« Best of »
Infections nosocomiales
Réanimation

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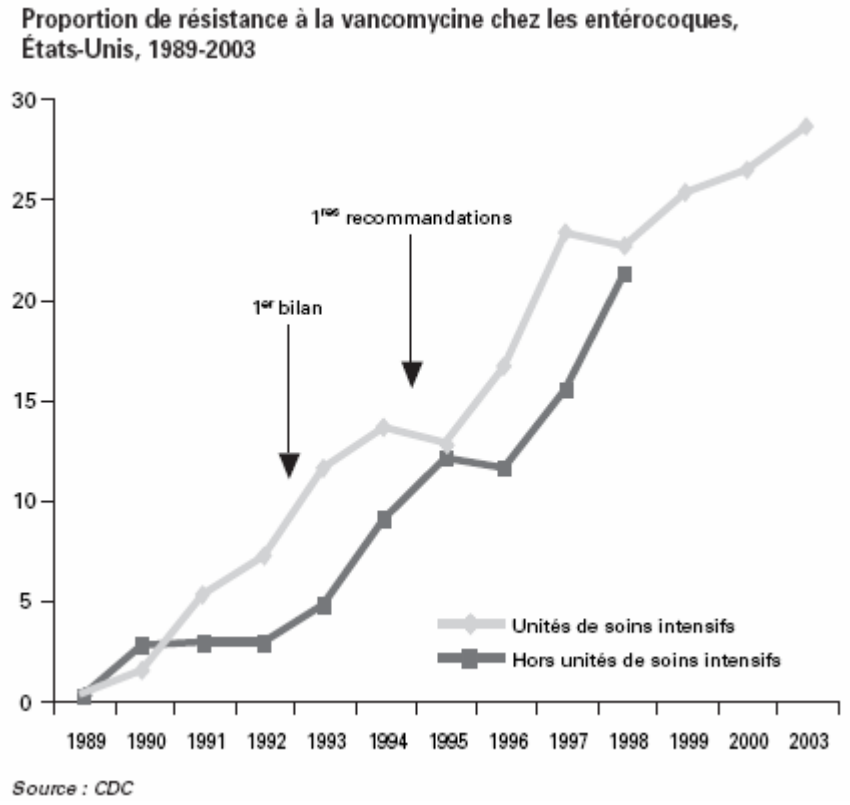
Enterocoque résistant a la vancomycine

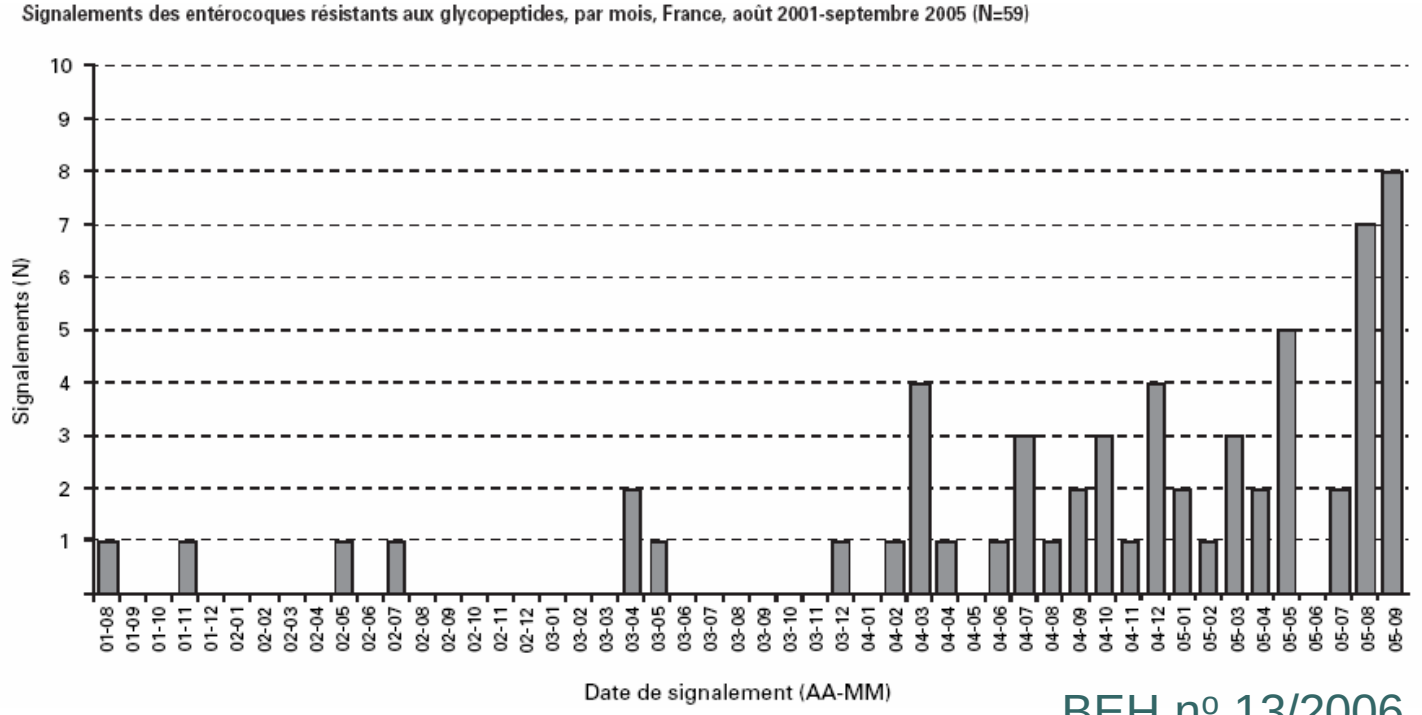
- USA
  - Description en 1989-90
  - Situation endémique dans les hôpitaux (25-30% ERV en 2003)



BEH nº 13/2006

Enterocoque résistant a la vancomycine

- France
  - Proportion ERV stable jusqu'en 2003 (<2%)
  - ↗ en 2004 espèce *E. faecium* mécanisme *vanA*
  - Diffusion = mode épidémique



