

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

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The *mra* (*murein* 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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1  GTCGACAGCCATCATGATGCTGTTGCGTATTGATTATAAAACGCGTCTGGAGAAAGCGCAGGCGTTTGTACGAGGTTCCAGCATGAGTGGTCAAGGAAGCGGATTAATGGTGTGGCAGGC
    (murG) M S G Q G K R L M V M A G
121  GGAACCGGTGGACATGTTCCCGGACTGCGCGTTCGCCACCATCTAATGGCTCAGGGTTGGCAAGTTCGCTGGCTGGGACTCGCCAGCCGTATGGAACCGGACTAGTCCCAAACAT
    G T G G H V F P G L A V A H H L M A Q G W Q V R W L G T A D R M E A D L V P K H
241  GGCATGCAAAATGATTTTCATTCGCTGCGTGGTGGAAAGGTATAAAAGCACTGATAGCTGCCCGCTGCGTATCTTCAACGCGCTGGCGTAAGCGCGGGCGGATATGAAAGCG
    G I E I D F I R I S G L R G K I K A L I A A P L R I F N A W R Q A A R A I M K A
361  TACAACCTGACGGTGGCTGCGTATGGAGGCTACCGTGCAGGTCGCGTGGCGCGTGGCTAGGCGATTCGGTTCATGATGAACAAAAGGATTTGGCGGCTTAACC
    Y K P D V V L C M G G Y V S G P G D L A A W S L G T P V V L H E Q N G I A G L T
481  AATAAATGGCTGGCAAGATGCCACCAAGTGAAGCGCTTCCAGTGGCTTCCCTAATCGGGAAGTAGTGGTAACCGCTGCTACCGATGTTGGTDLA L P L E Q
    N K W L K I A T K V M Q A F P G A F P N A E V V G N P V R T D V L A I P L E Q
601  CAACGTTTGGCTGGACGTGAAGTCCGGTTCGTGCTGGTGTAGTGGGTGCTTCAGGCGCGCAGCCATCTTAACAGACAATGCCGAGCTTGGTGGCAATGGTGTTCAGT
    Q R L A G R E G P V R V L V G G S Q G A R I L N Q T M P Q V A A K L G D S V T
721  ATCTGGCATCAGAGCGCAAGGTTCCGCAACAATCCGTTGAACAGCGGATGCGGAAAGCGGGCAACCGCAGCATAAAGTGACCGAATTTATTGATGATAGCGCGCGGCTATGCGTGG
    I W H Q S G K G S Q Q S V G Q A Y A E A G Q P H K V T E F I D D M A A A Y A W
841  GCGGATGTCGCTGTTGCGCTGCGGTAAACGGTGAAGTGAAGTGCAGCGCGCAGGACTACCGCGCTTTCTGTGCGCTTCAACATAAAGACCGCCAGCAATACTGGAATCCGCTA
    A D V V C R S G A L T V S E I A A A G L P A L F V P F Q H K D R Q Y V W N A L
961  CCGCTGGAAAAGCGGCGCAGCCAAAATATCGAGCAGCCAGCTTAGCGTGGATGCTGCGCAACACCGTCCGCGGGTGGTGGCAGAAACCTTATTAACTGGCAGAACCGCC
    P L E K A G A A K I I E Q P Q L S V D A V A N T L A G W S R E T L L T M A E R A
1081  CGCGCTGCATCCATTCGGATGCCACCGAGCGAGTGGCAAATGAAAGTGAAGCGGCTTCCCGGCGCTATGAGCGATGCCCTTTCATCGTATGAATTTAAGAAATTAATGGCTGAA
    R A A S I P D A T E R V A N E V S R V A R A †
1201  GAATGAATACACAACAATGGCAAACTGCGTTCATCGTCCCGCAATGGTGGCGTTCGGCACATACATTTTGTCCGCAATGGTGGTGGCGGTATGGCCGATTTGCCAAAGTTCGG
    (murC) M N T Q Q L A K L R S I V P E M R R V R H I H F V G I G G A G M G G I A E V L
1321  CCAATGAAGGTTATCAGATCAGTGGTCCGATTTAGCGCAAAATCCGCTCAGCAGCAGTAAATGAACTCGGCTGCGAGATTTATTTCAACCATCGCCGGAACAGTACGTGATGCCA
