

## **Research Article**

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# Enzyme Functionality: Zn2+-Chelating Peptide and Reaction of Zinc Enzymes

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**Citation:** Enzyme Functionality: Zn2+-Chelating Peptide and Reaction of Zinc Enzymes. Sci J Mat Sci & Eng. 2019; 1(1): 001-008.

Submitted: 16 May 2019; Approved: 22 May 2019; Published: 24 May 2019

#### Abstract

The display of peptide sequences on the surface of bacteria is a technology that offers exciting applications in biotechnology and medical research. Type 1 fimbriae are surface organelles of Escherichia coli which mediate d-mannose-sensitive binding to different host surfaces by virtue of the FimH adhesin. FimH is a component of the fimbrial organelle that can accommodate and display a diverse range of peptide sequences on the E. coli cell surface. In this study we have constructed a random peptide library in FimH. The library, consisting of ~40 million individual clones, was screened for peptide sequences that conferred on recombinant cells the ability to bind Zn2+. By serial selection, sequences that exhibited various degrees of binding affinity and specificity toward Zn2+ were enriched. None of the isolated sequences showed similarity to known Zn2+-binding proteins, indicating that completely novel Zn2+-binding peptide sequences had been isolated. By changing the protein scaffold system, we demonstrated that the Zn2+-binding seems to be uniquely mediated by the peptide insert and to be independent of the sequence of the carrier protein. These findings might be applied in the design of biomatrices for bioremediation purposes or in the development of sensors for detection of heavy metals.

### **INTRODUCTION**

The potential threat of heavy-metal and radionuclide pollution for ecosystems and public health has led to an increased focus on the development of systems for their sequestration and removal from soil, sediment, and wastewater. So far, decontamination techniques have been based mostly on traditional physiochemical methods, but in recent years interest has also centered on the application of biotechnology to efficient waste treatment. To this end, a number of biological remediation systems have been established in bacteria, algae, fungi and plants (5, 11, 17, 26).

Expression of heterologous peptides in naturally occurring surface proteins has become a powerful tool in generating microorganisms with binding affinity toward specific target molecules. This technique has been employed in the development of recombinant live vaccines, reagents for diagnostics, antibody production, screening of peptide libraries, and design of microbial biocatalysts and has recently constituted an attractive approach to development of bacterial bioadsorbents for heavy-metal removal purposes (2, 9, 10, 15).

Random peptide library expression is a highly versatile technology. Systems in which such libraries are expressed in connection with a surface protein scaffold allow the screening of a huge number of peptides ( $\sim$ 108) from which binders to a particular molecular target can be isolated by various panning techniques (6).

A well-characterized scaffold system for display of heterologous peptides is based on type 1 fimbriae. These are hair-like surface organelles present on most members of the Enterobacteriaceae. Type 1 fimbriae are found in up to 500 copies on the cell; they are heteropolymers, and each fimbria consists of about 1,000 copies of the major structural subunit, FimA. The d-mannose-specific FimH adhesin, located on the tip and perhaps also intercalated along the organelle, is also a structural component. By site-directed mutagenesis, we have previously identified permissive sites in FimH that allow the insertion and surface display of heterologous se

quences without altering the overall structure and function of FimH (14, 21). Such sites have been used for display of vaccine-relevant epitopes (14). Recently, we have successfully used the FimH protein as a molecular scaffold for the display of random peptide libraries (7, 19, 20). In this paper we report the identification of novel Zn2+-binding peptides selected from a FimH-displayed random peptide library. Our results indicate that the zinc binding can be a unique property of the displayed peptide and independent of the protein scaffold.

### **MATERIALS AND METHODS**

Bacterial strains, plasmids, and growth conditions. In this study we used the E. coli K-12 strain S1918 (F' lacIq  $\Delta$ malB101 endA hsdR17 supE44 thil relA1 gyr-96  $\Delta$ fimB-H::kan) (3). Cells were grown in Luria-Bertani medium supplemented with the appropriate antibiotics. Our FimH display system consists of two plasmids, the FimH expression vector pLPA30 and an auxiliary plasmid pPKL115. Plasmid pLPA30 is a pUC18 derivative containing the fimH gene downstream of the lac promoter. A BglII linker, located in a position corresponding to amino acid 225 (14), was used for integration of the random library. Plasmid pPKL115 is a pACYC184 derivative containing the whole fim gene cluster with a translational stop linker inserted in the fimH gene (14).

