Analysis of the Capsule Biosynthetic Locus of *Mannheimia* (Pasteurella) *haemolytica* A1 and Proposal of a Nomenclature System

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A 16-kbp DNA region that contains genes involved in the biosynthesis of the capsule of *Mannheimia* (Pasteurella) *haemolytica* A1 has been characterized. The gene cluster can be divided into three regions like those of the typical group II capsule biosynthetic clusters in gram-negative bacteria. Region 1 contains four genes (wzt, wzm, wzf, and wza) which code for an ATP-binding cassette transport apparatus for the secretion of the capsule materials across the membranes. The *M. haemolytica* A1 wzt and wzm genes were able to complement *Escherichia coli* kpsT and kpsM mutants, respectively. Further, the ATP binding activity of Wzt was demonstrated by its affinity for ATP-agarose, and the lipoprotein nature of Wza was supported by [3H]palmitate labeling. Region 2 contains six genes; four genes (orf1/2/3/4) code for unique functions for which no homologues have been identified to date. The remaining two genes (nmaA and nmaB) code for homologues of UDP-N-acetylglucosamine-2-epimerase and UDP-N-acetylmannosamine dehydrogenase, respectively. These two proteins are highly homologous to the *E. coli* WecB and WecC proteins (formerly known as RffE and RffD), which are involved in the biosynthesis of enterobacterial common antigen (ECA). Complementation of an *E. coli* rffE/D mutant with the *M. haemolytica* A1 nmaA/B genes resulted in the restoration of ECA biosynthesis. Region 3 contains two genes (wbrA and wbrB) which are suggested to be involved in the phospholipid modification of capsular materials.

*Mannheimia* (Pasteurella) *haemolytica* A1 is the principal microorganism responsible for bovine pneumonic pasteurellosis, a major cause of sickness and economic loss to the feedlot industry (15, 46). Some of its characterized virulence factors include leukotoxin, a sialoglycoprotease, neuraminidase, and transferrin-binding proteins (9). In addition, the bacterium produces an extracellular capsular polysaccharide (CPS) which has been implicated to play a role in pathogenesis. The role of CPS in the virulence of a number of gram-negative pathogens has been well documented. Some of these activities include adherence (11), prevention of desiccation (30), and resistance to host immune defense (29).

For *M. haemolytica* A1, the activities of CPS in virulence and protection have not been well defined. It has been reported that CPS is important in the adherence of the bacterium to alveolar surfaces (6, 45) and inhibition of complement-mediated serum killing (7) as well as inhibition of the phagocytic and bactericidal activities of neutrophils (12, 43). Preliminary studies by Yates et al. (47) using crude CPS preparations of *M. haemolytica* A1 suggested that the capsule conferred some protection against experimental pasteurellosis; however, it was unclear which molecule(s) in the preparation was responsible for this protection. On the contrary, Conlon and Shewen (10) showed that purified *M. haemolytica* A1 CPS did not elicit protection against experimental challenge. It has been suggested by Gatewood et al. (19) that the antigenic nature of the CPS could be influenced by the culture conditions and that only CPS produced during growth in the host could stimulate a protective immune response.

The CPS of *M. haemolytica* A1 is composed of a disaccharide repeat of N-acetylmannosaminuronic acid (ManNAcA) β1,4 linked with N-acetylmannosamine (ManNAc) (2). ManNAcA is one of the sugar moieties in enterobacterial common antigen (ECA) (26). Other than this, little is known about the biosynthesis of CPS. As a first step in understanding the biosynthesis of the CPS and elucidating its role in pathogenesis and in immune protection, we report here the isolation and characterization of the genetic locus that contains the capsule biosynthetic genes of *M. haemolytica* A1.

**Proposal of nomenclature scheme.** There are numerous reports in the literature that identified and named the various genes and proteins involved in CPS biosynthesis. For example, the genes that code for the ATP-binding transporter that have been named are *kps* in *Escherichia coli* (38), *hex* in *Haemophilus influenzae* (22), *ctr* in *Neisseria meningitidis* (17), *cpx* in *Actinobacillus pleuropneumoniae* (44), and *hex* in *Pasteurella multocida* (8), to name a few. These cognate genes and proteins have been shown in most cases to be functionally interchangeable by complementation studies. These various gene designations create confusion in the literature, especially when researchers are examining homologous functions or the construction of hybrid genes and proteins. As more genetic loci involved in CPS biosynthesis are characterized, additional nomenclature will be introduced. During a consultation, P. Reeves suggested a uniform nomenclature for the genes in the CPS cluster that follows the scheme that has been established for the genes in bacterial polysaccharide biosynthesis (34). Using the *M. haemolytica* A1 CPS biosynthetic cluster as an example, it is proposed that the four genes in region 1 that