    A N E G Y Q I S G S D L A P N P V T Q Q L M N L G A T I Y F N H R P E N V R D A
1441  GCGTGGCTGTTGTTCCAGCGCGATTTCTGCGGATAACCCGGAATTTGCGCGCTCATGAAGCGGCTATTCGGTGAATCCGTCGTCGCGCAATGCTGGTGAATTAATGGCTTTCGTC
    S V V V S S A I S A D N P E I V A A H E A R I P V I R R A E M L A E L M R F R
1561  ATGGCATCCCATTTGGCGAACCCGCAACGCAACGACACACCGCGATGGTTCAGCATCTACGCAAGAGCGGGCTCGACCCCACTTGGTAAACCGGGTGGTAAAGCGGGCGG
    H G I A I A G T H G K T T T T A H V S I Y A E A G L D P T F V N U G L V K A A
1681  GGGTTCATCGCGCTTTGGGCAATGGTGGTACCTGATGGCCAGCAGATGAGAATGATCGTTCCTGCTGCAACCGATGGCGATTTCCACCAATGCAACCGCCAGCACA
    G V H A R L G H G R Y L I A E A D E S D A S F L H L Q P M V A I V T N G I E A D H
1801  TGATACCTACGAGGCGCTTTGAGAATTTAAACAGACTTTTATTATTTCTGACAACTCGCGTTCAGTAAAGATATCAGCAGATGGCCCGCAGGGCACTTACGCTGCTGCCGAGCAAA
    M D T Y Q D F E N L K Q T F I N F L H N L P F Y G R A V M C V D V D P C C E L
1921  TACCAGGCTGGGCGCTCAGACCCAGCTTACGGCTTCAGCGAAGTCCGCGTGTAGAAAGATATCAGCAGATGGCCCGCAGGGCACTTACGCTGCTGCCGAGCAAA
    L P R V G R Q T T T Y G F S E D A D V R V E D Y Q I G P Q G H F T I L R Q D K
2041  AGCCGATCGGCTCAGCTGATGCGGCAAGTGGTATAACCGCTGAAACCGCGGAGCTGCGGTTCGCGTTCGCTACGGAAGAGGGCATTCACGACAGGGCTATTTGCCGCGCTTGA
    E P H R V T L N A F G R H N A R N A A A A V A V A T E E G I D D E A I L R A L E
2161  GCTTCAGGGAGTGGTGGCGTTCGCTGCGTAAATCCCGCTGGAGCCAGTAAATGGTAAAGCGGTCAGCGAATGGCTGATGCTAGCGCCACCCAGCGGAAATGG
    S F Q G T G R R F D F L G E F P L E V V G K S G T A M L V D D V G H H P T E V
2281  ACCGCCAATTAAGCGCGCGCGGCTGGCGGATAAAACCTGGTAACTGCTGTTACAGCCGCGCTTTACCGTACCGCGGAGCTGATGATGATTTCCCAATGGCTGACCG
    D A T I K A A R A G W P D K N L V M L F Q P H R F T R T R D L Y D D F A N V L T
2401  AGTTGATCCCTGATGCTGGAAGTATTCGGCTGGCGAAGCGCCAAATCCCGGAGCGGCAACCGCTTCGCTGTCGCGCAATTCGTGGAGCTGGGAAAATTCATCCATTCGG
    Q V D T L M L E V Y P A G E A P I P G A D S R S L C R T I R G R C K I D P I L
2521  TGGCGGATCCCGCGGGTACCGAGATGCTGGCAGGATTAACCGGTAACGACCTGATCTGTTACAGGGGCTGGTAAATTTGGAAAAATTCGCCATTCCTGAAATCAAC
    P P H R V A E M L A P V L T G N D I L V Q G A G N I T G K I A R S L A E I K
2641  TGAACCGCAACTCCGAGGAGAACCACTGACTGATAAAATCCGGCTCTGTTGGTGGGACCTCCGCTGAGCGGGAAGTTCTCTGAAATTCGGCAGCGGCTGTTAGCCGCTG
    L K P Q T P E E Q H D †
    (ddl) M T D K I A V L L G G T S A E R E V S L N S G A A V L A G L
2761  CGTGAAGCGGCTTACGCGCTATCTGTCGAC
    R E G G I D A Y P V D
    
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