BEH nº 13/2006

Enterocoque résistant a la vancomycine

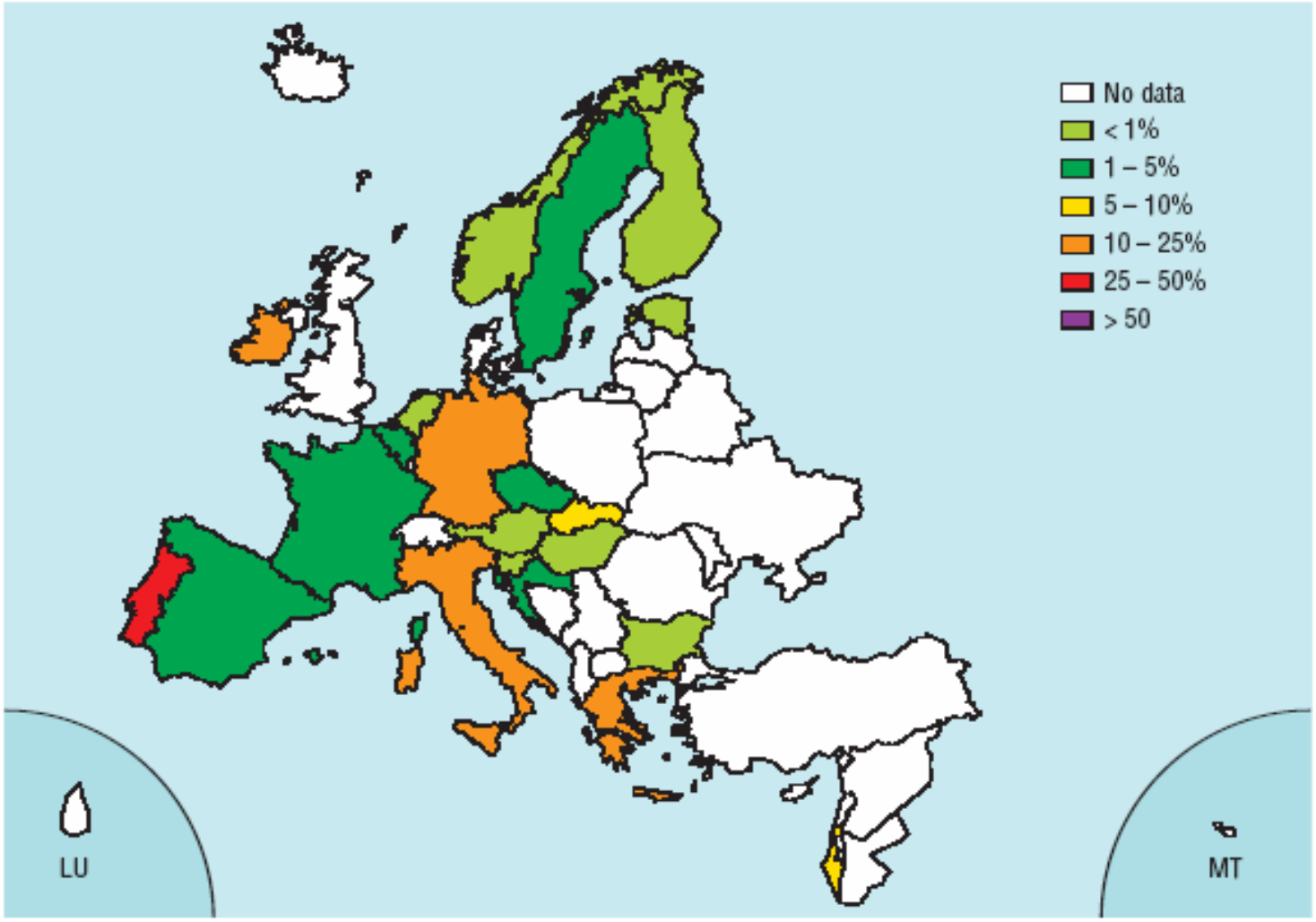


Figure 5.9. *Enterococcus faecium*: proportion of invasive isolates resistant to vancomycin in 2004.

Enterocoque résistant a la vancomycine

- Les enjeux
  - Apparition de SARM résistants aux glycopeptides par transfert de résistance *vanA*
  - ↗ morbidité mortalité chez les patients bactériémiques ERV
- Détection *E. faecium vanA*: pas de difficulté technique

Genotyping and Preemptive Isolation to Control an Outbreak of Vancomycin-Resistant *Enterococcus faecium*

E. M. Mascini,[1] A. Troelstra,[2] M. Beitsma,[2] H. E. M. Blok,[2] K. P. Jalink,[2] T. E. M. Hopmans,[2] A. C. Fluit,[2] R. J. Hené,[3] R. J. L. Willems,[2,4] J. Verhoef,[2] and M. J. M. Bonten[2,4,5]

Clinical Infectious Diseases 2006; 42:739–46

Table 1. Summary of infection-control measures during the 3 periods of the outbreak.

Measure	Period I (June 2000–October 2000)	Period II (November 2000–June 2001)	Period III (July 2001–January 2003)
Cohorting of patients	4 Cohorts: epiVRE patients, roommates of epiVRE patients, wardmates of epiVRE patients, and newly admitted patients	3 Cohorts: epiVRE patients, possibly epiVRE patients, and newly admitted patients	No cohorts
Cohorting of nursing staff	Cohorted as much as possible into 4 cohorts; for visiting staff, contact isolation of all patients	Cohorted as much as possible into 3 cohorts	No specific measures
Isolation of epiVRE patients	Contact isolation in a single room (patients labeled in hospital information system)	Contact isolation in a single room (patients labeled in hospital information system)	Contact isolation in a single room (patients labeled in hospital information system)
Isolation of possibly epiVRE patients	For roommates of epiVRE patients, contact isolation in a cohort or single room until 3 negative culture results; for ward contacts of epiVRE patients, treatment in cohort until 3 negative swab test results (no contact isolation)	Preemptive isolation of all patients hospitalized in the NG ward between January and November 2000, regardless of culture results (patients labeled in hospital information system)	None
Environmental disinfection	Disinfection of rooms of epiVRE patients after discharge	Disinfection of rooms of epiVRE patients after discharge	Disinfection of rooms of epiVRE patients after discharge
VRE screening	Obtainment of swabs from noncolonized and possibly epiVRE patients 3 times weekly	Obtainment of swabs from noncolonized and possibly epiVRE patients once weekly	Obtainment of swabs from noncolonized and possibly epiVRE patients once weekly until September 2001 and once monthly thereafter