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code for the ATP-binding transporter be designated \textit{wza}, \textit{wzf}, \textit{wzm}, and \textit{wzt} in the order of their genetic organization, that the two genes in region 2 that code for homologues of the ManNAcA pathway be designated \textit{nmaA} and \textit{nmaB}, and that the two genes in region 3 that code for functions in phospholipid modification be designated \textit{wbrA} and \textit{wbrB}. The remaining four genes in region 2 with uncharacterized functions are designated \textit{orf1}, \textit{orf2}, \textit{orf3}, and \textit{orf4} until their functions are determined. When the same gene from different organisms is being referred to, a suitable subscript will be added, e.g., \textit{wza}_{M.B}. A summary of this proposed scheme, together with enzymatic functions of the encoded proteins and the names from other systems, is presented in Table 1.

### MATERIALS AND METHODS

#### Bacterial strains, plasmids, and culture conditions.

The \textit{E. coli} strain XL1-Blue (Strategene, La Jolla, Calif.) was used for the cloning of all recombinant plasmids. \textit{E. coli} strain CSR603 (41) was used for the maxi-cell labeling experiments. \textit{E. coli} RS2436 (EV36 \textit{\DeltakapT}) and RS2604 (EV36 \textit{\DeltakapM}) was recovered from R. Silver (University of Rochester, Rochester, N.Y.). \textit{E. coli} 21566 (mutant \textit{rffD} and \textit{rffE}) was obtained from D. Bitter-Suermann (University of Hannover, Hannover, Germany). Plasmid pCW-1C (44), which encodes the \textit{RI} linkers ligated to randomly sheared DNA and packaged into the \textit{E. coli} plasmid system (Stratagene). The \textit{M. haemolytica} A1 strain was isolated from George Weinstock (University of Texas, Houston, Tex.). The \textit{lambda} library was constructed by the use of EcoRI linkers ligated to randomly sheared DNA and packaged into the \textit{xZAP} vector system (Stratagene). \textit{E. coli} strains were cultured in Luria-Bertani broth supplemented with thymine (50 \mu g/ml) and with ampicillin (100 \mu g/ml) when required. \textit{M. haemolytica} A1 was cultured in brain heart infusion broth. All cultures were grown at 37°C unless stated otherwise.

#### Enzymes, chemicals, and restraints.

Restriction endonucleases, \textit{T4} DNA ligase, and protein and DNA molecular weight standards were purchased from Pharmacia Chemicals (Baie d’Urfe, Quebec, Canada), GIBCO/Bethesda Research Laboratories (Burlington, Ontario, Canada), or Bio-Rad Laboratories (Mississauga, Ontario, Canada) and used according to the manufacturer’s instructions.

#### Screening of \textit{lambda} library and characterization of cloned \textit{DNA}.

The \textit{lambda} library was plated out on \textit{E. coli} XL1-Blue cells to produce approximately 300 plates per plate. Plates were lifted from the agar plates, and the plasmid DNA was prepared for hybridization as described by the supplier. A 1.5-kbp HindIII DNA fragment from pCW-1C was isolated, radiolabeled with [\textit{\alpha}-\textit{32P}]dATP (ICN Pharmaceuticals), and used to hybridize against the \textit{M. haemolytica} A1 strain. The appropriate fragment was recovered from the plasmid according to the manufacturer’s instructions (Stratagene). Plasmid DNA was isolated from \textit{E. coli} cells using Qiagen columns (Chatsworth, Calif.). Standard techniques were used for restriction analysis, subcloning, ligation, and recovery of \textit{DNA} fragments (40).

Overlapping clones were isolated from the \textit{lambda} library by chromosome walking using internal fragments from the recombinant plasmid as probes. Briefly, an appropriate fragment was recovered from the plasmid after digestion and recovery from a low-melting-temperature agarose gel. The DNA was extracted from the gel by Gene-Clean (Bio101, La Jolla, Calif.), labeled with [\textit{\alpha}-\textit{32P}]dATP (ICN Pharmaceuticals), and used to hybridize against the \textit{lambda} library as described above. Plasmids from positively hybridizing plaques were recovered and mapped, and those that contained DNA beyond the previously cloned regions were chosen for further studies.