DNA techniques. Plasmid DNA was isolated using the QIAprep Spin Plasmid kit (Qiagen). Restriction endonucleases were used as specified by the manufacturer (Biolabs or Pharmacia). PCR amplifications to monitor the size and distribution of the random library were performed as previously described (24). The oligonucleotide primers used in these reactions were P1 (5'-CCTGCACAGGGCGTCGGCGTAC) and P2 (5'-GGAATAATCGTACCGTTGCG). The nucleotide sequences of inserts conferring on cells the ability to bind to metal oxides were determined by the dideoxynucleotide chain termination method (18).

Construction of the random peptide library. Construction of the random library was performed essentially as described by Brown (3). Briefly, a template oligonucleotide containing the sequence 5'-GGACGCAGATCT(VNN)9AGATCTAGCACCAGT-3' (where N indicates an equimolar mixture of all four nucleotides and V indicates an equimolar mixture of A, C and G) was chemically synthesized. A primer oligonucleotide, 5'-ACTGGTGCTAGATCT-3', was hybridized to the template oligonucleotide and extended with the Klenow fragment of DNA polymerase I. The double-stranded oligonucleotide was purified by phenol-chloroform extraction and digested with BglII to release an internal 33-bp fragment. This was purified by electrophoresis through a 12% polyacrylamide gel in Tris-borate-EDTA (TBE) and

eluted into a buffer containing 10 mM Tris-HCl (pH 8.0), 2 mM EDTA, and 0.15 M NaCl. The eluate was filtered through a 0.22-µm-pore-size Qiagen filter, concentrated by ethanol precipitation, -and redissolved in a buffer containing 10 mM Tris-HCl (pH 8.0), 1 mM EDTA, and 0.1 M NaCl. The redissolved 33-bp BglII fragment was ligated at various ratios to BglII-digested pLPA30. The ligation products were precipitated with ethanol and electroporated into S1918(pPKL115).

The diversity of the library was calculated to be  $4 \times 107$  individual clones based on extrapolation from the numbers of transformants obtained in small-scale platings. The transformation mixture was made up to 10 ml and grown for approximately seven generations ( $4 \times 109$  cells). Aliquots (1 ml) were frozen at  $-80^{\circ}$ C in 25% (vol/vol) glycerol. Each 1-ml aliquot contained approximately  $4 \times 108$  cells, which represented 10 times the library diversity. Random screening of clones by PCR revealed a predominance of one to three 33-bp oligonucleotide inserts; sequencing of the inserts from randomly selected clones revealed G+C contents ranging from 30 to 70%.

Enrichment procedure. Bacterial cells were bound to zinc ions by use of stripped Ni2+-nitrilotriacetic acid (NTA) solid matrix (Qiagen) recoated with Zn2+ by a standard method. The enrichment procedure for identifying Zn2+-binding clones from the random library was as follows. Mid-exponential-phase cultures were diluted into M63 salts (13) containing 20 mM methyl  $\alpha$ -d-mannopyranoside and 50% (vol/vol) Percoll (Pharmacia). The methyl  $\alpha$ -d-mannopyranoside was added to block the natural receptor-binding domain of the FimH adhesin. The use of Percoll permitted the formation of a density gradient on centrifugation, which resulted in a distinct band due to the Zn2+-NTA resin, and specific separation of any adherent bacteria from nonadherent bacteria. Under these conditions, bacteria expressing wild-type FimH proteins as components of type 1 fimbriae did not coseparate with the Zn2+-NTA resin. The resin and bacteria expressing the random peptide library within FimH were mixed and allowed to adhere at room temperature with gentle agitation. Centrifugation was then performed, and the resin and any adhering bacteria were recovered and inoculated into Luria-Bertani medium containing appropriate antibiotics. After overnight incubation, exponentially growing cultures were established and the enrichment procedure was repeated. Following each cycle of enrichment, aliquots of the populations were stored at -80°C. Plasmid DNA was prepared from each aliquot and used in PCR to monitor the size distribution of the inserts in the population as previously described (19).

