

The Canadian experience with molecular typing methods for *C. difficile*: PFGE, PCR ribotyping and genome sequencing

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Canadian Nosocomial Infection Surveillance Program (est. 1995)

Canadian Hospital Epidemiology Committee (CHEC) AMMI-
Canada

32 members in 9 provinces; 52 hospitals
12 with LTCFs; 13 adult & pediatrics, 8 pediatric facilities

AND

Health Care-Acquired Infections Division (Ottawa) and
Antimicrobial Resistance and Nosocomial Infections Lab,
National Microbiology Laboratory (Winnipeg), PHAC

Incidence and Severe Outcomes for CDI

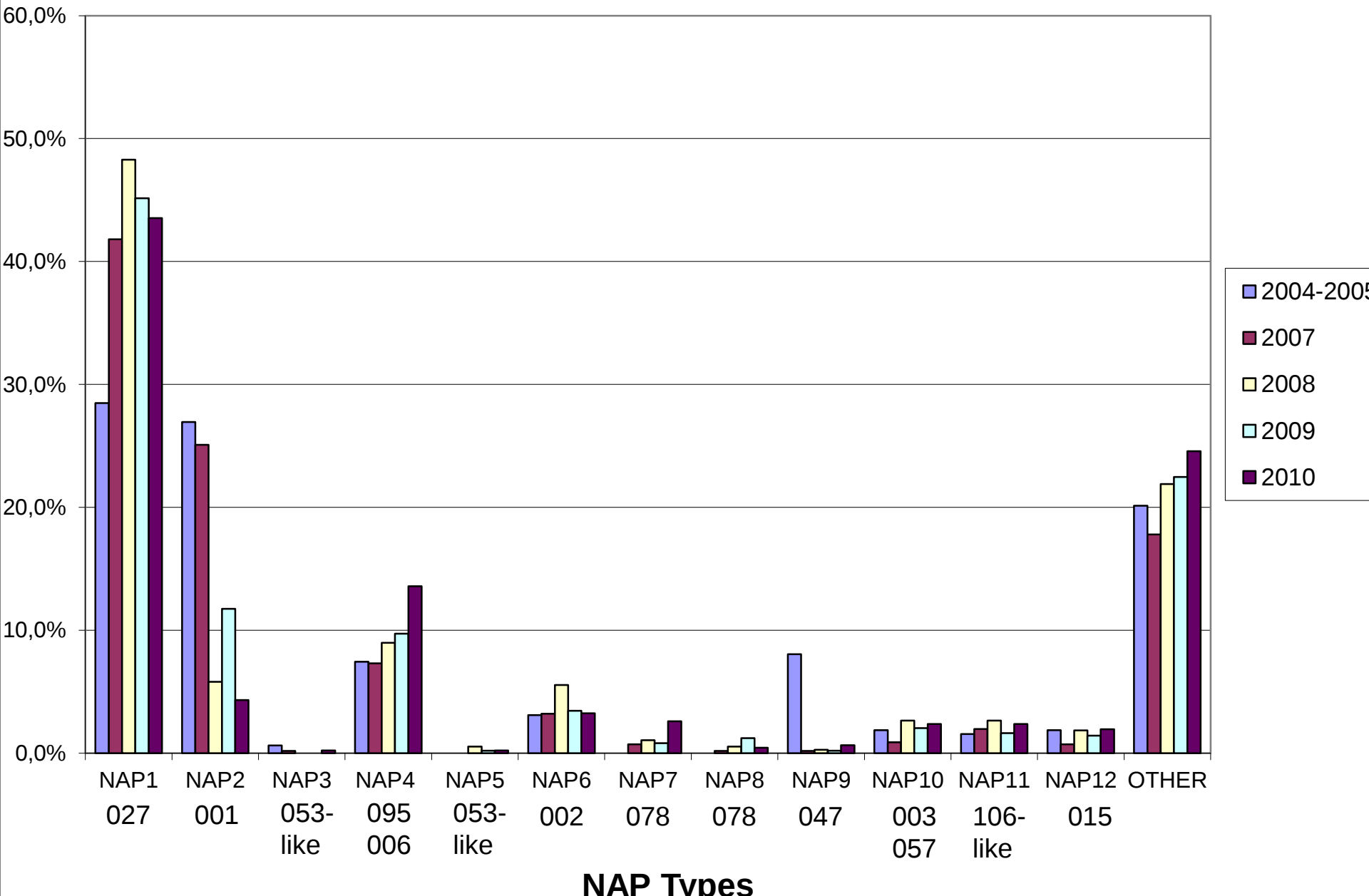
Canadian Nosocomial Infection Surveillance Program

