

# Detection of bacterial pathogens by phage antibody display

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## 1. Introduction

*Vibrio parahaemolyticus* is a halophilic Gram-negative facultative anaerobe commonly found in estuarine waters and in seafood like shellfish. It has been implicated in outbreaks of gastro-enteritis in several countries [1]. Food borne illness caused by *V. parahaemolyticus* results chiefly from the consumption of insufficiently heated or raw seafood, especially in the summer months. The standard method for detection of *V. parahaemolyticus* (Bacteriological Analytical Manual procedure) is a culture-based procedure which can take up to four days for positive identification.

Recent outbreaks of *V. parahaemolyticus* related illnesses have heightened the need to develop a rapid and reliable method to detect this pathogen in shellfish. PCR methods, based on the amplification of the toxin producing genes, unfortunately give false positive results with other *Vibrio* species [2]. In our studies we have used phage antibody display to differentiate between pathogenic *V. parahaemolyticus* and other pathogenic and non-pathogenic *Vibrio* sp.

## 2. Methods

### 2.1. Bacterial cultures

Cultures of *V. parahaemolyticus* and other *Vibrio* sp. were obtained from the National Collection of Type Cultures, London and the ATCC.

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### 2.2. Panning

The human synthetic scFv (NISSIM) library was used as a source of antibody fragments of different specificities (greater than  $10^8$ ) [3].

Five rounds of panning were used to select for antibodies specific for surface markers on *V. parahaemolyticus*. Pooled cultures of *V. parahaemolyticus* (cell density =  $8 \times 10^8$  cells/ml at  $A_{600}$ ) were used in 4 rounds of positive panning. One round of negative panning was carried out using pooled cultures of non-*parahaemolyticus* *Vibrios* (cell density =  $8 \times 10^8$  cells/ml at  $A_{600}$ ) to try and remove all cross-reactive phage.

The negative panning step was carried out after the first round of positive panning. The titre of eluted phage was checked after each round of panning.

### 2.3. ELISA

ELISA was used to determine binding specificity of phage clones. Phage clones after the 5th (and last) round of panning were grown up in 96-well round bottom ELISA plates overnight.

Flat bottom 96-well ELISA plates were coated with  $10^8$  cells/well of different strains of *V. parahaemolyticus* and strains of other non-*parahaemolyticus* sp. overnight. Phage supernatant was obtained by growing up individual phage clones overnight at  $30^\circ\text{C}$  and then spinning the cells at 2500 rpm for 10 minutes. Supernatant containing phage antibody was added to the wells and the phage were allowed to bind for 2 hours. Excess unbound phage was then washed off, and the bound phage detected by adding anti-M13 HRP conjugated antibody for 1 hour followed by the addition of tetramethylbenzidine (TMB) substrate. The absorbance was measured at 450 nm using an ELISA reader (MRX microplate reader, Dynex technologies). Irrelevant phage (anti-NIP) was used as a negative control.

Table 1

ELISA (Absorbance at 450nm) of phage clones binding to different strains of *Vibrio* sp

	1	2	3	4	5	6	7	8
A	*	*	*		*	*	*	
B	*	*	*		*	◇	*	
C	*	*	*	*	△	*	△	△
D	*	*	*	*				
E		*	*			*	*	
F	*	*	*	△		*	*	

Key: Readings greater than 1.000 at A<sub>450</sub> have been considered positive.

◇ = *Vibrio parahaemolyticus* NCTC 10884.

\* = *Vibrio parahaemolyticus* NCTC 10903 + NCTC 10884 (1 : 1 ratio).

△ = *Vibrio mimicus* NCTC 11346 and *Vibrio harveyi* NCTC 11435 (1 : 1 ratio) (cultures used for negative panning).

Table 2

Binding percentages of selected phage antibodies against *Vibrio* sp. (Percentage binding of anti-NIP was used as blank)

Clone	<i>Vibrio parahaemolyticus</i> NCTC 10903	<i>Vibrio parahaemolyticus</i> NCTC 10884
A1	11.3%	7.7%
B3	21.3%	21.9%
B5	27.6%	27.8%
C2	33%	30.5%
E3	16.6%	12.5%
F7	16.9%	8.15%

#### 2.4. FACS analysis

Repeatedly strong binding clones were selected for screening their binding properties using a FACSCalibur flow cytometer. Single cultures of *V. parahaemolyticus* as well as pooled cultures were used for analysis.

### 3. Results

After the final round of panning, 48 clones were picked for screening by ELISA. ELISA was carried out using individual cultures of *V. parahaemolyticus* NCTC 10903 and *V. parahaemolyticus* NCTC 10884 as well as pooled cultures mixed in a ratio of 1 : 1. Cell density was maintained at 10<sup>8</sup> cells/well. Out of 48 clones, 28

clones showed repeated strong binding to both strains of *V. parahaemolyticus*. Preliminary results have been shown in Table 1. Clone B6 was the only clone that was positive with *V. parahaemolyticus* NCTC 10884 and negative with NCTC 10903. It may therefore represent a clone that is strain specific.

ELISA was also carried out using pooled cultures of *V. mimicus* NCTC 11346 and *V. harveyi* NCTC 11435 in a 1 : 1 ratio. Only four clones of the 28 were cross reactive with the above cultures.

CDR3 insert size was determined using PCR as previously described [3]. BstN1 restriction digestion of a PCR fragment covering the whole scFv region was also carried out as previously described [4].

Six phage clones out of the 28 were picked at random and were analyzed for their binding specificities using flow cytometry. All 6 clones were positive for *V. parahaemolyticus* on FACS analysis. The percentage binding to each strain was also determined (Table 2).

### 4. Discussion

Using phage display, we have been able to isolate antibodies that bind to *V. parahaemolyticus*. We are now in the process of screening these antibodies against a broad range of *Vibrio* and other related sp., from different sources, to determine their specificity.

### References

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- [2] Y.B. Kim et al., Identification of *V. parahaemolyticus* strains at the species level by PCR targeted to the *toxR* gene, *Journal of Clinical Microbiology* **37**(4) (1999), 1173–1177.
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