Alternatively, overlapping \textit{DNA} was identified by restriction mapping of the genomic \textit{DNA} by Southern hybridization using an appropriate fragment from the cloned \textit{DNA}. Briefly, the \textit{DNA} fragment was labeled with digoxigenin and hybridized against total genomic DNA digests according to the protocol from the supplier (Boehringer Mannheim). A suitable \textit{DNA} fragment was recovered from an agarose gel and cloned into \textit{plasmid pHBlueScript SKII+} (Stratagene). DNA from recombinant plasmids was sequenced to identify overlapping \textit{DNA} and into newly cloned regions.

The nucleotide sequence of the cloned \textit{DNA} was determined by the dideoxy sequencing method according to our laboratory procedure (24) by using a combination of manual and automated sequencing approaches. Automated sequencing was performed at the Laboratory Services Division at the University of Guelph by using a 377 Prism automated sequencer (Applied Biosystems, Foster City, Calif.).

#### Nucleotide sequence and homology analyses.

The nucleotide sequences were analyzed using the software programs Gene Runner (Hastings Software, New York, N.Y.) and PC/Genome (IntelliGenetics, Mountain View, Calif.). Nucleotide and amino acid sequence homology comparisons were carried out with GenBank DNA and protein sequence databases using the National Center for Biotechnology Information BLAST network server (3). The sequences were also examined using the \textit{db-BLAST} analysis (9).

#### Plasmid labeling of plasmid-encoded \textit{proteins}.

The proteins expressed from recombinant plasmids were radiolabeled in an \textit{E. coli} maxi-cell system according to our laboratory procedure (1, 41). Briefly, \textit{E. coli} CSR603/pPHCPX2.2 (or pPHCPX10.1) cells were subcultured from a saturated culture into fresh Davis minimal medium supplemented with 0.5% Casamino Acids and ampicillin. After 2 h of growth, 10 ml of the culture was irradiated with an UV lamp at 400 mW/cm² on a petri plate. After growth for another 2 h, 100 \mu l of D-cycloserine (2 mg/ml) and with the culture was grown overnight. A 3-ml aliquot was centrifuged and washed, and the cells were resuspended in 0.5 ml of Davis minimal medium supplemented with threonine and proline at 100 \mu g/ml and arginine and leucine at 150 \mu g/ml. The cell suspension was grown for 1 h at 37°C, after which 25 \mu g of \textit{Trans}\textsuperscript{35S}-label (ICN Pharmaceuticals) or 50 \mu Ci of \textit{[\textit{35S}]H}palmitate (New England Nuclear, Guelph, Ontario, Canada) was added. After labeling for 2 h, the cells were recovered and washed once with the supplemented Davis medium. The \textit{[\textit{35S}]H}palmitate-labeled sample was washed twice with methanol, air dried, and resuspended in 100 \mu l of 2% sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) sample buffer. A 20- to 30-\mu l aliquot was analyzed by SDS-PAGE and autoradiography. The \textit{35S}-labeled sample was used for the ATP-agaro binding experiment (see below).

#### Functional analysis of open reading frames (ORFs).

(i) Complementation of \textit{E. coli} \textit{kpsT} or \textit{kpsM}.

\textit{E. coli} strains RS2436\textit{\DeltakapT} and RS2604\textit{\DeltakapM}, which were defective in the biosynthesis of the K1 CPS, were complemented with pPHCPX2.2. Briefly, the \textit{E. coli} strains were transformed with pPHCPX2.2 or the pHBlueScript vector and selected by ampicillin resistance. \textit{E. coli} RS2604 cells were grown at 25°C to avoid selecting for secondary mutations. The transformants were examined for phage sensitivity to the K1 capsule specific phages E.

