

Nucleotide sequence of the fim3 gene from *Bordetella pertussis* and homology to fim2 and fimX gene products

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The gene encoding the serotype 3 pilin subunit (fim3) of *Bordetella pertussis* (1) strain SA1, was isolated by screening a cosmid (pHC79) library with synthetic oligonucleotides. These were designed on the basis of the published amino acid sequence of serotype 2 pilin subunit (2). The nucleotide sequence of a 609 bp long pilin structural gene, reported in Fig. 1, was identified as fim3 by comparison with the fim3 NH_2-terminal peptide sequence (3). Fig. 2 shows the homology among the deduced amino acid sequences of serotype 2, 3 and×(4) pilin subunits, which amounts to 60.7%, 57.7% and 60.3% between fim3 and fim2, fim3 and fimX and fim2 and fimX, respectively. (Bars indicate the identical residues between fim3 and fim2 or fimX proteins, while dots show the ones in common only between fim2 and fimX. Occasional gaps were introduced to allow maximal alignment.)

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Fig. 1

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ATGTCCAAGTTTTTCATACCCTGCCTTGCGCGCGCGCGTTATCCTTGCCGCCTCGCCCGTACTGCCAGCGCTGGCCAACGACGGCACCATCGTCATCACCG   100
GCAGCATCTCCGACCAGACCTGCGTCATCGAAGAGCCCAGCACCCTCAACCATATCAAGGTCGTGCAACTGCCCAAGATTTCCAAGAACGCGCTCAGGAA   200
CGACGGCGACACCGCCGGCGCCACGCCCTTCGACATCAAGCTGAAGGAATGCCCCCTGGGCGCGCTCAAGCTGTATTTCGAGCCCGGCATCACCACCAAC   300
TACGACACGGGCGATCTGATTGCCTACAAGCAGACCTACAACGCATCCGGCAACGGCAACCTGAGCACCGTGTCGTCCGCCACCAAGGCCAAGGGCGTGG   400
AGTTCCGCCTGGCCAACCTCAACGGCCAGCACATCCGCATGGGCACGGACAAAACCACGCAAGCCGCGCAAACCTTTACCGGCAAGGTCACCAATGGCAG   500
CAAGAGCTACACCCTGCGCTATCTCGCCTCGTACGTGAAGAAACCCAAGGAAGATGTCGACGCGGCCCAGATCACCAGCTACGTCGGCTTTTCCGTCGTC   600
TACCCCTGA                                                                                                  609
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Fig. 2

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fim2  DDGTIVITGTITDTTCVIEDPSGPNHTKVVQLPKISKNALKANGDQAGRTPFIIKLKDCPSSLGNGVKAYFEPGPTTDYSTGDLRAYKMVYATN   94
fim3  NDGTIVITGSISDQTCVIEEPSTLNHIKVVQLPKISKNALRNDGDTAGATPFDIKLKECPLG...ALKLYFEPGITTNYDTGDLIAYKQTYNAS
fimX  EDGTIVITGTITDQTCTIEDPS.PGYIKVVHLPTISKSALKNAGDVAGRTRFDIKLKDCP.TTVNTLKLYFEPGPTTDYGTKDLKAYKQAWYVD

      PQTQLSNITAATEAQGVQVRISNLNDSKITMGANEATQQAAGFDPEVQTGGTSRTVTMRYLASYVKK.NGDVEASAITTYVGFSVVYP*          182
      GNGNLSTVSSATKAKGVEFRLANLNGQHIRMGTDKTTQAAQTFTGKVTNG..SKSYTLRYLASYVKKPKEDVDAAQITSYVGFSVVYP*
      AATLLKSPPSVTEAKGVQIRLMNLNGKQIPMGETEPNQHAAAFSGTMQAGQGQKSFTLHYLAGYVKKASGEVEATMLTTYVGFSVVYP*
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