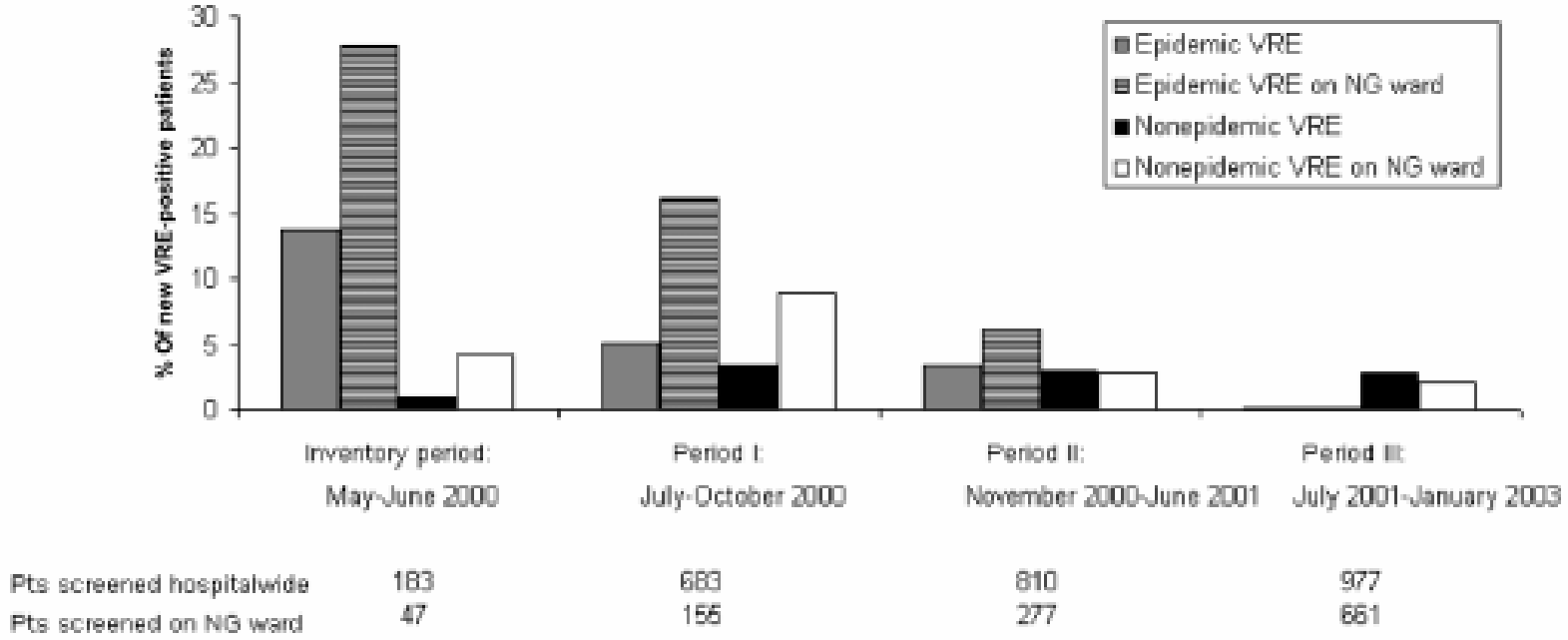


Figure 1. Percentages of newly identified patients colonized with epidemic (clusters I and II) and nonepidemic vancomycin-resistant *Enterococcus faecium* (VRE) during the different outbreak periods, 2000–2003. NG, nephrology/gastroenterology; Pts, patients.

Nosocomial Spread of *Enterococcus faecium* Resistant to Vancomycin and Linezolid in a Tertiary Care Medical Center

Thomas E. Dobbs,[1] Mukesh Patel,[1] Ken B. Waites,[2*] Stephen A. Moser,[2] Alan M. Stamm,[1] and Craig J. Hoesley[1]

Department of Medicine[1] and Department of Pathology,[2] University of Alabama at Birmingham, Birmingham, Alabama 35249-7331

JOURNAL OF CLINICAL MICROBIOLOGY, Sept. 2006, p. 3368–3370

- Résistance entérocoque décrite précocement après introduction du linézolide aux USA
- Nombre limité de cas et stable jusqu'en 2004 (<0,5%)
- 1 cas en mai 2004 → 60 souches en 2005 = 21% des *E. faecium* d'un même hôpital ➔ étude rétrospective

- Souches étudiées n=40
- Champs pulsé 1 clone 19/21 souches
- Nouveau clone (? des LSVRE)
- Mutation G2576T sur 23S rRNA

- 22 responsables d'infection (probable)
- Décès=9 au total (6/22)
- Parcours des patients dans l'hôpital ?
- ATB avant LRVRE
  - Fluoroquinolone 34/40, Vancomycine 32/40
  - Linézolide 6/40

- Stratégie
  - Sensibilisation précautions standards et isolement contact
  - Cohorting patients et personnel
  - Screening écouvillon rectal juillet → décembre 2005
  - Réserves prescription fluoroquinolones/vancomycine ultérieurement

Emergence of Linezolid Resistance in the Vancomycin-Resistant *Enterococcus faecium* Multilocus Sequence Typing C1 Epidemic Lineage

Maria Grazia Bonora,[1] Maurizio Solbiati,[2] Erminia Stepan,[3] Antonella Zorzi,[3] Aldo Luzzani,[4] Maria Rosaria Catania,[5] and Roberta Fontana[1,3]*

JOURNAL OF CLINICAL MICROBIOLOGY, Mar. 2006, p. 1153–1155

- Surveillance active en réanimation en 2004 (janv.-déc.), 127 patients
- 35 ERV en infection/colonisation
- 6 LR et 8 LI

TABLE 1. Clinical data of patients infected or colonized by linezolid-resistant *E. faecium* and molecular typing of linezolid-resistant isolates

Patient (sex/age [yr])	Ward[a]	Underlying disease(s)	Risk/outcome[b]	Strain code	Type or site of infection (isolation date [mo/day/yr])	Linezolid MIC (μg/ml)	PFGE type[c]	MLST type	Detection of G2576 mutation	Detection of T2576 mutation
P1 (male/64)	TICU	Kidney transplant	Prolonged hospitalization (58 days), ICU care, linezolid use, discharged	SM902	Ascites (03/25/04)	4 (LI)	D_{04}	78	Yes	No
				SM912	Ascites (05/05/04)	8 (LR)	D_{04}		Yes	Yes
P2 (female/71)	NICU	Communicans artery aneurysm	Prolonged hospitalization (81 days), ICU care, linezolid use, discharged	SM922	Urine (07/12/04)	8 (LR)	C_{04}	78	Yes	Yes
				SM924	Rectal (07/13/04)	8 (LR)	$C_{1,04}$		Yes	Yes
				SM925	Rectal (07/21/04)	8 (LR)	C_{04}			
P3 (female/64)	ICU	Ictus, diabetes	Died after 8 days of hospitalization	SM941	Rectal (10/19/04)	8 (LR)	F_{04}	78	Yes	Yes
P4 (female/75)	NICU	Communicans artery aneurysm	Prolonged hospitalization (56 days), ICU care, discharged	SM934	Rectal (09/22/04)	64 (LR)	$A^*_{2n,04}$	78	Yes	Yes
P5 (male/74)	ICU	Necrotizing pancreatitis	Prolonged hospitalization (46 days), ICU care, linezolid use, death	SM943	Ascites (11/02/04)	64 (LR)	$A^*_{2,04}$	78	Yes	Yes
P6 (male/67)	ICU	Spontaneous esophageal rupture, mediastinitis, peritonitis	Hospitalization overlapping P5, ICU care, discharged	SM936	Rectal (10/01/04)	64 (LR)	$A^*_{2,04}$	78	Yes	Yes
				SM944	Ascites (11/18/04)	64 (LR)	$A^*_{2,04}$		Yes	Yes

First Nosocomial Outbreak of Vancomycin-Resistant *Enterococcus faecium* Expressing a VanD-Like Phenotype Associated with a *vanA* Genotype

Thierry Naas,[1]* Nicolas Fortineau,[1] Renaud Snanoudj,[2] Colette Spicq,[1] Antoine Durrbach,[2] and Patrice Nordmann[1]

JOURNAL OF CLINICAL MICROBIOLOGY, Aug. 2005, p. 3642–3649 Vol. 43, No. 8

- 6 phénotypes de résistance aux glycopeptides
  - VanA: haut niveau de résistance vancomycine et teicoplanine acquis inductible, plasmide → transfert horizontal, 7 gènes *van*
  - VanD: faible niveau de résistance vancomycine et sensible ou intermédiaire teicoplanine

