Research Article

Structural and immunological characterization of *E. coli* derived recombinant CRM$_{197}$ protein used as carrier in conjugate vaccines

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It is established that the immunogenicity of polysaccharides is enhanced by coupling them to carrier proteins. Cross reacting material (CRM$_{197}$), a nontoxic variant of diphtheria toxin (DT) is widely used carrier protein for polysaccharide conjugate vaccines. Conventionally, CRM$_{197}$ is isolated by fermentation of *Corynebacterium diphtheriae* C7 (β$_{197}$) cultures, which often suffers from low yield. Recently, several recombinant approaches have been reported with robust processes and higher yields, which will improve the affordability of CRM$_{197}$-based vaccines. Vaccine manufacturers require detailed analytical information to ensure that the CRM$_{197}$ meets quality standards and regulatory requirements. In the present manuscript we have described detailed structural characteristics of *Escherichia coli* based recombinant CRM$_{197}$ (rCRM$_{197}$) carrier protein. The crystal structure of the *E. coli* based rCRM$_{197}$ was found to be identical with the reported crystal structure of the C7 CRM$_{197}$ produced in *C. diphtheriae* C7 strain (Protein Data Bank (PDB) ID: 4EA0). The crystal structure of rCRM$_{197}$ was determined at 2.3 Å resolution and structure was submitted to the PDB with accession number ID 5I82. This is the first report of a crystal structure of *E. coli* derived recombinant CRM$_{197}$ carrier protein. Furthermore, the rCRM$_{197}$ was conjugated to Vi polysaccharide to generate Typhoid conjugate vaccine (Vi-rCRM$_{197}$) and its immunogenicity was evaluated in Balb/C Mice. The Vi-rCRM$_{197}$ conjugate vaccine was found to generate strong primary α-Vi antibody response and also showed a booster response after subsequent vaccination in mice. Overall data suggest that *E. coli* based recombinant CRM$_{197}$ exhibits structural and immunological similarity with the C7 CRM$_{197}$ and can be used as a carrier protein in conjugate vaccine development.

Introduction

Over the past three decades, many routine childhood and adult vaccines have been developed using conjugation technology. Conjugate vaccines are developed by covalent attachment of an antigenic polysaccharide to a nontoxic carrier protein. Conjugation to a nontoxic carrier protein enhances the immunogenicity of polysaccharide antigens, enabling host defence against diseases caused by encapsulated pathogens. Conjugation transforms the T cell-independent response of polysaccharide vaccines to a T cell-dependent one. Conjugate vaccines have been demonstrated to be immunogenic and capable of inducing immunological memory and high avidity antibodies. Unlike unconjugated polysaccharides, conjugate vaccines also elicit protective responses in the immature immune system of young infants and the senescent immune system of the elderly [1-3].
Cross reacting material (CRM197) is widely used as a carrier protein in conjugate vaccines [3]. CRM197 protein is a nontoxic variant of diphtheria toxin (DT, molecular weight: ~58 kDa) with a single mutation (Glycine to Glutamate substitution at position 52) that eliminates its toxicity [4,5]. The protein nonetheless retains the same immunostimulant properties as DT and it is used to generate safe and effective polysaccharides conjugate vaccines for all age groups [6,7].

CRM197-based polysaccharides conjugate vaccines have already been developed to confer protection against important bacterial pathogens such as Streptococcus pneumoniae (Prevnar), Haemophilus influenzae type b (HibTITER, Vaxem-Hib) and Neisseria meningitidis serogroup A, C, Y and W-135 (e.g. Menofo and Menjugate). These vaccines have been successfully used to immunized hundreds of millions of people worldwide. Several conjugate polysaccharides vaccines using CRM197 as carrier protein are under preclinical and clinical evaluation. These include vaccines against Staphylococcus aureus, Streptococcus agalactiae (Group B Streptococcus), Salmonella Typhi, Salmonella Paratyphi, Mycobacterium tuberculosis and several pneumococcal conjugate vaccines [3,8-14].

CRM197 is synthesized as a single chain holoprotein, which comprises two domains fragment A (catalytic domain) and fragment B (transmembrane domain), bound together by a disulfide bridge. The B domain contains a subdomain for binding to the HB-EGF cell receptor and another subdomain for translocation into eukaryotic cells. In vitro, mild trypsin treatment and reduction divdes the toxin into two functional moieties (the 'nicked form'). The receptor-binding subdomain of fragment B has an all-β-sheet structure, in contrast with the transmembrane subdomain containing nine α-helices. Two disulfide bridges are present in the intact holoprotein: one bridge joins Cys158 to Cys201, linking fragment A to fragment B while a second bridge joins Cys461 to Cys471 within fragment B [15].