Binding assay and quantification. Mid-exponential-phase cultures standardized on the basis of their optical density at 550 nm (OD550) were washed and resuspended in M63 salts containing 20 mM methyl  $\alpha$ -d-mannopyranoside. Samples were incubated at room temperature for 15 min with gentle agitation before the addition of Zn2+-NTA agarose beads. After a 15-min incubation with gentle agitation, the beads were examined by phase-contrast microscopy (Carl Zeiss Axioplan microscope) and digital images were captured with a 12-bit cooled slow-scan charge-coupled device camera (KAF 1400 chip; Photometrics, Tucson, Ariz.) controlled by PMIS software (Photometrics).

The ability of individual clones to bind to Zn2+ was measured by counting cells attached to a selection of randomly chosen Zn2+-NTA beads and correlating the number of adhering cells to the bead size. The same procedure was used for quantification of cells binding to Ni2+-NTA and Cu2+-NTA beads.

Agglutination of yeast cells. The capacity of bacteria to express a d-mannose-binding phenotype was assayed by their ability to agglutinate yeast cells (Saccharomyces cerevisiae) on glass slides. Aliquots of washed bacterial suspensions at an OD550 of 1.0 and 10% yeast cells were mixed, and the time until agglutination occurred was measured.

Insertion of a CTB loop in fimH. Two oligonucleotides. oligonucleotide KK12 (5'-GATCT-GTTGAAGTTCCGGGATCCCAGCATATCGATAGT-CAGAAA AAAGCTA-3') and oligonucleotide KK13 (5'-GATCTAGCTTTTTTTCTGACTATCGATATGCTGG-GATCCCGGAACTTCAACA-3') encoding amino acids 50 to 64 of cholera toxin B chain (CTB), were designed so that they contained an internal BamHI site at amino acid position 54 and were flanked by BgIII overhangs. These oligonucleotides were annealed, phosphorylated, and ligated into pLPA30 digested with BglII. The resultant plasmid (pKKJ16) was checked by BamHI digestion and sequencing. Plasmid pKKJ16 (containing the loop of CTB in fimH) was transformed into S1918(pPKL115).

Engineering a Zn2+-binding peptide into the CTB3 loop in FimH. The Zn2+-binding sequence of pKKJ106 was amplified by PCR using primers KK77 (5'-GCCCGGATCCGAAAGCAGGGTCGACC-3') and KK78 (5'-GCCCGGATCCTTGGTGATGACGCTCTG-3') containing BamHI overhangs. The PCR product was digested with BamHI and ligated into pKKJ16 digested with BamHI. The resultant plasmid (pKKJ145) was checked by sequencing and transformed into S1918(pPKL115).

Fimbria purification. OD550-standardized overnight cultures were harvested by centrifugation and washed with phosphate-buffered saline (PBS). Cells were resuspended in PBS, and fimbriae were de tached from the cell surface by blending. The cell debris was removed by centrifugation, and the fimbriae in the supernatant were precipitated with acetone. The purified fimbriae were dried and resuspended in PBS (8).

Sodium dodecyl sulfate-polyacrylamide gel electrophoresis and Western immunoblotting. Purified fimbriae were treated with diluted HCl (pH = 2) and separated on 15% polyacrylamide gels by sodium dodecyl sulfate-polyacrylamide gel electrophoresis by using standard procedures (16). The gels were transferred to polyvinylidene difluoride microporous membrane filters using a semidry blotting apparatus. The membranes were blocked with 0.5% Tween 20 and incubated with anti-FimH (truncated) serum followed by horseradish peroxidase-conjugated anti-rabbit serum.

