

Nucleotide sequence involving *murG* and *murC* in the *mra* gene cluster region of *Escherichia coli*

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The *mra* (*mu*rein synthesis cluster *a*) region at 2 min on the *Escherichia coli* chromosome map carries the genes for peptidoglycan synthesis (1, 2): genes *murC, murD, murE, murF* and *ddl*, coding for five enzymes synthesizing UDP-N-acetylmuramyl-pentapeptide (*L*-alanyl-*D*-glutamyl-meso-diaminopimelyl-*D*-alanyl-*D*-alanine) from UDP-N-acetylmuramic acid by sequential addition of appropriate amino acids. The genes *pbpB* and *ftsW* (3) that code for septum-peptidoglycan synthetic proteins, *murG* (4) which produces a protein of unknown function and an open reading frame ORF-Y (5) were also located in the *mra* region. In the present study, we determined the base sequences of the *murG* and *murC* genes located between *ftsW* and *ddl* and thus completed the sequencing of the total 12 kb *mra* region which is flanked by a 5 kb region involving *ftsQ, ftsA, ftsZ* and *envA*. An open reading frame of 1065 bp capable of encoding a moderately hydrophobic peptide with 355 amino acid residues (Mw 37,814) was found for *murG*, and one of 1473 bp encoding a peptide with 491 amino acid residues (Mw 53,625) was found for *murC*. The proteins MurG and MurC were detected on SDS/PAGE in an *in vitro* protein synthesis system. Overlapping of the open reading frames of the *murG-murC* area and its flanking genes *ftsW* and *ddl* was observed. Considerable homologies were found in the deduced amino acid sequences of the product proteins of *murC, D, E* and *F*, i.e., four ligases that synthesize UDP-N-acetylmuramyl-pentapeptide, including putative ATP-binding domains GXXGKT/S (126–131 of MurC). MurG showed considerable homology with the corresponding region of the *Bacillus subtilis* chromosome.

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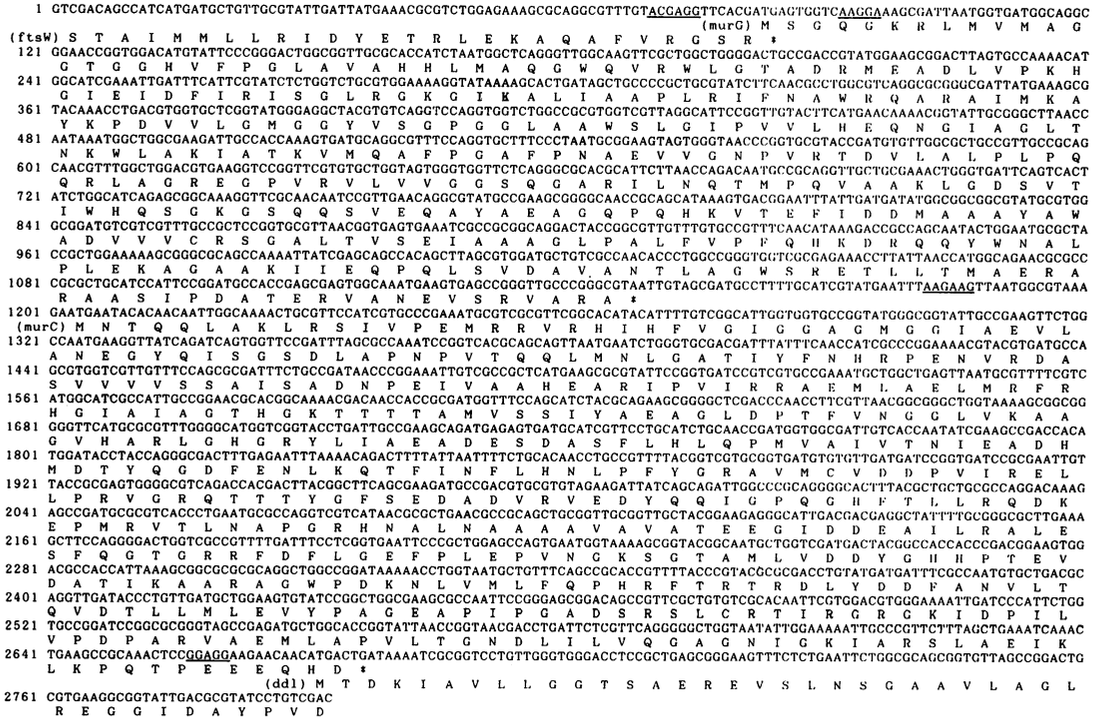

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