Since CRM197 is genetically nontoxic, chemical toxoiding is not required. This helps to preserve epitopes which would otherwise be lost. It has been suggested that preservation of T-helper epitopes explains the improved carrier effect of CRM197 compared with diphtheria toxoid [13]. The lack of toxicity in CRM197 has been examined in vivo and in vitro using lethality tests in guinea pigs, cytotoxic activity assays on HeLa cells and Vero cells and an ADP-ribosyltransferase enzymatic assay [16].

CRM197 is classically purified from culture supernatant of the Corynebacterium diphtheriae C7 (β197) tox negative (Tox−) strain [4]. The production of CRM197 from its C7 strain often suffers from low yield and also requires sophisticated laboratory conditions to cultivate the C. diphtheriae C7 strain. More recently, CRM197 has been produced in heterologous recombinant systems such as Escherichia coli and Pseudomonas fluorescens [17-19] with higher yield. The characterization of CRM197 protein produced from C. diphtheriae C7 strain has been published [15,16]. However, limited data are available for CRM197 produced from E. coli based recombinant source. Also, there is lack of information whether E. coli based recombinant CRM197 is structurally and immunologically equivalent to its incipient counterpart (C7 CRM197). In the present study, for the first time we have performed structural and immunological characterization of E. coli derived recombinant CRM197 protein. The data are particularly important because the increasing global demand of polysaccharide conjugate vaccines against encapsulated bacterial pathogens highlight the pressing need for high yield processes delivering well-characterized carrier protein that meets regulatory and safety requirements. The objective of present study was to: (i) express the rCRM197 protein from E. coli and its physicochemical characterization, (ii) determination of X-ray crystal structure of recombinant CRM197 and demonstration of its structural equivalence with C7 CRM197, (iii) development of polysaccharide conjugate vaccine using rCRM197 and demonstration of immunological functionality of rCRM197 as carrier protein.

Materials and methods
Cloning, expression and purification of CRM197
The codon optimized sequence corresponding to CRM197 gene was synthesized and cloned into pTWIN 1 vector (New England Biolabs, U.K.) using BamH1 and Sap1 restriction sites [18]. The pTWIN1_CRM197 plasmid was transformed into chemically competent BL21-DE3 E. coli expression host. Transformants were screened on LB agar plates supplemented with ampicillin (100 μg/ml). Five to ten randomly selected colonies were purified by repeated subculturing on LB + ampicillin (100 μg/ml) plate. Finally, a few colonies were selected and a research cell bank was generated. For the expression analysis of rCRM197 protein, clones were grown in 100-ml LB + Ampicillin (100 μg/ml) till mid log phase (OD₆₀₀ ~1). At this stage, culture was induced with 1 mM IPTG and was further grown to reach late log phase (OD₆₀₀ ~4–5). One millilitre culture from each transformant was centrifuged and pellet was resuspended into 100-μl SDS loading buffer and heated at 80°C for 10 min. Twenty microlitres of lysate was loaded on 8–12% Tri-Glycine gel and SDS/PAGE was run using 80 V constant current for ~2 h. Gel was stained with Coomassie Blue (make: Amresco, Cat No: 0472-25 G). The expression of rCRM197 was confirmed by comparing a band appearing at
Further, Western blot was performed using anti-CRM$_{197}$ antibody (Make: Santa Cruz Biotechnology, Cat No: SC2054). One of the clones expressing rCRM$_{197}$ protein has been used for fermentation and large-scale production of protein.

Fermentation inoculum was generated by inoculating one vial of research cell bank into seed flask containing 200-ml LB + ampicillin (100 µg/ml). Seed flask (containing growth media and inoculum) was grown to achieve OD$_{600}$ ~4 and inoculated into 20-l fermentation medium. Fermentation was performed in chemically defined medium. After fermentation was complete, cell mass was separated by centrifugation. The cell pellet was lysed by Micro fluidizer high pressure homogenization. Homogenized cell mass was centrifuged and pellet containing inclusion body protein was retained and used for rCRM$_{197}$ purification. The inclusion body was solubilized in buffer containing 6 M urea at 30°C and rCRM$_{197}$ was purified by refolding followed by ion exchange chromatography [18]. The solubilized inclusion body protein was refolded and purified by ion exchange chromatography method described by Stefan et al. [19].

C7 CRM$_{197}$ used as a reference in the studies was procured as a lyophilized powder from Sigma–Aldrich (Cat# D2189).