### TABLE 1. Proposed nomenclature for genes in the CPS biosynthetic cluster

<table>
<thead>
<tr>
<th>\textit{M. haemolytica} gene \textit{H. influenzae}</th>
<th>\textit{N. meningitidis}</th>
<th>\textit{A. pleuropneumoniae}</th>
<th>\textit{E. coli}</th>
<th>\textit{P. multocida}</th>
<th>Properties of the proteins</th>
</tr>
</thead>
<tbody>
<tr>
<td>\textit{wza}</td>
<td>\textit{hexD}</td>
<td>\textit{ctrA}</td>
<td>\textit{cpxD}</td>
<td>\textit{kpSE}</td>
<td>\textit{hexD}</td>
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<td>\textit{hexC}</td>
<td>\textit{ctrB}</td>
<td>\textit{cpxC}</td>
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<td>\textit{cpxB}</td>
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<td>\textit{hexA}</td>
<td>\textit{ctrD}</td>
<td>\textit{cpxD}</td>
<td>\textit{rffE} \textit{wecB}</td>
<td>\textit{rffD} \textit{wecC}</td>
</tr>
<tr>
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<td>\textit{nmaB} \textit{rffD} \textit{weC} \textit{ctrD} \textit{cpxA} \textit{kpsT} \textit{hexA}</td>
<td></td>
<td></td>
<td></td>
<td>ManNAc synthesis</td>
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<tr>
<td>\textit{wbrA}</td>
<td>\textit{lipA}</td>
<td></td>
<td></td>
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* Only those genes whose products have characterised activities were assigned nomenclature. A blank space indicates that no similar genes or homologues were present.
The nucleotide sequence reported in this paper has been deposited in GenBank under the accession no. AF170495.

RESULTS

Isolation and characterization of pPHCPX2.2. Using the 1.5-kbp HindIII fragment from the A. pleuropneumoniae cpx cluster as a probe, positively hybridizing plaques were isolated from the λ library and rescreened, and the plasmid was excised for further analysis. A plasmid designated pPHCPX2.2 (Fig. 1) that was recovered from one of the clones was shown to contain approximately 6 kbp of insert DNA that hybridized to the probe. Nucleotide sequence analysis showed that this DNA contains ORFs that are highly homologous to the ATP-binding cassette 2 subfamily transporters (20, 35). These transporters are involved in polysaccharide export across the inner and outer membranes in a number of gram-negative bacteria (see below).

Isolation of overlapping clones containing the remaining capsule biosynthetic cluster. Using the approach of chromosome walking, three additional λ clones were isolated, each containing insert DNA overlapping to the right of the cloned DNA in pPHCPX2.2 (Fig. 1). A fifth plasmid clone (pPHPHYB) that contains DNA further to the right of the cluster was also isolated by direct cloning of the DNA flanking pPHCAP701. Together, these five clones contained a total of 16 kbp of DNA that was analyzed.

It was immediately apparent from the analysis of the sequence data and assignment of ORFs that the M. haemolytica A1 CPS cluster has the same genetic organization as other well-characterized group II capsule biosynthetic clusters (5, 21, 37). The cluster was divided into three regions, and the proteins encoded in each region are examined in the following sections. The DNA that flanked the CPS cluster does not contain information that is involved directly in the biosynthesis of the capsule. However, they may code for regulatory functions, as in the case of the N. meningitidis CPS cluster.

Analysis of proteins in region I. Examination of the nucleotide sequence in region 1 identified four ORFs in tandem on the same DNA strand. These ORFs were designated wza, wzf, wzm, and wzt (Fig. 1) by following the proposal presented here (Table 1). Each of the encoded polypeptides showed high amino acid homology with the cognate Cpx proteins in A. pleuropneumoniae (44), the Bex proteins of H. influenzae (22), the Ctr proteins of N. meningitidis (17), and the Kps proteins of E. coli K5 (38). The E. coli K5 CPS cluster does not contain a Wza homologue, but a Wza homologue from E. coli 09a:K30 was included for comparison (13). Additional homology was also observed with ATP transport proteins from other bacterial systems, but for simplicity, only the A. pleuropneumoniae Cpx,
the H. influenzae Bex, the N. meningitidis Ctr, and the E. coli K5 proteins were included in this comparison (Table 2).

**Analysis of proteins in region 2.** Six ORFs were identified in region 2. Of the six, four showed no significant homology with sequences in the data banks by BLAST or psi-BLAST searches. The remaining two ORFs showed significant homologies to the E. coli wecB and wecC genes and were named nmaA and nmaB, respectively. The E. coli wecB and wecC genes (formerly named rffE and rffD, respectively) are involved in the biosynthesis of ECA (28). wecB codes for UDP-\textsuperscript{-}\textit{N}-acetylglucosamine-2-epimerase, which catalyzes the conversion of UDP-\textsuperscript{-}\textit{N}-acetylglucosamine (UDP-GlcNAc) to UDP-ManNAc. wecC codes for UDP-ManNAc dehydrogenase, which oxidizes UDP-ManNAc to UDP-ManNAcA. ManNAcA is one of the three sugars in ECA, whereas both ManNAc and ManNAcA are components of the M. haemolytica A1 CPS. A homology comparison of the corresponding proteins is shown in Table 2.

