

Nucleotide sequence: the β -hemolysin gene of *Staphylococcus aureus*

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We have cloned and determined the nucleotide sequence of the *Staphylococcus aureus* β -hemolysin gene (*hly*). The *hly* gene, located on a 4kb *Clal* fragment, contains 330 amino acids having a predicted molecular weight of 39kd. The amino acid composition of the predicted 39kd protein is in agreement with the data of Bernheimer et al. (1) and Fackrell (2), and the restriction map of the nucleotide sequence corresponds to the data of Coleman et al. (3). We note that, at the amino acid level, there is a 55.7% similarity over 200 residues between the Hly protein and a sphingomyelinase of *Bacillus cereus*. (4).

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                    50                                100
AGCTATATAAAGGAGTGAATAATGATGGTGA AAAAACA AAATCCAATTCAC TAAAAAAGTTGCAACACTTGCATTAGCAAAATTTATTAGTTGGTGCACCTACTGACAATAGTGC
--S D--          MetValLysLysThrLysSerAsnSerLeuLysLysValAlaThrLeuAlaLeuAlaAsnLeuLeuValGlyAlaLeuThrAspAsnSerAla

                    150                                200
AAAGCCGAATCAAGAANGATGACTGATTTGAAGTTAGTTAGTCATAACGTTTATATGTTATCGACCGTTTTGTATCCCAACTGGGGGCAATAAAGCCGCTGATTTAATCGGCACA
LysAlaGluSerLysLysAspAspThrAspLeuLysLeuValSerHisAsnValTyrMetLeuSerThrValLeuTyrProAsnTrpGlyGlnTyrLysArgAlaAspLeuIleGlyGln

                    250                                300                                350
TCTCTTATATAAAAAATGATGTCGTAATATCAATGAAGCATTGATAATGGTGCATCAGACAAATTTAAGTAAATGTGAAAAAAGAAATATCCTTATCAACACCTGTACTCGGC
SerSerTyrIleLysAsnAsnAspValValIlePheAsnGluAlaPheAspAsnGlyAlaSerAspLysLeuLeuSerAsnValLysLysGluTyrProTyrGlnThrProValLeuGly

                    400                                450
CGTTCTCACTCAGGCTGGGCAAAACTGAAGGTAGCTACTCATCACTGTTGCAGAAGATGGTGGCTAGCGATTGTAAGTAAATATCCTTATAAAGAAAAATCCAGCATGTTTCAAA
ArgSerGlnSerGlyTrpAspLysThrGluGlySerTyrSerSerThrValAlaGluAspGlyGlyValAlaIleValSerLysTyrProIleLysGluLysIleGlnHisValPheLys

                    500                                550                                600
AGCGGTTGTGGATTCCGATAATGATAGCAACAAGGCTTTGTTATACAAAAATAGAGAAAAATGGTAAGAAGCTTCAGTTATCGGTACACATACACAATCTGAAGATTCACGTTGTGGT
SerGlyCysGlyPheAspAsnAspSerAsnLysGlyPheValTyrThrLysIleGluLysAsnGlyLysAsnValHisValIleGlyThrHisThrGlnSerGluAspSerArgCysGly

                    650                                700
GCTGGACATGATCGAAAAATTAGAGCTGAACAAATGAAGAAATCACTGACTTTGTTAAAAAGAAAAATATCCCTAAAGATGAAACGGTATATATAGGTGGCGACCTTAATGTCAATAAA
AlaGlyHisAspArgLysIleArgAlaGluGlnMetLysGluIleSerAspPheValLysLysLysAsnIleProLysAspGluThrValTyrIleGlyGlyAspLeuAsnValAsnLys

                    750                                800
GGCCTCCAGAGTTC AAGATATGCTTAAAACTTGAATGTAATGATGTTCTATATGCAGGTGATAATAGCACATGGGACCTCAATCAAAATCAATTCGAAAATAATAATACCTAAT
GlyThrProGluPheLysAspMetLeuLysAsnLeuAsnValAsnAspValLeuTyrAlaGlyHisAsnSerThrTrpAspProGlnSerAsnSerIleAlaLysTyrAsnTyrProAsn

                    850                                900                                950
GGTAAACAGAACATTTAGACTATATATTACAGATAAAGATCATAAACAACCAAAACAATTAGTCAATGAAGTTGTGACTGAAAAACCTAAGCCATGGGATGTATATCGGTTCCCATAT
GlyLysProGluHisLeuAspTyrIlePheThrAspLysAspHisLysGlnProLysGlnLeuValAsnGluValValThrGluLysProLysProTrpAspValTyrAlaPheProTyr

                    1000
TACTACGTTTACAATGATTTTTTCAGATCAATACCCAACTCAAAGCCTATAGTAAATAGTGCTCACTAACAATAACTTTCCTGCTTCTTAAAAAGGACGAAGCGAGTTATATTG
TyrTyrValTyrAsnAspPheSerAspHisTyrProIleLysAlaTyrSerLys...

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