**Endonuclease assay for rCRM$_{197}$**

The assay was performed as described by Stefan et al. (2011) [19] with minor modifications. In brief, 2 µg rCRM$_{197}$ was mixed with 1 µg pUC57 plasmid DNA using endonuclease reaction buffer (10 mM Tris/HCl pH 7.6, 2.5 mM CaCl$_2$, 2.5 mM MgCl$_2$). Content was mixed by brief centrifugation (3000 g, 30 s) and incubated for different time points (0, 0.5, 1, 3, 5 and 18 h) at 25°C. The 0-h time point sample was used as a control. At each time point, reaction was terminated by the addition of 5 mM EDTA (final concentration) to each tube and frozen at −20°C. Thawed samples were mixed with DNA loading buffer and run on 1% agarose gel electrophoresis in 1× TAE buffer using 80 V constant voltage. DNA staining dye SYBR Safe gel stain (Invitrogen, Cat# S33102) was added to the agarose gel at the time of pouring. After the electrophoresis run was completed, the gel was analysed under UV transillumination (Bio-Rad ChemiDoc Gel imaging System).

**SDS/PAGE and Western immunoblot analysis**

Reducing and nonreducing SDS/PAGE and Western blot analyses were performed with purified rCRM$_{197}$ as per the standard protocol [20]. Four micrograms of purified rCRM$_{197}$ along with the reference CRM$_{197}$ was loaded on to 4–12% Tris-Glycine gels under reducing and nonreducing conditions. Gels were run at 80 V constant voltage until blue dye reached the bottom of the gel. SDS/PAGE molecular weight markers (New England Biolabs, Cat# P7712S) were used for molecular weight calibration. After Coomassie Brilliant Blue staining, the image was captured using transilluminator (Bio-Rad ChemiDoc system). For Western immunoblotting, 2 µg protein was separated by SDS/PAGE and transferred to nitrocellulose membrane (0.45 µm, Bio-Rad, Cat# 1620115). The blot was probed with α-CRM$_{197}$ rabbit polyclonal primary antibody (Abcam, Cat# ab151222) by incubating the membrane for 1 h. After the primary incubation, the membrane was further incubated in HRP-conjugated secondary antibody (rabbit) (make: Santa Cruz Biotechnology, Cat No: SC2054). Bands were visualized using 3,3′-diaminobenzidine (DAB) substrate and the image captured using Bio-Rad ChemiDoc gel imaging system.

**Intact MS**

The intact mass of rCRM$_{197}$ was determined by LC-MS (ABSCIEX Triple TOF 5600+) using the published protocol [21,22]. Protein samples were buffer exchanged by centrifugal ultrafiltration (Amicon Ultra-0.5 ml, 10 K MWCO, 14000 g, 15 min, 4°C) and analysed by LC-qToF using the manufacturer’s protocol.

**Amino acid composition analysis**

rCRM$_{197}$ was subjected to high sensitivity amino acid analysis (AAA). The analysis was performed on samples desalted by ultrafiltration (Vivaspin 6 spin columns with a 10-kDa polyethersulfone filter: Sartorius, Cat# VS0601). Samples were resuspended in 20% acetonitrile (ACN) containing 0.1% trifluoroacetic acid (TFA) and subjected to gas phase hydrolysis (6 N HCl at 110°C). α-amino butyric acid (AABA) was run as an internal standard prior to sample analysis. Cysteine analysis was performed after performic acid oxidation followed by hydrolysis as above. Hydrolysates were analysed using a Waters Acquity UPLC system with AccQTag Ultra chemistry. Samples were analysed in duplicate and the mean reported [23,24].
Western immunoblotting with structural monoclonal antibodies against CRM$_{197}$/DT

rCRM$_{197}$ samples along with reference were run in SDS/PAGE. The gel was transferred to nitrocellulose membrane and Western immunoblotting was done using five different monoclonal antibodies (mAbs) against DT/CRM$_{197}$. These mAbs were 7F2 (Abcam, Cat. No: ab8310), 8A4 (Abcam, Cat. No: ab8308), 3B6 (Abcam, Cat. No: ab8307), 1H2 (Abcam, Cat. No: ab8306) and HYB 123-09 (Statens Serum Institute, Cat. No: 66045). The SDS/PAGE and Western blot methods were as described above.

Determination of crystal structure of rCRM$_{197}$ by X-ray crystallography

Center for the Structural Genomics of Infectious Diseases (CSGID) standard protocols were used to determine the structure of CRM$_{197}$ [25-27].