Patient[m]	Isolate	Onset[a] (days)	Sex[b]	Age (yr)	Infection status[c]	Underlying disease[d]	Treatment[e]	MIC[f] (μg/ml) of VA/TEC	PFGE[n]	PCR[g]		
										vanA	IS*16*	IS*16-vanY*
I	8	20	M	85	UTI	Prostatic cancer	None	256/16	A	+	+	+
II	13	15	F		Peritonitis	Lymphoma	LZD, SXT	12/4	A	+	+	+
III	11	20	F	64	Bacteremia	Transplantation + ESRD	None	24/6	A	+	+	+
IV	9	7	F	77	UTI	Diabetes + ARF	None	24/6	A	+	+	+
	10[h]	21	F	77	C	Diabetes + ARF	–	16/8	A	+	+	+
V	5	21	M	80	Peritonitis	ESRD	LZD, SXT	256/8	A	+	+	+
VI	4	22	F	67	UTI	Diabetes + ARF	None	24/8	A	+	+	+
VII	1	4	F	63	UTI	Transplantation + ESRD	None	12/6	A	+	+	+
VIII	3	15	F	68	C	ESRD	–	24/6	A	+	+	+
IX	14	10	F	75	C	Myeloma	–	24/8	A	+	+	+
X	2	11	F	48	C	Transplantation	–	12/6	A	+	+	+
XI	12	8	F	45	C	Transplantation	–	256/48	A	+	+	–
XII	20[i]	23	F	54	C	Transplantation	–	256/32	B	+	+	–
	21	23	F	48	C	Transplantation	–	32/8	A	+	+	+
XIII	17	10		59	C	Transplantation + polycystic kidney disease	–	24/8	A	+	+	+
XIV	15	5	M	55	C	Nephroangiosclerosis	–	256/16	A	+	+	+
XV	16	24	F	39	C	Transplantation	–	96/16	A	+	+	+
XVI	18	15	F	44	C	Immunoglobulin A nephropathy	–	32/6	A	+	+	+
XVII	19	21	F	69	C	Amyloid kidney	–	24/12	A	+	+	+
XVIII	23	4	M	75	C	Myeloma	–	16/6	A	+	+	+
XIX	22	4	M	65	C	Liver cirrhosis	–	32/16	A	+	+	+
XX	24	23	F	45	C	Transplantation	–	32/12	A	+	+	+
XXI	28	2	M	69	C	Transplantation + diabetes	–	256/6	A1	+	+	+
XXII	25	14	F	30	C	ESRD	–	16/6	A	+	+	+
XXIII	27	5	M	77	C	ESRD	–	256/48	A	+	+	–
XXIV	29	24	F	62	C	ARF	–	32/12	A	+	+	+
C1[j]	6							256/48	C	+	–	–
C2[k]	7							48/0.5	D	–	–	–
C3[l]	26							0.25/0.25	E	–	–	–

26 souches, 24 patients (30-85 ans), 7 infectés, 18 colonisés

Clostridium difficile

- Depuis le début des années 2000 : Canada (Québec) et États-Unis
  - multiplication par 10 des infections à *C. difficile*
  - infections nosocomiales sévères et épidémiques
  - apparition de la souche 027 en 2003, et actuellement
    - 80% des souches de *Cd* isolées au Québec, environ 50% dans certains États des États-Unis.
    - situation endémique, 30% de récidive (vs 10%), 10-15% de mortalité (vs 1,5-2%)

Clostridium difficile

- Depuis 2004 : Europe
  - Grande-Bretagne: 2400 décès (vs 900 habituellement)
  - Pays-Bas (2005), 35% des souches sont 027
  - Belgique (2005), 67% des souches sont 027
- Début 2006:
  - premiers cas en France, dans la région Nord – Pas de Calais

The NEW ENGLAND JOURNAL of MEDICINE

ESTABLISHED IN 1812 DECEMBER 8, 2005 VOL. 353 NO. 23

An Epidemic, Toxin Gene–Variant Strain of *Clostridium difficile*

L. Clifford McDonald, M.D., George E. Killgore, Dr.P.H., Angela Thompson, M.M.Sc., Robert C. Owens, Jr., Pharm.D., Sophia V. Kazakova, M.D., M.P.H., Ph.D., Susan P. Sambol, M.T., Stuart Johnson, M.D., and Dale N. Gerding, M.D.

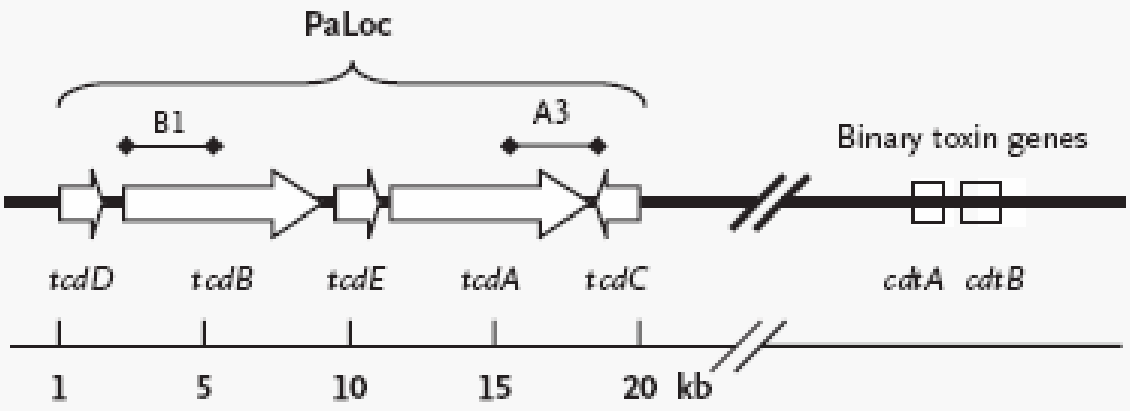


Figure 1. Major Genes in the Pathogenicity Locus (PaLoc) of *Clostridium difficile* and Relation to the Genes for Binary Toxin.

- 187 isolats de 8 établissements ayant décrit une épidémie depuis 2001

Table 1. Isolates of *Clostridium difficile* According to Health Care Facility and the Proportion of Isolates Belonging to the BI/NAP1 Strain.

Health Care Facility	Date of Onset of Outbreak	No. of Isolates Tested	BI/NAP1 Strain
			no. (%)
Georgia	Oct. 2001	46	29 (63)
Illinois	July 2003	14	6 (43)
Maine, Facility A	March 2002	13	9 (69)
Maine, Facility B	July 2003	48	30 (62)
New Jersey	June 2003	12	9 (75)
Oregon*	April 2002	30	3 (10)
Pennsylvania, Facility A	2000–2001	18	7 (39)
Pennsylvania, Facility B	Oct. 2003	6	3 (50)
Total		187	96 (51)

