

B Cell Epitope Mapping of the *Vibrio cholera* Toxins A, B, and P and an ELISA assay

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Supplementary Figures

Figure S1- List of *Vibrio cholerae* [toxin A (P01555), B (P01556), and P (P29485)] synthetic peptides and position in the cellulose membrane of Spot synthesis.

Figure S2- Purification of the peptide B (Vc/TxB-11) by HPLC using an XBridge BEH C18 (2.7 μ , 5 cm x 4.6 mm) column coupled to a Water HPLC system at a flow rate of 1.2 ml min⁻¹ using mobile phases A [0.05% formic acid in water (18 M Ω x cm)] and B [(0.05% formic acid in ACN (acetonitrile acid)) (v/v) in water. Detection at 200-300 nm using a diode array.

Figure S3- Mass spectrometry. The peptide B (Vc/TxB-11) was solubilized in deionized water to a final concentration of 10 μ g/ml and then added formic acid to a final concentration of 0.1%. The mass spectrometer used was the Water UPLC model Acquity-I Class. The samples were electronically injected by the equipment at 1 μ l/min. The range used for ion detection ranged from 1000-11500 m/z.

Peptide	Sequence	Peptide	Sequence	Peptide	Sequence
A1	GSGSGMVKIIIFVFFI	B1	NDVLGAYSPHPDEQE	C1	VKRQIFSGYQSDIDT
A2	MVKIIFVFVFFIFLSSF	B2	AYSPHPDEQEVSALG	C2	FSGYQSDIDTHNRIK
A3	FVFFFIFLSSFSYAND	B3	PDEQEVSALGGIPYS	C3	SDIDTHNRIKDELGS
A4	FLSSFSYANDDKLYR	B4	VSALGGIPYSQIYGW	C4	DTHNRIKDELGS
A5	SYANDDKLYRADSRP	B5	GIPYSQIYGWYRVHF	C5	GSGSGMIKLKFGVFF
A6	DKLYRADSRRPDEIK	B6	QIYGWYRVHFGVLDE	C6	MIKLKFGVFTTVLLS
A7	ADSRPPDEIKQSGL	B7	YRVHFGVLDEQLHRN	C7	FGVFFTLLSSAYAH
A8	PDEIKQSGLMPRGQ	B8	GVLDEQLHNRGYRD	C8	TVLLSSAYAHGTPQN
A9	QSGGLMPRGQSEYFD	B9	QLHRNRYGRDYYSN	C9	SAYAHGTPQNITDLC
A10	MPRGQSEYFDRGTQM	B10	RGYDRYYNSLDIAP	C10	GTPQNITDLCAEYHN
A11	SEYFDRGTQMNNLY	B11	RYYSNLDIAPAAADGY	C11	ITDLCAEYHNTQIYT
A12	RGTQMNNLYDHARG	B12	LDIAPAAADGYGLAGF	C12	AEYHNTQIYTLDKI
A13	NINLYDHARGTQTGF	B13	AADGYGLAGFPPEHR	C13	TQIYTLNDKIFSYTE
A14	DHARGTTQGTVRHDD	B14	GLAGFPPEHRAWREE	C14	LNDKIFSOTESLAGK
A15	TQTGFVRHDDGYVST	B15	PPEHRAWREEPWIHH	C15	FSYTESLAGKREMAI
A16	VRHDDGYVSTSISLR	B16	AWREEPWIHHAPPGC	C16	SLAKREMAIITFKN
A17	GYVSTSISLRAHLV	B17	PWIHHAPP CGNAPR	C17	REMAIITFKNGAIFQ
A18	SISLRAHLVGQTIL	B18	APP CGNAPR SSMN	C18	ITFKNGAIFQVEVPG
A19	SAHLVGQTILSGHST	B19	GNAPR SSMN TCD EK	C19	GAIFQVEVPGSQHID
A20	GQTILSGHSTYYIYV	B20	SSMSNT CDEKT QSLG	C20	VEVPGSQHIDSQKKA
A21	SGHSTYYIYVIATAP	B21	TCDEKT QSLGV KFLD	C21	SQHIDSQKKAIERMK
A22	YYIYVIATAPNMFNV	B22	TQSLGV KFLDEY QSK	C22	SQKKAIERMKDTLRI
A23	IATAPNMFNVDVLG	B23	VKF LDEY QSKV KQR	C23	IERMKDTLRIAYLTE
A24	NMFNVNDVLGAYSPH	B24	EYQSKV KRQIFSGYQ	C24	DTLRIAYLTEAKVEK
D1	AYLTEAKVEKLCVWN	E1	DEHKTLI ENV KLGQY	F1	YEQKTL ECT KNGSGS
D2	AKVEKLCVWN NKTPH	E2	LIENV KLGQY RINII	F2	EQKTL ECT KNGSGSG
D3	LCVWN NKTPH AIAAI	E3	KLGQY RINII IQV IVS	F3	
D4	NKTPH AIAAI SMANG	E4	RINII IQV IV SENV VD	F4	
D5	HAI AAIS MANG GSG	E5	QIV ISEN VV DED ACS	F5	
D6	GSGSGM GYV RVI YQF	E6	ENV VDE ADCS QK KV	F6	
D7	MGY VRVI YQFP DN LW	E7	EADC SQK KV KERIK	F7	
D8	VIY QFP DN LW NECT	E8	QK KV KERIK IEWG K	F8	
D9	PDNL WWNE CTN QV YY	E9	KERIK IEWG KIN VVP	F9	
D10	WNE CTN QV YY AQD PM	E10	IEWG KIN VV PYL VFS	F10	
D11	NQV YYA QD PM KPERL	E11	INV PYL VFS ALV YA	F11	
D12	AQD PM KPERL IGBT P	E12	YL VFS ALV Y ALL PV	F12	
D13	KPERL IGP SII QT K	E13	AL Y VALL PVI WWS YG	F13	
D14	IGTP SII QT KLL KIL	E14	LL PVI WWS YG QW YQH	F14	
D15	II QT KLL KIL CEY HP	E15	WWS YG QW YQHE LAG I	F15	
D16	LL KIL CEY HPA PCPN	E16	QW YQHE LAG I THD LR	F16	
D17	CEY HPA CPN DQ I I K	E17	E LA GITH DLR D LAR L	F17	
D18	APCP NDQ I I KAL WPH	E18	THD LR D LAR L PGI TI	F18	
D19	DQ I I KAL WPH GFI SS	E19	DL AR L PGI TI QK L SE	F19	
D20	ALW PHG FISSES LTQ	E20	PG ITI QK L SE QK L TF	F20	
D21	GFI SSES LTQ A I KRT	E21	QKL SE QK LTF AI DQH	F21	
D22	ESLT QAI KTR DF L N	E22	QKL TFA IDQ HQ CSV N	F22	
D23	AI KTR DF L N DE HKT	E23	AIDQ HQ CSV NYE QKT	F23	
D24	RDF LN DE HK T L I EN	E24	QCS VNY E QKT L ECT K	F24	
G1		G9	QE VR KY FCV	G17	QE VR KY FCV
G2		G10		G18	
G3	KE VP ALTA VET GAT N	G11	KE VP ALTA VET GAT N	G19	
G4		G12		G20	
G5	GYPKDGN AFN NL DR	G13	GYPKDGN AFN NL DR	G21	
G6		G14		G22	
G7	YDY DVP DY AGY PY DV	G15	YDY DVP DY AGY PY DV	G23	
G8		G16		G24	YDY DVP DY AGY PY DV

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