Sitting drop crystallization plates were set up at room temperature and crystals of rCRM$_{197}$ were obtained by mixing 22.9 mg/ml of protein in 0.15 M sodium chloride, 0.01 M Tris/HCl buffer (pH 8.3) with the crystal screen solution of 0.2 M lithium sulfate, 0.1 M Bis-Tris buffer (pH 5.5), 25% (w/v) PEG 3350 (Qiagen, Classics II suite (G2), in a 1:1 ratio. Harvested crystals were transferred to the reservoir solution before being flash-frozen in liquid nitrogen. Diffraction data were collected at 100 K at the Life Sciences Collaborative Access Team at the Advance Photon Source, Argonne, Illinois (APS BEAMLINE 21-ID-F). Data were processed using HKL-3000 for indexing, integration and scaling. The crystal structure of recombinant CRM$_{197}$ (Protein Data Bank (PDB) ID: 5182) was determined by molecular replacement using PDB entry 4AE0 as a search model. The structure was refined with Refmac 5 [28]. Models were displayed in Coot and manually corrected based on electron density maps [29]. All structure figures were prepared using PyMOL Molecular Graphics System, version 1.3 (Schrödinger, LLC). The structure was submitted to the PDB (PDB_ID: 5182).

Generation of typhoid conjugate vaccine (Vi-rCRM$_{197}$) using rCRM$_{197}$ and immunogenicity assessment

rCRM$_{197}$ was conjugated with Vi polysaccharide antigen to generate Vi-rCRM$_{197}$ conjugate vaccine (typhoid conjugate vaccine). The Vi polysaccharide was produced by fermentation of Citrobacter freundii as per method described by Rondini et al. [30]. The C. freundii strain was provided by Dr Laura B. Martin, GSK Vaccine Institute of Global Health, Siena, Italy. The Vi-CRM$_{197}$ conjugate was prepared according to the method reported by Kossaczka et al. [31] and as detailed by Micoli et al. [8]. Briefly, rCRM$_{197}$ was derivatized with adipic acid dihydrazine (ADH). Then, Vi (purified from C. freundii) was activated with N-hydroxy succinimide and 1-ethyl-3(3-dimethylaminopropyl) carbodiimide hydrochloride and linked to the derivatized rCRM$_{197}$ protein generating Vi-rCRM$_{197}$ conjugate vaccine. The ADH derivatized rCRM$_{197}$ (rCRM$_{197}$-ADH) was mixed with activated Vi polysaccharides in 1:1 ratio and incubated at room temperature for 5–6 h. The resulting conjugate was purified by HIC (hydrophobic interaction chromatography) using phenyl sepharose (GE) resin.

The immunogenicity of Vi-rCRM$_{197}$ was performed as per procedures described by Rondini et al. [30]. Four to six weeks old female Balb/C mice were used in the experiment. A group of 30 mice were subcutaneously immunized with three doses of Vi-rCRM$_{197}$, unconjugated Vi polysaccharide and PBS (placebo control). A 100μl dose of Vi-rCRM$_{197}$ conjugate vaccine containing 2.5 μg Vi, unconjugated Vi polysaccharide (2.5 μg) and PBS (control) were administrated in mice on day 1 followed by booster dose at days 14 and 21. Fourteen days after first immunization, ten randomly selected mice from each group were terminally bled to collect the post-dose 1 sera. Remaining animals (20 each) were given the second dose of vaccine. Seven days after second immunization (day 21), ten mice from each group were terminally bled and post-dose 2 sera was collected. Finally, remaining ten mice were given the third dose of vaccine. The final sera (post-dose 3) was collected at day 28 by bleeding of remaining mice from each group. Mouse sera was subjected to ELISA analysis and anti-Vi IgG response was measured as per the procedure described by Micoli et al. [8].

Results

Determination of molecular weight and identity of E. coli derived rCRM$_{197}$

rCRM$_{197}$ appears as a ~58 kDa band in SDS/PAGE and Western blot analyses performed under both nonreducing and reducing conditions. This is consistent with the reported molecular weight of CRM$_{197}$ of 58.4 kDa [16]. Gels run under nonreducing conditions help to evaluate possible covalent and noncovalent aggregation in the samples and to detect impurities. rCRM$_{197}$ contains two disulfide bonds, one linking chains A and B and a second within the
Intact mass determination by MS

MS is a powerful analytical tool as it measures an intrinsic property of a molecule, its mass, with very high sensitivity and therefore it is used in a wide range of applications [22]. The intact mass of rCRM\textsubscript{197} was obtained by deconvolution of mass/charge (m/z) ratio. Data obtained by TOF-MS showed most abundant mass of 58413 Da compared with a theoretical calculated mass of 58421 Da based on amino acid sequence (Figure 2). This result confirms the molecular weight of the purified rCRM\textsubscript{197} protein i.e. \( \sim \)58.4 kDa. Similar data have also been reported both for a recombinant CRM\textsubscript{197} produced in \textit{Pseudomonas fluorescens} and C7 CRM\textsubscript{197} [21,32].
The major abundant peak of 58.4 kDa has been observed which is similar to the expected/theoretical molecular weight of CRM$_{197}$ protein.