Pulsotype NAP1, Profil de restriction enzymatique type B1

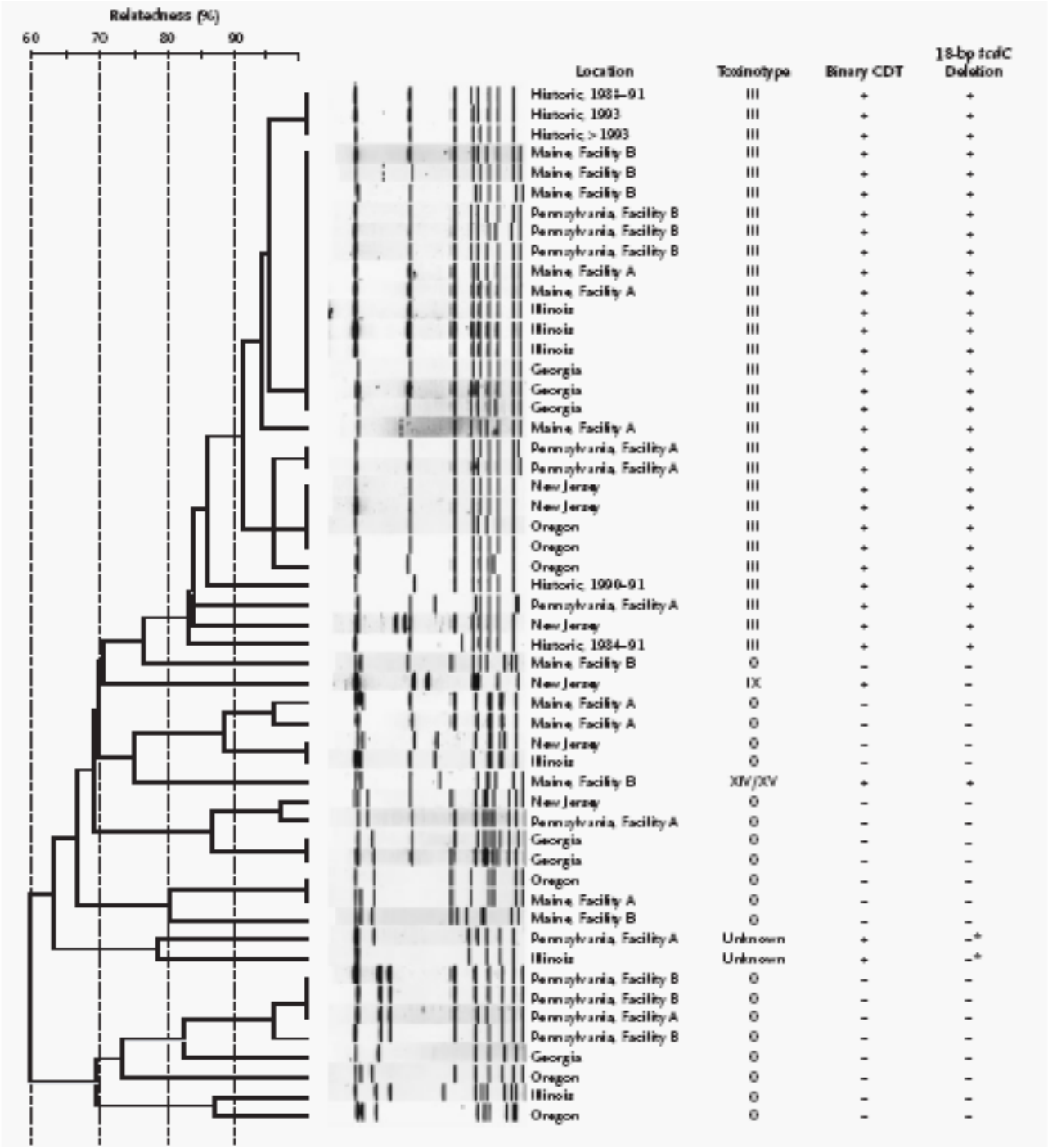

Relatedness (%)
60
70
80
90
Location
Toxinotype
Binary CDT
18-bp tcdC Deletion
Historic, 1985–91 III + +
Historic, 1993 III + +
Historic, >1993 III + +
Maine, Facility B III + +
Maine, Facility B III + +
Maine, Facility B III + +
Pennsylvania, Facility B III + +
Pennsylvania, Facility B III + +
Pennsylvania, Facility B III + +
Maine, Facility A III + +
Maine, Facility A III + +
Illinois III + +
Illinois III + +
Illinois III + +
Georgia III + +
Georgia III + +
Georgia III + +
Maine, Facility A III + +
Pennsylvania, Facility A III + +
Pennsylvania, Facility A III + +
New Jersey III + +
New Jersey III + +
Oregon III + +
Oregon III + +
Oregon III + +
Historic, 1990–91 III + +
Pennsylvania, Facility A III + +
New Jersey III + +
Historic, 1984–91 III + +
Maine, Facility B 0 – –
New Jersey IX + –
Maine, Facility A 0 – –
Maine, Facility A 0 – –
New Jersey 0 – –
Illinois 0 – –
Maine, Facility B XIV/XV + +
New Jersey 0 – –
Pennsylvania, Facility A 0 – –
Georgia 0 – –
Georgia 0 – –
Oregon 0 – –
Maine, Facility A 0 – –
Maine, Facility B 0 – –
Pennsylvania, Facility A Unknown + –*
Illinois Unknown + –*
Pennsylvania, Facility B 0 – –
Pennsylvania, Facility B 0 – –
Pennsylvania, Facility A 0 – –
Pennsylvania, Facility B 0 – –
Georgia 0 – –
Oregon 0 – –
Illinois 0 – –
Oregon 0 – –

Table 2. Resistance of Current BI/NAP1 *Clostridium difficile* Isolates, Current Non-BI/NAP1 Isolates, and Historic BI/NAP1 Isolates to Clindamycin and Fluoroquinolones.*

Antimicrobial Agent	Current BI/NAP1 Isolates (N=24)	Current Non-BI/NAP1 Isolates (N=24)	P Value†	Historic BI/NAP1 Isolates (N=14)	P Value‡
	no. with intermediate resistance or resistant (%)§			*no. with intermediate resistance or resistant (%)*	
Clindamycin	19 (79)	19 (79)	1.0	10 (71)	0.7
Levofloxacin	24 (100)	23 (96)	1.0	14 (100)	1.0
Gatifloxacin	24 (100)	10 (42)	<0.001	0	<0.001
Moxifloxacin	24 (100)	10 (42)	<0.001	0	<0.001

A Predominantly Clonal Multi-Institutional Outbreak of *Clostridium difficile*–Associated Diarrhea with High Morbidity and Mortality

Vivian G. Loo, M.D., Louise Poirier, M.D., Mark A. Miller, M.D., Matthew Oughton, M.D., Michael D. Libman, M.D., Sophie Michaud, M.D., M.P.H., Anne-Marie Bourgault, M.D., Tuyen Nguyen, M.D., Charles Frenette, M.D., Mirabelle Kelly, M.D., Anne Vibien, M.D., Paul Brassard, M.D., Susan Fenn, M.L.T., Ken Dewar, Ph.D., Thomas J. Hudson, M.D., Ruth Horn, M.D., Pierre René, M.D., Yury Monczak, Ph.D., and André Dascal, M.D.

N Engl J Med 2005;353:2442-9.

Table 2. Age-Specific Incidence and Mortality Attributed to *Clostridium difficile*–Associated Diarrhea.