**Analysis of the proteins in region 3.** Two ORFs were identified in region 3. The first ORF is homologous to kpsC, lipA, and phyA of the E. coli K5 (38), N. meningitidis (18), and P. multocida (8) CPS clusters, respectively, and was designated wbrA. The next ORF is homologous to kpsS, lipB, and phyB from the same CPS clusters and was designated wbrB. In N. meningitidis, the two proteins LipA and LipB have been shown to be responsible for substitution of phospholipids on the CPS at the reducing ends of the polysaccharide chains (18). This lipid modification is necessary for the translocation of the CPS to the cell surface and the anchoring of CPS to the outer membrane (18). Therefore, it is likely that the two homologous M. haemolytica A1 proteins perform the same functions during CPS biosynthesis.

**Functional analysis of M. haemolytica A1 Wz* proteins.** To demonstrate the function of the Wz* transport proteins, the plasmid pPHCPX2.2 was transformed into E. coli kpsM or kpsT mutants which are defective in the synthesis of the K1 capsule. In E. coli K1, KpsM and KpsT have been hypothesized to form an inner membrane complex for the transport of CPS (31, 33). Based on the homology comparison, we predicted that Wzm is a functional homologue of KpsM and that Wzt is a functional homologue of KpsT. After transformation of the E. coli mutants, the colonies were examined for phage sensitivity to phages E and K1F. The results showed that the E. coli mutants were complemented by pPHCPX2.2 and phage sensitivity was restored. Even though the complementation studies were not carried out with subclones which carry only wzm or wzt separately, the extensive similarities between the proteins as well as similar complementation data from other systems are consistent with the interpretation that the M. haemolytica Wzm and Wzt proteins are functional homologues to E. coli KpsM and KpsT, respectively. Minimally, these data showed that the M. haemolytica A1 transporter is capable of translocating the E. coli K1 capsular materials across the membranes.

The analysis of Wzt showed that it contains the typical ATP-binding domains (42) which are also present in the homologous BexA, CtrD, and KpsT proteins. The results in Fig. 2 demonstrate the function of Wzt in translocating CPS to the cell surface.
expected for Wzt expressed from the plasmid pPHCPX2.2. This binding assay demonstrated that the Wzt protein exhibits ATP binding activity as predicted.

The analysis of Wza suggested that it is a lipoprotein homologous to BexD and CtrA. Wza contains the typical lipoprotein leader as well as the signal peptidase II cleavage site. To demonstrate that Wza is a lipoprotein, plasmid-encoded proteins expressed from pPHCPX2.2 were labeled with \( ^{3}H \)palmitic acid in the \( E. coli \) maxi-cell system. The results in Fig. 3 show that a 43-kDa protein corresponding to the predicted molecular mass of Wza was labeled with \( ^{3}H \)palmitic acid, supporting the prediction that Wza is a lipoprotein.

**Complementation of ECA biosynthesis.** Based on the above analysis, region 2 of the \( M. haemolytica \) A1 CPS cluster contains two genes which are involved in the biosynthesis of UDP-ManNAc and UDP-ManNAcA. To demonstrate the activities of these two gene products, they were tested for functional complementation of the \( E. coli \) wecB/C genes. When the plasmid pNMA was transformed into \( E. coli \) 21566 (mutant wecB and wecC), it was observed that ECA biosynthesis was restored (Fig. 4). This showed the activities of the \( M. haemolytica \) A1 nmaA and nmaB genes and demonstrated that the biosynthesis of the amino sugars for incorporation into CPS in \( M. haemolytica \) A1 utilized a pathway similar to that of the production of UDP-ManNAc and UDP-ManNAcA from UDP-GlcNAc in ECA biosynthesis.