**Endonuclease activity**

Mild endonuclease activity is an inherent property of CRM$_{197}$ and its parent molecule DT [4] and is considered as an indicator of the correctly folded bioactive form of the protein. Incubation of CRM$_{197}$ with supercoiled plasmid DNA in the presence of divalent cations (e.g. Ca$^{++}$ and Mg$^{++}$) results in DNA cleavage [19,33]. Incubation of pUC57 plasmid DNA with rCRM$_{197}$ in a 2:1 ratio for different times and analysis of the DNA by agarose gel electrophoresis confirmed the positive nuclease activity in the protein. During incubation, rCRM$_{197}$ was able to linearize the supercoiled DNA. No endonuclease activity was seen in the 0-h time point sample but it increased with the incubation time (Figure 3). This endonuclease assay can be used as an in-process control assay for CRM$_{197}$ protein produced from insoluble inclusion bodies. Similarly, earlier reports in which endonuclease activity was used to establish the purity and correctness of refolding of rCRM$_{197}$ produced in *E. coli* is also reported [19]. Previous reports also showed that both DT and CRM$_{197}$ should have fragment A-associated nuclease activity [33].

**Determination of amino acid composition**

Acid hydrolysis followed by high-sensitivity AAA has been performed with rCRM$_{197}$ and compared with reference CRM$_{197}$. After acid hydrolysis, amino acid mixture was analysed by ultra performance liquid chromatography (UPLC) using the Waters AccQTag Ultra chemistry. All samples were analysed in duplicate and results expressed as an average. The amino acid composition of rCRM$_{197}$ closely matches (within 1–2% variability range) with reference and with the theoretical values of CRM$_{197}$ protein (Figure 4). AAA can be used to confirm the primary amino acid composition of protein. The overall data suggest that rCRM$_{197}$ produced in *E. coli* has similar amino acid composition as CRM$_{197}$ produced by *C. diphtheriae C7* strain (reference CRM$_{197}$) [15].

**Immunoblotting with α-CRM$_{197}$ mAbs**

Three independent lots of rCRM$_{197}$ were run in SDS/PAGE and were probed with five different mAbs with specificity to different epitopes on the protein in Western immunoblotting experiments. All these mAbs recognized the protein at similar level and showed a major immune-reactive band at ~58 kDa, the expected size of the protein (Figure 5). The reference CRM$_{197}$ was recognized at similar level as rCRM$_{197}$. However, a slight difference in the recognition pattern was observed with respect to different mAbs, which suggests differential affinity of different mAbs for recognition of CRM$_{197}$. mAb mapping of CRM$_{197}$ has been found useful to assess potential nicking of A and B chains that could be seen in Western blot. A similar study was performed with different mAbs raised against CRM$_{197}$ for their ability to bind DT and six functional mutants CRM$_{197}$, CRM$_{176}$, CRM$_{228}$, CRM$_{1001}$, CRM$_{45}$ and CRM$_{30}$ by immunoblotting.
Figure 3. Demonstration of functional activity in rCRM$_{197}$ samples purified from inclusion body

pUC57 plasmid was incubated with rCRM$_{197}$ for different time points and the mix was run on 1% agarose gel. Native CRM$_{197}$ possesses a mild endonuclease activity and this assay is used to prove the restoration of biological activity and conformation integrity of the protein purified from insoluble inclusion body. The purified rCRM$_{197}$ exhibits the endonuclease activity as evident by nicking of supercoiled plasmid DNA incubated with the protein (Lanes 2–7).

Figure 4. High-sensitivity AAA profile of rCRM$_{197}$ and CRM$_{197}$

Both the proteins showed similar elution profile during AAA chromatogram of high-sensitivity AAA of CRM$_{197}$. (A) AAA chromatogram of BioE rCRM$_{197}$ and (B) AAA chromatogram of reference CRM$_{197}$. Both the proteins showed similar elution profile. The peak data were extrapolated and plotted in bar diagram (C). Blue bar: theoretical number of amino acid residues, Red bar: experimental amino acid residues of rCRM$_{197}$ and Green bar: experimental amino acid residues of reference CRM$_{197}$.