Age	No. of Cases	No. of Cases/ 1000 Admissions*	Attributable 30-Day Mortality Rate
yr			%†
<40	76	3.5	2.6
41–50	85	11.2	1.2
51–60	191	20.0	3.2
61–70	272	24.4	5.1
71–80	523	38.3	6.2
81–90	458	54.5	10.2
>90	114	74.4	14.0

Table 3. Characteristics of Case Patients and Control Patients.*

Characteristic	Case Patients (N=237)	Controls (N=237)	P Value
Age — yr			0.48
Median	75	75	
Interquartile range	66–82	66–82	
Male sex — no. (%)	115 (48.5)	126 (53.2)	0.3
Charlson index†	2.6±1.9	2.6±2.0	0.66
Ward			0.82
Medicine	133 (56.1)	142 (59.9)	
Surgery	78 (32.9)	70 (29.5)	
Geriatrics	17 (7.2)	15 (6.3)	
Oncology	9 (3.8)	10 (4.2)	
Community hospital — no. (%)	68 (28.7)	67 (28.3)	0.9
Days at risk for *C. difficile*–associated diarrhea			0.02
Median	13	16	
Interquartile range	6–25	8–29	
No. of antibiotics received	1.9±1.1	1.3±1.3	<0.001
Any exposure to antibiotics — no. (%)	188 (79.3)	141 (59.5)	<0.001
Cephalosporins	115 (48.5)	65 (27.4)	<0.001
Clindamycin	19 (8.0)	6 (2.5)	0.007
Fluoroquinolones	128 (54.0)	75 (31.6)	<0.001
Chemotherapy — no. (%)	17 (7.2)	13 (5.5)	0.45
Proton-pump inhibitors — no. (%)	112 (47.3)	111 (46.8)	0.92
Histamine H_2–blockers — no. (%)	47 (19.8)	47 (19.8)	1.0
Enteral feeding — no. (%)	44 (18.6)	28 (11.8)	0.04

Table 4. Multivariate Model of the Risk of *Clostridium difficile*–Associated Diarrhea According to the Use of Antibiotics among Case Patients, as Compared with Matched Controls, January 11 through June 26, 2004.*

Antibiotic	Odds Ratio	95% Confidence Interval
Any cephalosporin	3.8	2.2–6.6
First-generation	2.4	1.2–4.6
Second-generation	6.0	2.1–17.5
Third-generation	3.0	1.4–6.8
Any fluoroquinolones	3.9	2.3–6.6
Ciprofloxacin	3.1	1.8–5.4
Gatifloxacin or moxifloxacin	3.4	1.5–7.7
Levofloxacin	0.6	0.2–1.9
Clindamycin	1.6	0.5–4.8
Aminoglycosides	0.7	0.3–1.9
Macrolides	1.3	0.6–2.9
Intravenous vancomycin	1.3	0.5–3.1
Penicillins combined with β-lactamase inhibitor	1.2	0.7–2.3
Penicillins	0.7	0.3–2.9
Carbapenems	1.4	0.3–6.3

Toxin production by an emerging strain of *Clostridium difficile* associated with outbreaks of severe disease in North America and Europe

Michel Warny, Jacques Pepin, Aiqi Fang, George Killgore, Angela Thompson, Jon Brazier, Eric Frost, L Clifford McDonald

www.thelancet.com Vol 366 September 24, 2005

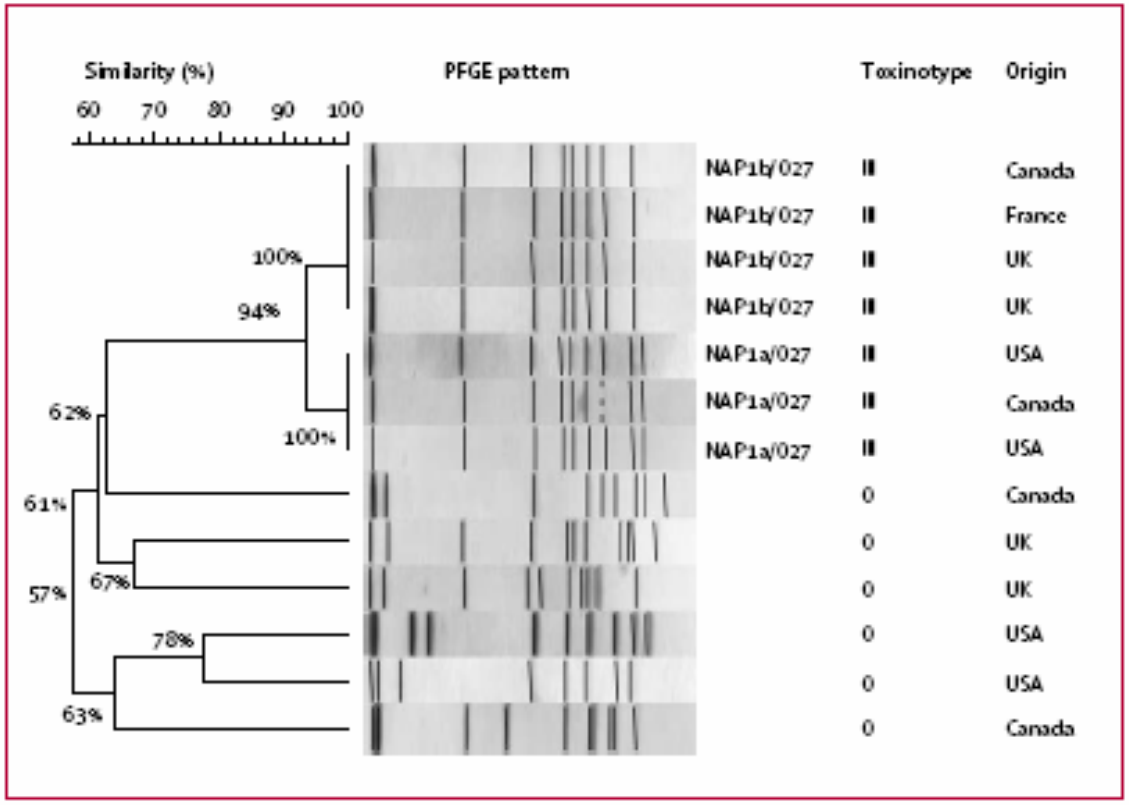


Figure 1: PFGE analysis of *C difficile* study isolates from various geographical locations

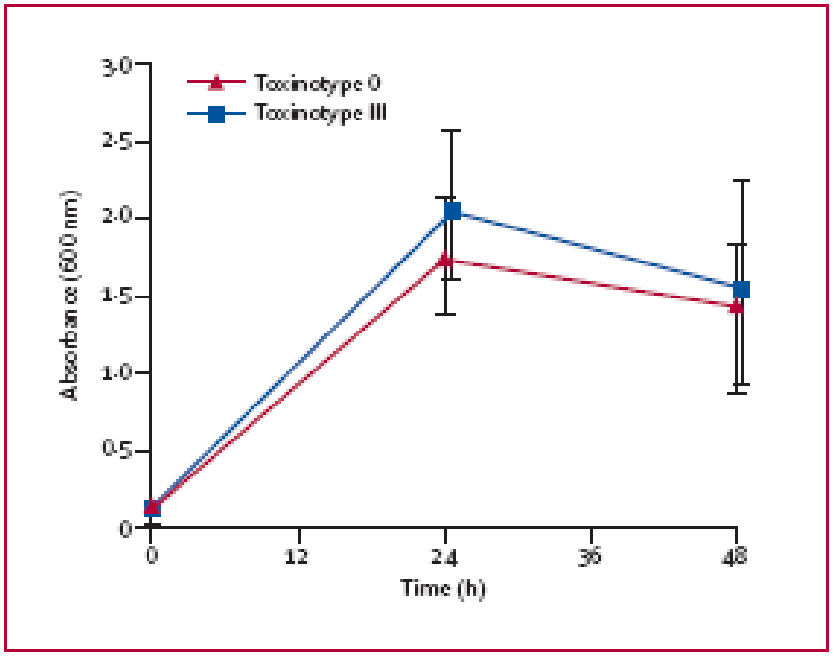


Figure 2: Growth curves of toxinotype 0 and toxinotype III (NAP1/027)
Mean cell density and SDs are shown.

