

Nucleotide sequence of the Fbp gene from *Neisseria meningitidis*

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The gene that encodes the major iron regulated protein (Fbp) of *Neisseria gonorrhoeae* has been cloned and sequenced (1). Results of N-terminal amino acid sequence analysis (2) and reactivity with monoclonal and polyclonal antibodies (3) suggested that a similar protein was present in the other pathogenic species of *Neisseria*, *Neisseria meningitidis*. Sequence analysis of the Fbp gene has confirmed this homology. We have cloned the Fbp gene of *N. meningitidis* (strain 80084313, serogroup A) on two genomic *TaqI* fragments in pUC 13 using probes from the *N. Gonorrhoeae* Fbp gene. Sequence data from the *N. meningitidis* Fbp gene was compared to that of *N. gonorrhoeae* (strain F62) from the start of the leader peptide through 141 bases of the 3' untranslated region. Eight differences were observed; however, only two of them resulted in an amino acid change (amino acid 136, val to ala; amino acid 146, ile to

val). Figure 1 shows the meningococcal Fbp sequence with the bases that differed from the gonococcal Fbp sequence underlined and the corresponding gonococcal sequences below. The amino acids in parenthesis are where the two conservative amino acid substitutions occurred. The arrows indicate a possible transcription termination signal and the asterisk denotes the first amino acid of the mature protein.

REFERENCES

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M K T S I R Y A L L A A A L T A A T P A L A D I T V Y N G Q H
ATGAAAACATCTATCGGATACGCACTGCTTGCCGACGGCTGACCGCGCAACCCCGCGCTGGCAGACATTACCGGTACAACGGCCAACAC 27
      C
K E A A Q A V A D A F T R A T G I K V K L N S A K G D Q L A G
AAAGAAGCAGCACAAAGCCGTTGCAGATGCCTTTACCCGGGCTACCGGCATCAAAGTCAAACAGTGCCAAAGGGCAGCAGCTTCCCGGT 120
      G
Q I K E E G S R S P A D V F Y S E Q I P A L A T L S A A N L L
CAAATCAAAGAAGAAGGCAGCCGAAGCCCGCGCAGTATTCTATTCCGAACAAATCCCGCACTCGCCACCCTTCCGCGCAACCTCCTA 213
      C
E P L P A S T I N E T R G K G V P V A A K K D W V A L S G R S
GAGCCCTGCCCGCTCCACCATCAACGAAACACGCGCAAAGCGTGCCGGTTGCCGCCAAAAAGACTGGGTGGCACTGAGCGGACGTTTCG 306
      C
R V V V Y D T R K L S E K D L E K S V L N Y A T P K W K N R I
CGCGTCGTCGTTTACGACACCCGCAAACTGTCTGAAAAAGATTTGGAAAAATCCGTCCTGAATTACGCCACGCCGAAATGGAAAAACCCGCATC 399
      C
G Y (A) P T S G A F L E Q (V) V A I V K L K G E A A A L K W L K G
GGTTACGCCGCCACTTCCGGCCGCTTCTTGAACAGGTTGTCCGCATCGTCAAACACTGAAAGGCGAAGCGGCCGATTGAAATGGCTCAAAGCA 492
      T
L K E Y G K P Y A K N S V A L Q A V E N G E I D A A L I N N Y
CTGAAAGAATACGGCAAGCCTTACGCTAAAAACTCCGTCGCCCTTCAAGCGGTTGAAACGGCGAAATCGATGCCGCCCTCATCAACAACCTAC 585
      C
Y W H A F A R E K G V Q N V H T R L N F V R H R D P G A L V T
TACTGGCAGCCTTTCGCGCGTGAAAAAGGCGTACAAAATGTCCACACCCGCTGAATTCGTCGCCACAGAGATCCCGCGCACTCGTTTACC 678
      C
Y S G A V L K S S Q N K D E A K K F V A F L A G K E G Q R A L
TATTCGGCGCAGTGTAAAAATCCTCCAAAAACAAGGATGAGGGCAAAAAATTCGTCGCCCTTCTCGCCGCAAGGAAGCAGCGCCGCTG 771
      C
T A V R A E Y P L N P H V V S T F N L E P I A K L E A P Q V S
ACCGCCGTCCGTCGCAATATCCTTTGAATCCGCACGTGGTATCCACTTTCATTTGGAACCCATCGCCAAGTTGGAAGCACCCCAAGTGTCC 864
      C
A T T V S E K E H A T R L L E Q A G M K
GCCACCCTGTTTCGAAAAAGAACACGCCACCCGGCTGCTTGAGCAAGCCGGTATGAAATAAGCCGTTTTTCGGATTGTCAAACGGGTGGACA
      C
TTTATACGTCCGCCGTTTTGCGGATGAAAAACACTATGTCTCCTAAAAAATACCCATTGGCTTACCGGCTCATCTACTGATCGCCCT
GCCGCTTACCCTGCCT

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