### RESULTS

Library construction in FimH. A random peptide library based on oligonucleotides 33 bp in length with BglII overhangs was constructed for display in the type 1 fimbria adhesin FimH (Fig. (Fig.1).1). To this end, we used a vector (pLPA30) containing the fimH gene with a BgIII linker inserted at codon position 225 and under the transcriptional control of the lac promoter (14). Insertions in this position have previously been shown to permit the expression of heterologous sequences without affecting the properties of FimH. The inserted double-stranded oligonucleotides consisted of nine random codons flanked by BglII restriction sites (encoding Arg-Ser). Due to the presence of BgIII overhangs, various numbers of double-stranded oligonucleotides were inserted in fimH, further adding to the complexity of the library. To express FimH variants as constituents of fimbriae, an auxiliary plasmid (pKKL115), containing all fim genes except fimH, was used for transcomplementation of the fimH-containing plasmid. Expression from the binary plasmid system led to display of chimeric FimH in the context of fully functional fimbriae.



FIG. 1: Overview of random peptide display in type 1 fimbriae. (A) The binary plasmid systems used in heterologous display by FimH. Plasmid pPKL115 contains the entire fim gene cluster with a translational stop linker inserted in the fimH gene (indicated by the solid triangle). The FimH expression vector pLPA30 is shown, along with the BgIII insertion site at amino acid 225 and the two primers (P1 and P2) used to monitor the size and distribution of the random library. (B) Genetic structure of the random library inserted into fimH. The two oligonucleotides were annealed and extended with the Klenow fragment of DNA polymerase I, and the product was purified after digestion with BgIII. N indicates an equimolar mixture of all nucleotides, and V indicates an equimolar mixture of A, C, and G. The use of a VNN coding system prevents the introduction of functional stop codons in an amber-suppressing host.

Selection and identification of Zn2+-binding sequences. Cells able to adhere to Zn2+ were isolated from the FimH-displayed random library after repetitive rounds of selection. The cells were allowed to bind to Zn2+-NTA beads, and binding cells were separated from nonbinders by density gradient centrifugation in 50% (vol/vol) Percoll. Bacteria adhering to the Zn2+-NTA beads were recovered and transferred to fresh growth medium. The enrichment procedure was repeated, and the insert distribution of the population was monitored by PCR (data not shown). No change in the insert population was observed in a control experiment, in which neither Zn2+-NTA nor Percoll was present during the enrichment procedure. However, a notable change in the insert distribution was observed after three rounds of enrichment with Zn2+-NTA. Cells obtained from the third enrichment cycle were spread onto agar plates, and cultures were established from 20 single colonies. The ability of cells expressing the enriched peptides to adhere to Zn2+-NTA was examined by phase-contrast microscopy (Fig. (Fig.2).2). Of the 20 clones, 15 displayed a Zn2+-binding phenotype. To ensure that the observed binding phenotype was indeed FimH based, each of the fimH-encoding plasmids was isolated and retransformed into S1918(pPKL115). The new recombinant clones displayed the same binding phenotype as the original isolates, indicating that the binding phenotype was indeed plasmid encoded. Furthermore, the agglutination titers of these cells were similar to that of a control strain expressing wild-type FimH, indicating that the presence of the inserts had not significantly altered the amount of surface-displayed FimH.



FIG. 2: Phase-contrast microscopy showing adherence to Zn2+-NTA beads by S1918(pPKL115) cells containing plasmid pLPA30 (wild-type fimH) (A) or plasmid pKKJ114 (random library clone isolated after selection for adherence to Zn2+-NTA beads) (B).

Most of the isolated sequences contained one or more histidine residues, as expected given the important role played by this amino acid in Zn2+ binding. It is a well-established fact that histidine is able to chelate divalent metal ions, as seen in a number of proteins with zinc finger motifs and metallothioneins (25). However, one sequence (pKKJ113) devoid of histidines was also identified from the library, showing that histidine is not an absolute requirement for binding to Zn2+. Indeed, cells expressing the peptide sequence of plasmid pKKJ113 mediated stronger Zn2+ binding than did cells expressing peptides containing multiple histidine residues. Furthermore, plasmid pKKJ113 displayed a very high degree of binding specificity toward Zn2+ compared to its specificity toward Ni2+. Previously, Barbas et al. (1) identified a number of Zn2+-binding peptides from a phage-displayed semisynthetic combinatorial antibody library. We did not observe any similarities between our Zn2+-binding sequences and those identified by Barbas et al. (1). This might be due to the genetic structure of the libraries and the different selection and enrichment procedures employed.

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