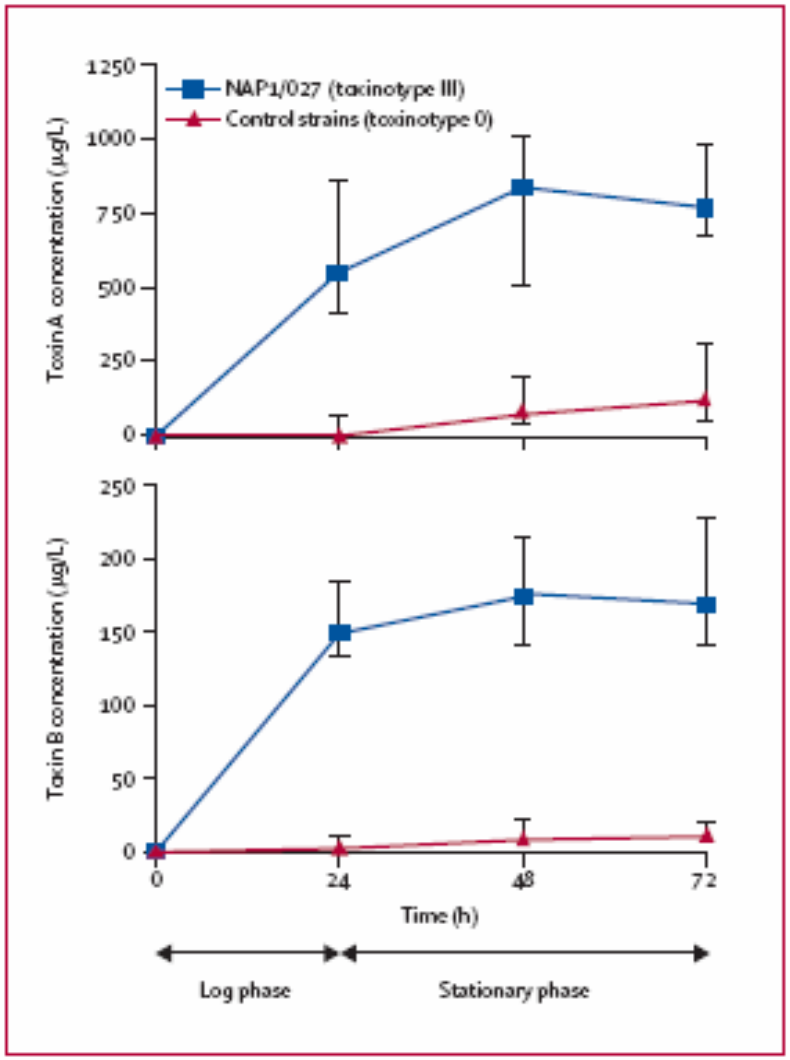
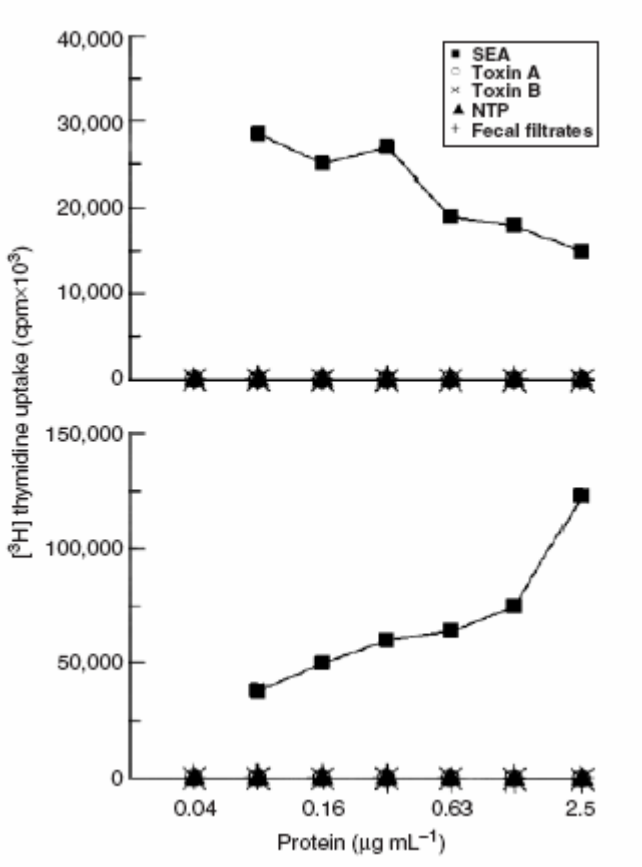


Figure 3: In vitro production of toxins A and B by *C difficile* isolates
Median concentration and IQRs are shown. *C difficile* strains included 25 toxinotype 0 and 15 NAP1/027 strains (toxinotype III) from various locations.

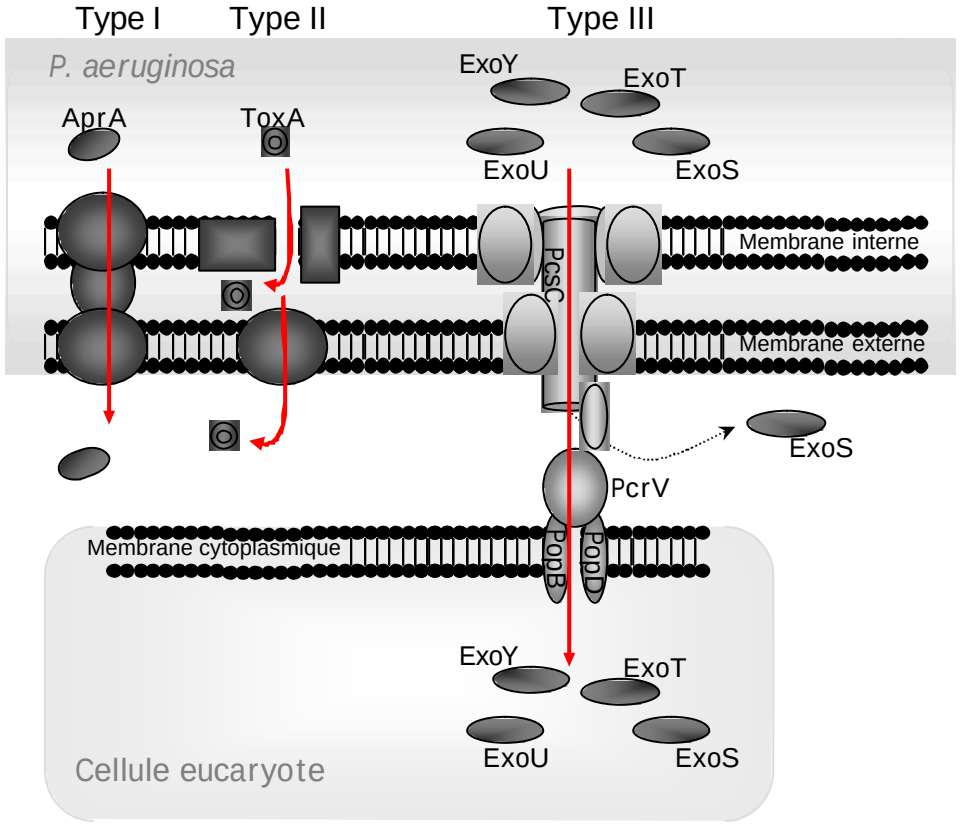
Clostridium difficile lacks detectable superantigen activity

