also in the article by Razew et al. (*Staphylococcus aureus* sacculus mediates activities of M23 hydrolases. *Nat Commun* 14, 6706 (2023)). They showed that mature lysostaphin and lysostaphin catalytic domain hydrolysed the same Gly-Gly bonds.

Moreover, full-length LytM is catalytically inactive. This is because the linker between its N-terminal and catalytic domains occludes the catalytic site (Odintsov et al. Latent LytM at 1.3 Å

resolution. J. Mol. Biol. 225, 775 (2004)). LytM catalytic domain without its N-terminal segment is active (Odintsov et al (2004) and Firczuk et al. Crystal structure of active LytM. J. Mol. Biol 354, 578 (2005)).

1. Impact and novelty:

(1) the current study provided evidence suggesting the novel function of LytM in cleaving D-Ala-Gly. The impact of this finding is unclear. The manuscript discussed Enterococcus faecalis EnpA. But how about other M23 endopeptidases? What is biological relevance?

EnpA was specifically mentioned because it has been reported to also cleave the D-Ala-Gly bond. Structural similarities between the enzymes could reveal the basis for this bond specificity. Moreover, the focus of the study was not to reveal the biological function of LytM but rather to understand which amino acid substitutions lead to differences in specificities in the two structurally very similar enzymes.

(2) A very similar study published recently showed that the activity of LSS and LytM is regulated by PG cross-linking: LSS cleaves more cross-linked PG and LytM cleaves less cross-linked PG (Razew, A., Laguri, C., Vallet, A., et al. Staphylococcus aureus sacculus mediates activities of M23 hydrolases. Nat Commun 14, 6706 (2023). The results of this paper are different from the current study whereby both LSS and LytM prefer cross-linked substrates (Fig. 2JKL). Moreover, no D-Ala-Gly cleavage was observed by LytM using purified PG substrate from Razew A et al. An explanation of inconsistent results is needed here. In my opinion, the knowledge generated from the current study has not been fully settled. If the results can be validated, the contribution to the field is incremental, but not substantial.

Another point raised by the Reviewer concerned the inconsistent results between our study and the recent paper by Razew et al. (2023) regarding LytM D-Ala-Gly cleavage. The explanation might lie in the type of NMR data acquired and its interpretation. We identified all hydrolysis products using ¹H, ¹³C multiple bond correlation NMR spectra acquired from samples dissolved in deuterated buffers. Use of C-H signals is advantageous in that they are not prone to chemical exchange phenomena and enable unambiguous chemical shift assignment. Based on shown NMR spectra, Razew and co-workers identified cleaved muropeptide bonds by observing product glycine peaks in ¹H, ¹⁵N correlation spectra, specifically amide peaks of product C-terminal glycines appearing in the 114-117 ppm ¹⁵N region of spectra of samples treated with LytM/LSS. D-Ala-Gly cleavage, however produces an N-terminal glycine, whose signal due to chemical exchange is not typically observed in regular N,H correlation spectra. Razew and co-workers validated their observations with UPLC-MS analysis. However, to our understanding, their data analysis was based on the assumption that LytM cleaves between Gly4-Gly5 (or Gly1-Gly2 using our numbering), and accordingly only masses corresponding to potential products containing 1 to 4 glycines anchored to the lysine side chain were considered.

(3) The authors emphasized a few times in the text that it is superior to use NMR technology. In my opinion, NMR has certain advantages, such as measuring the efficacy of cleavage, but it is not that superior. It should be complementary to other methods such as mass spectrometry. In addition, more relevant solid-state NMR using intact PG or bacterial cells was not discussed in the study. I am of the opinion that the corresponding text should be revised.

We value and agree with the Reviewer's opinion that NMR spectroscopy is complementary to other methods e.g., mass spectrometry. However, in this particular case, NMR provided simultaneously information on reaction kinetics as well as scissile bonds in the substrates,

which allowed us to compare rates of hydrolysis in different PG fragments and reshape the substrate specificities of LytM/LSS. We also agree that solid-state NMR is a wonderful technique. In our revised manuscript, we will edit the text accordingly.

1. The conclusions are not fully supported by the data

As mentioned above, the conclusions from synthesized peptide substrates may not necessarily reveal physiological functions. The conclusions need to be validated by more physiological substrates.

As pointed out above in our response to the potential weaknesses of this study, the aim of this work was not to reveal the physiological function of LytM but to glean information on its substrate specificity that echoes its functional role in a substrate level. Hitherto LytM has been shown to cleave amide bonds between glycines without providing detailed information about the specific scissile bonds in the established PG components in *S. aureus* cell wall. The same holds true for lysostaphin as well. This study provides concomitantly information on the rates of hydrolysis and scissile bonds of these two enzymes. We deduced that LytM, and especially lysostaphin substrate specificity is defined by D-Ala-Gly cross-linking, which is a structural property, whereas Razew et al. (2023) discuss about “more cross-linked” and “less cross-linked PG”, which is a supramolecular asset or density.

1. There are some issues with the presentation of the figures, text, and formatting.

We are grateful to the Reviewer for bringing up issues in figures and text. We will address these in the revised version of the manuscript.

Reviewer #2 (Public Review):

Summary:

*This work investigates the enzymatic properties of lysostaphin (LSS) and LytM, two enzymes produced by *Staphylococcus aureus* and previously described as glycyl-glycyl endopeptidases. The authors use synthetic peptide substrates mimicking peptidoglycan fragments to determine the substrate specificity of both enzymes and identify the bonds they cleave.*

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- *The manuscript is difficult to read in places and some figures are not always presented in a way that is easy to follow. This being said, the authors have made a good effort to present their experiments in an engaging manner. Some recommendations have been made to improve the current manuscript but these remain minor issues.*

We thank the Reviewer for providing positive feedback on our manuscript and for appreciating the systematic work behind this study which aims to unknot the substrate specificity of two *S. aureus* PG hydrolyzing enzymes. We are grateful for the comments aiming to improve the presentation of the current version of manuscript and we will take these into account while preparing the revised version of the manuscript.