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Nucleotide sequence of the pilin gene from *Bacteroides nodosus* strain 238 (Serogroup G)

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Among the field isolates of *Bacteroides nodosus*, the causative agent of ovine footrot, eight serogroups designated A to H have been distinguished (1). Comparison of the coding sequence of pilin from *B. nodosus* 238, a representative of serogroup G, with pilins of other serogroups shows that serogroups fall into two quite distinct subsets, A,B,C,E,F and G in one set, and D and H in the other. Pilins within each subset show greater than 60% identity, while between subsets no greater similarity is present than between *B. nodosus* pilins and the homologous pilins of *Moraxella bovis*, *Neisseria gonorrhoeae* and *Pseudomonas aeruginosa* (<40%). Nucleotide sequences immediately downstream of the coding region, available for serogroups A,G,D and H, also indicate a close relationship between members of the same subset, while showing little, if any, relationship between members of the different subsets. These data and the demonstrated compatibility of pilin expression between bateria of different families (2) suggest that DNA transfer between species be considered as a possible source of subset diversity.

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ATCCGCGCAC GGTAAAAAGC CGCGGATTTC CGTTTGTCCT TCTGCTAACG CTGCTAATAA TAAGGCGCGA TGCGACATTG ATTTATCGCC GCATATCGTT

ATTTCGCCGG AAAGCGCAGA GACGGGCGCG GTGTGCCATA TATTCATCAT TATTCCTTTT TGTGAAACGG GCGTTATTGT GCCGGAAAAA TGGGAGAAAA

AATGCAAAAA AAGCGCGCGC ACCAGAAAAA TAATTTTTTA AACAATTGTT TTTAAATATA AAAATAATGT TGGCATTGAT GACGCATAAT GAAAGGCGTC

AGGCAACTGA CTCTAAACAA GATGATATTT AAATGTTCAC ATTCTTAATA GGAGAATATG ATG AAA AGT TTA CAA AAA GGT TTC ACC TTA ATC
                                                                  Met Lys Ser Leu Gln Lys Gly Phe Thr Leu Ile

GAA CTC ATG ATT GTG GTT GCA ATT ATC GGT ATC TTA GCT GCT TTC GCT ATC CCT GCA TAC AAC GAC TAC ATC GCT CGT ACC
Glu Leu Met Ile Val Val Ala Ile Ile Gly Ile Leu Ala Ala Phe Ala Ile Pro Ala Tyr Asn Asp Tyr Ile Ala Arg Thr

CAG GTT TCA GAA GGC GTT AGC TTG GCT GAT GGT TTA AAA ATC CGT ATC GCT GAC AAC TTA CAA GAT GGT AAA TGT ACC TCT
Gln Val Ser Glu Gly Val Ser Leu Ala Asp Gly Leu Lys Ile Arg Ile Ala Asp Asn Leu Gln Asp Gly Lys Cys Thr Ser

GAA GGA GAT CCT GCA TCT GGC GAA GTA GGT AAC ACA GAT ATG GGT AAG TAC GCT CTT GCT ACA ATT GAA GGA ACC CCT GAT
Glu Gly Asp Pro Ala Ser Gly Glu Val Gly Asn Thr Asp Met Gly Lys Tyr Ala Leu Ala Thr Ile Glu Gly Thr Pro Asp

GCC AAC CTT GCA GGA CTT ACC CCT AAG GAT CCA AAT GGT TGT AAA GTT AAG ATT GAA TAT GGT AAG GGA ACT GCT GGA GAT
Ala Asn Leu Ala Gly Leu Thr Pro Lys Asp Pro Asn Gly Cys Lys Val Lys Ile Glu Tyr Gly Lys Gly Thr Ala Gly Asp

AAC ATT TCT CCT TTA ATT AAG GGT CAA ATG TTG GTG CTT AAC CAA TTA GTT AAC GGC AGT TAT GAC AAA GAT TCA TCT TCT
Asn Ile Ser Pro Leu Ile Lys Gly Gln Met Leu Val Leu Asn Gln Leu Val Asn Gly Ser Tyr Asp Lys Asp Ser Ser Ser

ACC GTG AAA CCT AAA TTC CTT CCT AAA GCA TTG AAA GAA GCT ACT CCA TAGTAGTTGC GTATATAGCT TACTTAAAAG CCTCTCTCTT
Thr Val Lys Pro Lys Phe Leu Pro Lys Ala Leu Lys Glu Ala Thr Pro

GAGAGGCTTT TTTTATGGTT TATTGTGTTT CTATCATTTA AACAAAAGAA AATTAACTCA TAATCATCTA CTCTATATCT TGTCTAAGTA GGAGTATA
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Legend. Sequence of the pilin gene from *B. nodosus* 238. A potential promoter consensus sequence and transcription termination signal are underlined.

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