The results showed a difference in the recognition pattern of mAbs specific to different part of the protein. Our data are of particular importance because protein is purified from insoluble inclusion body after refolding. There is potential chance of misfolding and or improper folding that might impact the conformation of the protein. Hence, the
data also confirm that rCRM197 has attained the correct conformational structure after purification from insoluble inclusion bodies [35].

**Determination of crystal structure of E. coli rCRM197 by X-ray crystallography**

The crystal structure of *E. coli* derived recombinant CRM197 was determined at 2.3 Å resolution and the structure was submitted to the PDB with the PDB ID: 5I82. Previous studies have elucidated the structural features of DT in different conditions, such as in the apo conformation, at acidic pH, in complex with NAD, with dinucleotide inhibitor adenyl 3′–5′ uridine 3′-monophosphate and with an extracellular fragment of its receptor [36–39]. More recently, the structures of C7 CRM197 in the apo form and in complex with the NAD hydrolysis product nicotinamide have been determined [16]. This showed that the single amino acid substitution of G52E that is the difference between CRM197 and DT, results in an intrinsic flexibility of the active-site loop [16]. All these studies were performed on DT and CRM197 produced by *C. diphtheriae*. However, there is very limited information available on CRM197 protein produced from the recombinant *E. coli*. To verify if the rCRM197 produced from insoluble inclusion body protein have the overall similar 3D structure of the protein, we determined the X-ray crystal structure of rCRM197. Furthermore, the crystal structure of rCRM197 confirms the presence of structural determinants that ablated the toxicity of DT and resulted in CRM197 (G52E mutation).

The structure was determined at 2.3 Å resolution by molecular replacement using a search model, the coordinates of the apo form of C7 CRM197 (PDB entry 4EA0). Data collection, refinement and the final model validation statistics for the structure of rCRM197 (PDB ID: 5I82) have been given in Table 1. The asymmetric unit contains four molecules of rCRM197 (chains A, B, C and D). The four chains interact as dimers (chains A–B and chains C–D) by domain swapping, with each monomer in ‘open’ conformation, a typical packing that has already been described for both DT and CRM197 (Figure 6) [16]. The overall fold of each chain is similar to C7 CRM197 (PDB: 4AE0). In fact, by superimposing the single chains or the two homodimers (chains A–B and C–D), the RMSD results were less than 0.17 Å (A and B, 428 out of 507 Ca, RMSD of 0.17 Å; A and C, 424 out of 508 Co, RMSD of 0.17 Å; A and D, 426
Table 1 Refinement statistics of CRM_{197} (PDB ID: 5I82)

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PDB ID 5I82

Figure 6. Crystal structure of monomeric form of *E. coli* derived rCRM_{197} protein (PDB ID: 5I82)

(A) Superimposition of the monomer of rCRM_{197} and C7 CRM_{197}. (B) Chain A (cartoon colored as ruby) and chain B (transparent, dark grey ribbon) of rCRM_{197} are superimposed on the monomer of wild-type CRM_{197} (PDB code: 4AE0, cartoon colored as yellow) and its symmetry-related molecule (transparent, yellow ribbon). (C) Catalytic domains consisting of residues 1–187, (T) Transmembrane domain consisting of residues 201–384, (R) Receptor domain consisting of residues 387–535. The dimers show the swapping of the T domains in the open conformation.

out of 504 Cα, RMSD of 0.10 Å; AB and CD, 839 out of 1011 Cα, RMSD of 0.17 Å) [40], demonstrating that these are very similar.

The dimers in the crystal structure of rCRM_{197} and C7-CRM_{197}, are equivalent. By superimposing the A and B chains of rCRM_{197} on to C7-CRM_{197} and its symmetry-related molecule that forms the dimer, 924 out of 998 Cα superimposed with RMSD of 0.38 Å (Figure 6). The overall fold of the monomer rCRM_{197} is equivalent to C7-CRM_{197}, with an overall RMSD of 0.34 Å for 451 out of 498 superimposed Cα atoms (Figure 6). Since overall structure is
Figure 7. The glycine to glutamate mutation at amino acid position 52 (G52E) in rCRM_{197}.
Zoom in the active site loop CL2 where G52E mutation has taken place. The mutation creates a structural distortion in active site loop of DT thereby eliminating its toxicity (consequently CRM_{197} is formed). The image depicts the structural superimposition of the DT (PDB code: 1SGK; thin blue ribbon), C7-CRM_{197} (PDB code: 4AE0, yellow cartoon) and rCRM_{197} (PDB code: 5I82: chain A as ruby cartoon, chain B as red cartoon, chain C as light red cartoon and chain D as firebrick color cartoon). The data demonstrate that rCRM_{197} possesses G52E point mutation that converted DT into CRM_{197}. The same point mutation was also evident in C7-CRM_{197}.

