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Systematically analysis antibacterial activity of CHAP catalytic domain of *Staphylococcus aureus* phage lysin Ply187

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Lysins are murein hydrolases encoded by bacteriophage and can kill bacteria effectively. To obtain highly effective antibacterial lysins, we need to systematically analyze the activity of its catalytic domains. The coding sequence of the catalytic domain of Ply187 ($CHAP_{Ply187}$) was synthesized and constructed into a recombinant expression plasmid to generate pET28a-$CHAP_{Ply187}$, which was transformed into a BL21(DE3) *E. coli* strain. The recombinant $CHAP_{Ply187}$ protein was produced by IPTG induction and purified by a two-step method, reaching >95 percent purity. Compared with the catalytic domain of lysostaphin (CAT_{Lysn}), $CHAP_{Ply187}$ showed similar antibacterial potency and the activity was similarly affected by a series of metal ions. $CHAP_{Ply187}$ however showed a much broader antibacterial spectrum, exhibited optimal activity in a wider range of the pH and could tolerate higher ionic strength. The research work will help to design potent recombinant lysins against drug resistant bacteria.

Biography

Qingshan Huang has completed his PhD from Fudan University and Postdoctoral studies from Fudan University Life School. He is an Associate Professor at Fudan University and is interested in the development of anti-infective and anti-tumor protein agents by using molecular biology, cell biology, bioinformatics and other approaches. He has published more than 50 papers in reputed journals.

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