

**Role of *Pseudomonas aeruginosa* Low-Molecular-Mass Penicillin-Binding Proteins in AmpC Expression,  $\beta$ -lactam Resistance and Peptidoglycan Structure**Alaa Ropy<sup>1</sup>, Gabriel Cabot<sup>2</sup>, Irina Sánchez-Diener<sup>2</sup>, Cristian Aguilera<sup>1</sup>,  
Bartolome Moya<sup>2</sup>, Juan A. Ayala<sup>1\*</sup> and Antonio Oliver<sup>2\*</sup>[+](#) Author Affiliations**ABSTRACT**

This study aimed to characterize the role of *Pseudomonas aeruginosa* Low-Molecular-Mass penicillin-binding proteins (LMM-PBPs), namely PBP4 (DacB), PBP5 (DacC) and PBP7 (PbpG), in peptidoglycan composition,  $\beta$ -lactam resistance and ampC regulation. For this purpose, we constructed all single and combined mutants of *dacB*, *dacC*, *pbpG* and *ampC* in from wild-type PAO1 strain. Peptidoglycan composition was determined by HPLC, ampC expression by RT-PCR, PBPs patterns by Bocillin-FL binding test and antimicrobial susceptibility by MIC testing for a panel of  $\beta$ -lactams. Microscopy and growth rate analysis revealed no apparent major morphological changes for any of the mutants compared to wild-type PAO1. Of the single mutants, only *dacC* led to significantly increased pentapeptide levels, showing that PBP5 is the major DD-carboxypeptidase in *P. aeruginosa*. Moreover, our results indicate that PBP4 and PBP7 would play a significant role as DD-carboxypeptidase only if PBP5 is absent, together with their inferred DD-endopeptidase activity. As expected, the inactivation of PBP4 lead to a significant increase in ampC expression (around 50-fold), but, remarkably, the sequential inactivation of the three LMM-PBPs produced a much further increase (1000-fold) which correlated with peptidoglycan pentapeptide levels. Finally, the  $\beta$ -lactam susceptibility profiles of the LMM-PBPs mutants correlated well with ampC expression data. However, the inactivation of ampC in these mutants evidenced as well a role of LMM-PBPs, especially PBP5, in intrinsic  $\beta$ -lactam resistance. In summary, in addition to assessing for the first time the effect of *P. aeruginosa* LMM PBPs in peptidoglycan structure, our results represent a step forward in understanding the impact in  $\beta$ -lactam resistance, apparently driven by the interplay between their role on AmpC induction,  $\beta$ -lactam trapping and DD-carboxypeptidase/ $\beta$ -lactamase activity.

**FOOTNOTES**

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