Figure 8. The presence of correct disulfide bonds in \textit{E.coli} derived rCRM_{197}.
Zoom in the disulfide bond C186-C201 (A) and C461-C471 (B) in rCRM_{197} (PDB ID: 5I82). Two disulfide bonds has been identified in at the expected position of the resolved structure of rCRM_{197}.

preserved between C7 CRM_{197} and rCRM_{197}, it is unlikely that there will be any significant differences between these two molecules in terms of T epitopes that can potentially impact the efficacy of rCRM_{197}.

Furthermore, previous studies showed that the substitution G52E induces the dislocation of the active-site loop CL2 in C7-CRM_{197} with respect to DT [16]. The intrinsic flexibility of CL2 results in a localized low quality electron density map in the C7-CRM_{197} structure [38,39]. In our crystal structure of rCRM_{197}, we have also observed a low electron density in the active loop CL2, consistent with the previous results (Figure 7). This confirms the structural basis of lack of toxicity in rCRM_{197}.

Another important biochemical and structural features of DT, as well as C7 CRM_{197}, is the presence of the disulfide bond C186-C201 that maintains the A and B fragments bound together in the nicked form after the proteolytic cleavage of the chain. The structure revealed that the disulfide bond is conserved in rCRM_{197} (Figure 8).
Immunogenicity of Vi-rCRM\textsubscript{197} conjugate vaccine in mice

Immunogenicity of typhoid conjugate vaccine (Vi-rCRM\textsubscript{197}) generated using \textit{E. coli} derived rCRM\textsubscript{197} as carrier protein was evaluated in Balb/c mice. Mice were immunized with three doses of conjugate vaccine Vi-rCRM\textsubscript{197} and anti-Vi IgG immune response was measured by ELISA. Sera from mice immunized with PBS was used to generate the baseline. Vi-rCRM\textsubscript{197} immunized mice were able to elicit strong Anti-Vi IgG antibody response. Mice immunized with unconjugated Vi polysaccharide (Control) showed only basal level of Anti-Vi IgG. The Anti-Vi antibodies response also found to be bootable as seen in a steep increase in IgG titre after second dose of vaccine (Booster) (Figure 9). The Anti-Vi IgG response was in mice immunized with Vi-rCRM\textsubscript{197} conjugate vaccine was found to be \textasciitilde{}16-fold higher than the baseline response (PBS) after booster dose whereas un-conjugated Vi showed only 2 fold increase in the anti-Vi IgG over baseline. Noteworthy, the response of anti-Vi IgG in mice immunized with conjugate vaccine was 10-12 fold higher than the un-conjugated Vi.

As per the recommendation of World Health Organization-Technical Report Series (WHO-TRS) on typhoid conjugate vaccine, the conjugate vaccine should induce an immune response that is at least four-fold higher than the response induced by un-conjugated Vi, and a booster response should occur after the second dose in animals (WHO-TRS, 2013) [41]. The conjugate vaccine generated by using rCRM\textsubscript{197} as carrier protein comfortably meets the WHO immunogenicity criteria for typhoid conjugate vaccine, as it induces more than four-fold Anti-Vi IgG and also exhibits a booster response in mice. The data confirm the immunological functionality of rCRM\textsubscript{197} as carrier protein and suggests that it is able to convert T-independent response of polysaccharides in mice into T-dependent one and therefore booster antibody response is resulted. These data corroborate that rCRM\textsubscript{197} conjugation with Vi polysaccharide in mice can be resulted in immunogenic conjugates and therefore strengthening the suitability of rCRM\textsubscript{197} as a carrier protein for the development of conjugate vaccines.

To our knowledge, this is the first reported crystal structure of \textit{E. coli} derived rCRM\textsubscript{197} and first described comparison with C7-CRM\textsubscript{197}. In conclusion, rCRM\textsubscript{197} conserves the overall folding, making it structurally equivalent to C7-CRM\textsubscript{197}, which is used in many licenced conjugate vaccine such as meningitis, pneumococcal conjugate vaccine etc. [10-14].
Conclusion