**DISCUSSION**

The results here show that the genetic organization of the \( M. haemolytica \) A1 CPS biosynthetic cluster is the same as that reported for group II capsules. This is consistent with the hypothesis regarding the evolution of the CPS biosynthetic clusters in gram-negative bacteria (16, 39). The moles percent of G+C of the DNA in regions 1, 2, and 3 are 36.2, 35.7, and 36.8, respectively, which are very similar to the overall 39 mol% G+C of \( M. haemolytica \) A1 DNA (23). This indicates that these DNAs were probably not recently acquired by the bacterium. However, on closer analysis, the four uncharacterized ORFs in region 2 have a moles percent G+C of only 33.3. Since no significant homologies with these sequences were detected in the data banks, this region may be entirely unique to \( M. haemolytica \) A1 and might have been acquired elsewhere from an unidentified source.
of the cognate genes in *A. pleuropneumoniae* (44). This similar organization with related CPS clusters is consistent with analysis that suggests that one promoter upstream of *wza* regulates the expression of the *wez* genes in region 1. There is an alternative possibility that a second promoter may be present upstream of *wza*; experiments are in progress to address this issue. Separate promoters (in opposite orientations) between *nmaA* and *wbcA* could be involved in the regulation of expression of the genes in regions 2 and 3. The complementation of ECA biosynthesis using the insert DNA in pNMA suggested that a promoter located upstream of *nmaA* is responsible for its expression. In *E. coli* K5, three promoters have been identified for the expression of the genes in region 2 (37), whereas a separate promoter is responsible for the expression of *kpsT* and *kpsM* in region 3 (31). For *P. multocida*, it has been suggested that one promoter is responsible for the expression of the genes in regions 1 and 2 together, whereas a different promoter regulates the genes in region 3 (8). Transcriptional analysis will be performed on the *M. haemolytica* A1 CPS cluster to examine the expression of these genes and regulatory mechanisms involved in CPS biosynthesis.

The complementation of the *E. coli* K1 *kpsT* and *kpsM* mutants with *M. haemolytica* A1 *wzt* and *wzm* showed that the export of CPS through the inner membrane follows a similar mechanism as in the export of polysialic acid in *E. coli* K1. Analysis of the amino acid sequences showed that the KpsM and KpsT proteins from the K1 and K5 clusters are essentially identical. Further, the *cpx* genes from *A. pleuropneumoniae* have been shown to complement the *E. coli* K5 *kps* mutants (44), and we chose to complement the *E. coli* K1 mutants instead. According to the model proposed by Bliss and Silver (4), the KpsM and KpsT proteins are responsible for interaction with the polysaccharide chain to initiate the insertion of the complex into the inner membrane for export. To complete the export process, KpsE has been postulated to be involved in creating localized fusions of the inner and outer membranes and KpsD likely functions in the recruitment of a porin to facilitate export of the polysaccharide out of the cell. It would be of interest to examine the complementation of the remaining *wez* genes with the corresponding *E. coli* mutants to determine if the components in subsequent steps of export are interchangeable. Recently, it has been shown that in *E. coli* 09a:K30 cells, Wza forms ring-shaped multimeric complexes which may be involved in the translocation of CPS materials across the membranes (13).

One interesting observation from this work is the restoration of ECA biosynthesis in an *E. coli* *wecB/C* mutant by the *M. haemolytica* A1 *nmaA/B* genes. The *E. coli* mutant 21566 was generated by Tn10 mutagenesis and was originally thought to have a transposon insertion in *rffD* (*wecC*). However, it was shown by Marolda and Valvano (27) that in addition to a transposon insertion in *rffD*, 21566 also contains a small insertion in the upstream *rffE* gene, resulting in the loss of both epimerase and dehydrogenase activities. Therefore, the complementation experiment carried out with both *nma* genes showed that the two *M. haemolytica* A1 enzymes can complement both missing activities. The biosynthesis of ECA takes place at the inner membrane and involves a stepwise transfer of the amino sugars to the lipid carrier undecaprenyl monophosphate. The complementation results showed that the enzymes involved in the biosynthesis of UDP-ManNAcA from UDP-ManNac and UDP-GlcNAc in *E. coli* and *M. haemolytica* A1 cells are functional homologues. This also shows that the pathways for the synthesis of the amino sugars for incorporation into CPS or ECA are essentially the same.

The four ORFs in region 2 of the CPS showed no significant homologies with any of the sequences in the data banks. This region usually encodes functions involved in the biosynthesis of sugar moieties or glycosyl-transferase enzymes (37). Presently, there is no indication of the function(s) of these proteins and whether they are involved in capsule biosynthesis. Further characterization by mutagenesis experiments may help to elucidate their activities.

With the present data in hand, experiments are being done to examine the role of CPS in pathogenesis. DNA flanking the CPS cluster is being characterized to determine if any regulatory functions are encoded there, as in the CPS locus of *N. meningitidis*. In addition, using the gene replacement procedure described by Federova and Highlander (14), an acapsular mutant in which the *nmaA* and *nmaB* genes have been knocked out has been created (unpublished results). The properties of this acapsular mutant are being examined.

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