Anna Wanahita[1], Beckley Davis[3], Richard J. Hamill[2], Elizabeth A. Goldsmith[1], John R. Rodgers[3], Richard G. Cook[3], James G. Lamphear[3] & Daniel M. Musher[2,3]

[1]Michael E. Debakey Veterans Affairs Medical Center, Houston; and [2]Departments of Medicine, Molecular Virology and Microbiology and [3]Immunology, Baylor College of Medicine, Houston, Texas, USA



Pseudomonas aeruginosa



- Berthelot, P. et al. "**Genotypic and phenotypic analysis of type III secretion system in a cohort of Pseudomonas aeruginosa bacteremia isolates: evidence for a possible association between O serotypes and exo genes**." J.Infect.Dis. 188.4 (2003): 512-18.
- Hauser, A. R. et al. "**Type III protein secretion is associated with poor clinical outcomes in patients with ventilator-associated pneumonia caused by Pseudomonas aeruginosa**." Crit Care Med. 30.3 (2002): 521-28.
- Roy-Burman, A. et al. "**Type III protein secretion is associated with death in lower respiratory and systemic Pseudomonas aeruginosa infections**." J.Infect.Dis. 183.12 (2001): 1767-74.

Epigenetic acquisition of inducibility of type III cytotoxicity in *P. aeruginosa*

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- Certaines souches de *P. aeruginosa* ont un SSTT non inductible
- Présence d'une boucle de régulation positive sur le promoteur ExsA
- Possibilité d'un switch épigénétique du caractère inductible/non inductible

An indirect enzyme-linked immunosorbent assay for rapid and quantitative assessment of Type III virulence phenotypes of *Pseudomonas aeruginosa* isolates

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Annals of Clinical Microbiology and Antimicrobials

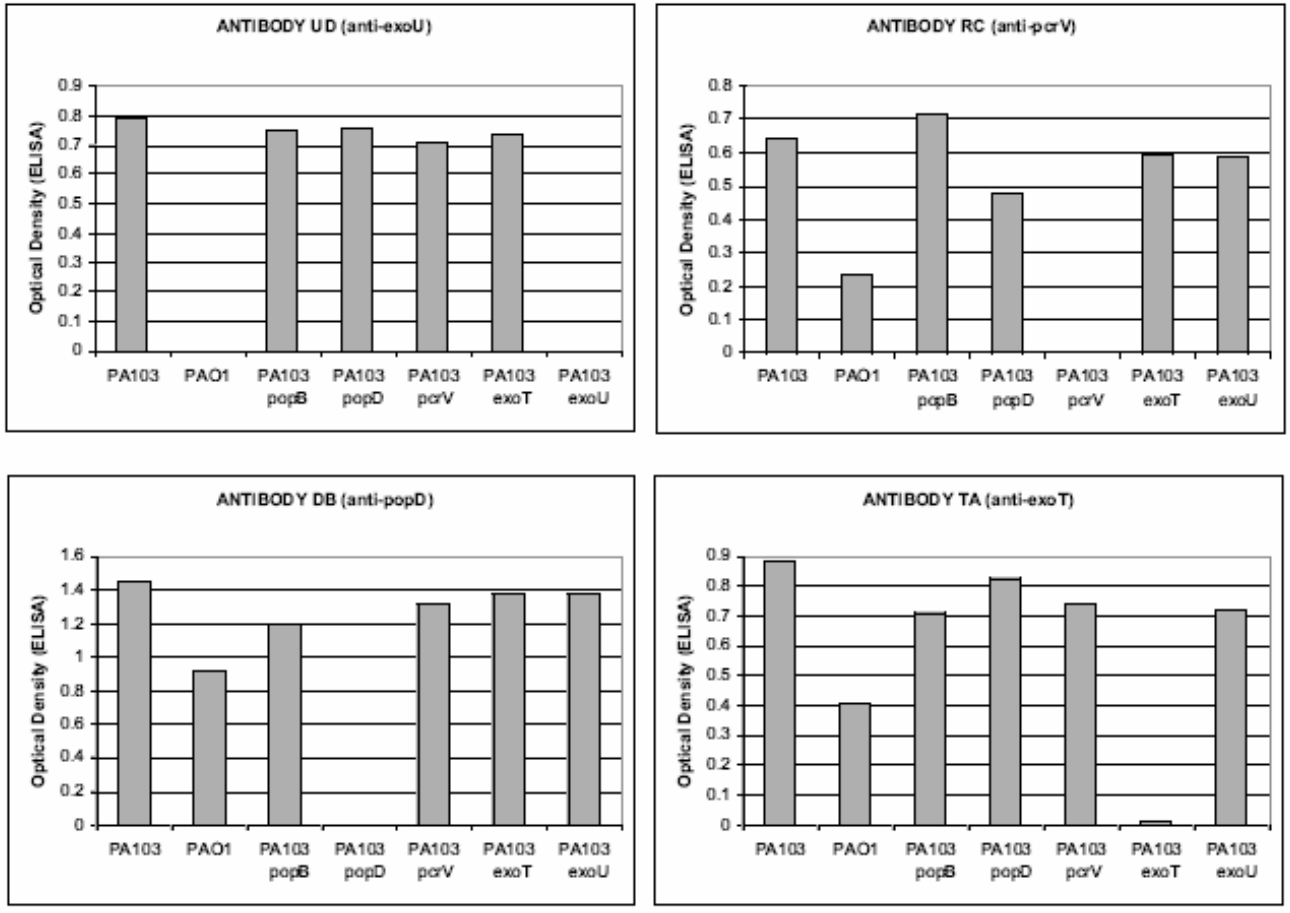

Table 4: Genotypes and phenotypes determined for 74 clinical isolates.

Genotype[a]		Phenotype[b]		Cell Rounding[c]	Cytotoxicity[c]
exoU+ *exoT*+ *popD*+ *pcrV*+	17	ExoU+ ExoT+ PopD+ PcrV+	15	14/15	14/15
		ExoU- ExoT- PopD- PcrV-	2	0/2	0/2
exoU- *exoT*+ *popD*+ *pcrV*+	55	ExoU- ExoT+ PopD+ PcrV+	46	44/46	0/31
		ExoU- ExoT- PopD- PcrV-	7	2/7	N.D.
		other[d]	2	1/2	N.D.
exoU- *exoT*- *popD*- *pcrV*-	2	ExoU- ExoT- PopD- PcrV-	2	0/2	N.D.