The present study provides the detailed structural and immunological characteristics of CRM197 carrier protein produced by heterologous expression in E. coli. In addition to reveal the scientific insights of rCRM197, the data presented in this work are also important in the context that regulatory guidelines on conjugate vaccines that emphasizes the need for in-depth characterization of carrier protein used in the conjugate vaccines development. Successful and broadly marketed carbohydrate conjugate vaccines are based on just a few FDA-approved carrier proteins. First-generation of carrier proteins such as DT and tetanus toxin require detoxification with formaldehyde, potentially eliminating part of the lysine residues needed for glycan attachment, thereby potentially compromising the conjugation efficacy. CRM197 is one of the most widely used and highly effective carrier protein for conjugate vaccine. Licensed conjugate vaccines such as HibTITER (Haemophilus influenzae type b associated diseases), Prevnar (pneumococcal diseases), and Menevo (meningococcal diseases) are containing CRM197 as a carrier protein. Majority of currently marketed glycoconjugate vaccines contain CRM197 as a carrier protein and access to high quality material will support the development and production of new conjugate vaccines. The data presented herein demonstrate for the first time structural and immunological characterization of rCRM197 produced in E. coli.

In a recent study, the recombinant CRM197 has also been expressed in E. coli using pET28a expression vector [42]. Unlike our study, CRM197 was expressed in Histidine-tagged form (His-CRM197) which requires a histidine removal step by enterokinase treatment. This process often poses the limitation during the scale-up of production process and inconsistencies with respect to batch to batch purity/impurity profiles of protein. The protein was purified at small scale by immobilized metal affinity chromatography (IMAC) with reasonable purity [42]. However, the in-depth analytical characterization of protein was also lacking in this study. In the present study, rCRM197 expression was done in pTWIN expression vector, which releases the expressed protein from fusion tag by self-splicing with high fidelity. CRM197 protein was purified at high scale (~20 L Fermentation Scale) using ion exchange chromatography and highly pure form of protein (>95%) was recovered as the final product.

Recently, we have studied the analytical comparability of five CRM197 proteins produced in three different expression systems (E. coli, P. fluorescens and C. diphtheriae C7). A comprehensive physicochemical analysis of the CRM197 molecules demonstrate that recombinant CRM197S expressed in E. coli are overall highly similar to those expressed in the traditional system (C. diphtheriae C7) in terms of primary sequence/post-translational modifications, higher order structural integrity, apparent solubility, physical stability profile and in vitro antigenicity [43]. However, the detailed structural analysis and its in vivo antigenicity/immunological characterization was lacking. As a part of further in-depth characterization, we have determined the 3D crystal structure of E. coli derived rCRM197. The rCRM197 has shown the equivalence with C7 CRM197 in terms of overall folding pattern, domain architecture and the presence of correct disulfide bonds. The absence of toxicity in CRM197 relies on a point mutation at amino acid position 52 that replaces Glycine with Glutamate (G52E) and renders protein nontoxicity. In the present study, the genetic basis of nontoxicity of E. coli based rCRM197 was also confirmed by X-ray crystallography. These data are important for scientific communities as well as industries working on conjugate vaccine development using CRM197 as carrier protein. The in vivo functionality of E. coli expressed recombinant CRM197 carrier protein has been demonstrated by conjugating it with Vi polysaccharide antigen of Salmonella Typhi thereby generating Vi-rCRM197 conjugate vaccine. The data confirm that the use of rCRM197 as a carrier protein in conjugate vaccine will be able to elicit the primary and a booster antibody response in animals. The Anti-Vi IgG elicited by Vi-rCRM197 conjugate vaccine was more than four-fold higher than the response generated by unconjugated Vi which is one of the benchmark for a protective typhoid conjugate vaccine [41]. The comparative immunogenicity of Vi polysaccharide conjugated to other carrier protein like tetanus toxoid (TT), diphtheria toxoid (DT) and C7 CRM197 is already published [44]. The immunogenicity of Vi-rCRM197 showed the comparable result in terms of overall fold change in Anti-Vi IgG over Vi and booster impact. The overall data presented in our study will potentially catalyse the efforts for the production of CRM197 protein in the recombinant system and its use as carrier protein in the conjugate vaccine development.

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Competing interests

A.G., R.P.N.M. and to R.S.P.Y. are full-time employees of Biological E. Ltd., Hyderabad, India. The other authors declare that they have no competing interests associated with the manuscript.

Author contribution


Abbreviations

AAA, amino acid analysis; ADH, adipic acid dihydrazine; ADP, adenosine diphosphate; CRM197, cross reacting material 197; CSGID, Center for the Structural Genomics of Infectious Diseases; DT, diphtheria toxin; FDA, Food and Drug Administration; HB-EGF, heparin binding epidermal growth factor; HRP, horseradish peroxidase; LC-qTOF, liquid chromatography-quadrupole time-of-flight; mAb, monoclonal antibody; PDB, Protein Data Bank; TAE, Tris-acetate-EDTA; WHO-TRS, World Health Organization-Technical Report Series.

References