	2004/05	2007	2008	2009	2010	2011*
Incidence (per 1,000 patient-admissions)	4.5	4.5	5.5	4.7	4.3	4.5
Incidence (per 10,000 patient-days)	6.4	6.9	7.0	5.8	6.3	5.3
Colectomy	1.0%	1.4%	2.0%	1.6%	1.2%	
ICU Admission	2.0%	2.2%	1.0%	2.2%	5.6%	
All Deaths	16.3%	15.5%	12.7%	14.3%	13.5%	
Attributable Deaths	5.6%	4.8%	4.8%	2.4%	5.4%	
Directly related	2.1%	1.4%	1.6%	0.1%	1.1%	
Indirectly related	3.5%	3.4%	3.2%	2.2%	4.3%	

*Incidence rates based on 9-months surveillance



National Distribution of NAP Types (2004-2010)



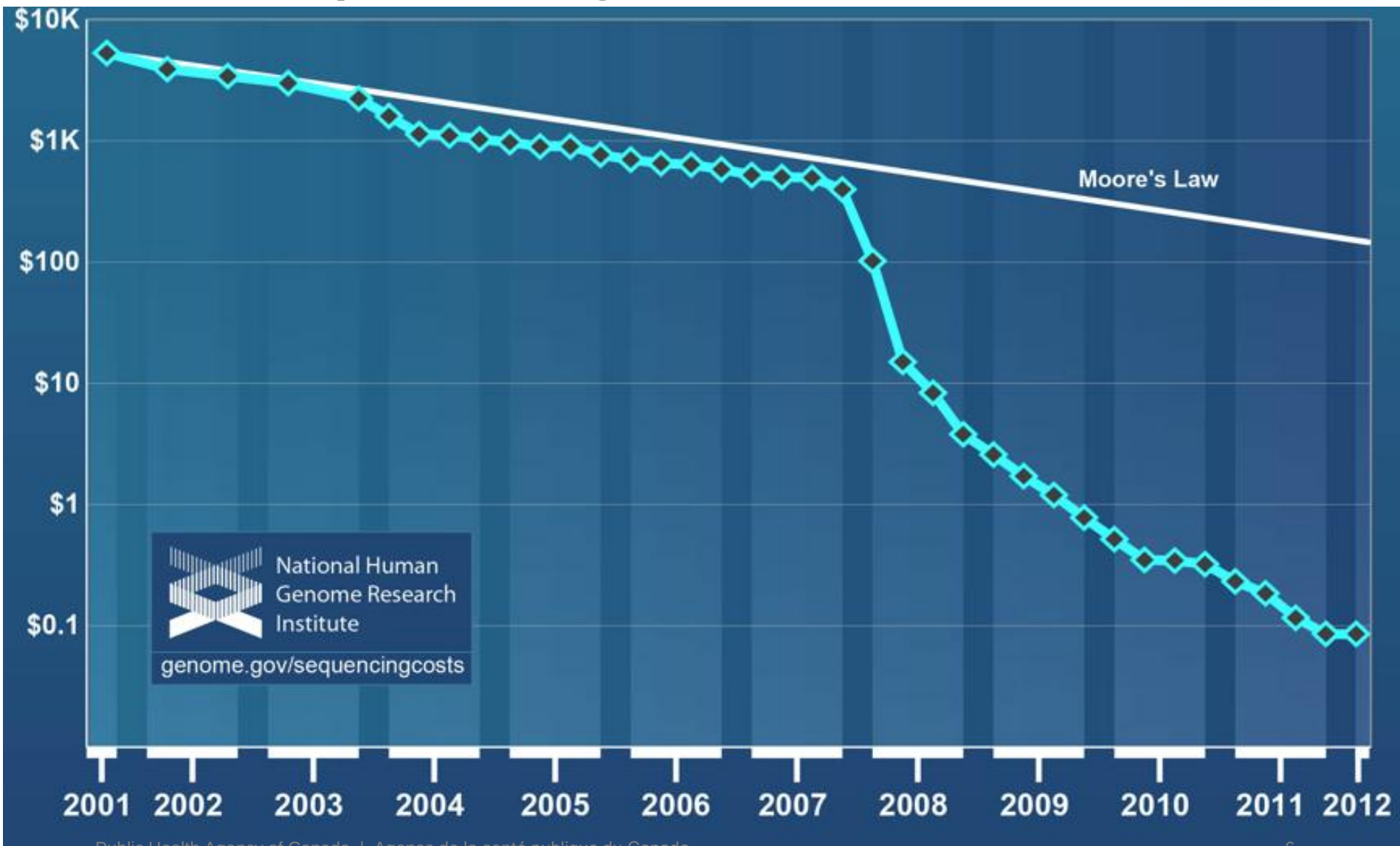


Future of *C. difficile* typing in Canada?

C. difficile Typing Future

- Currently working with Duncan MacCannell (CDC), Ed Kuijper (Leiden U), Mark Wilcox (Leeds) to standardize PCR-ribotyping
- Global database for comparing ribotypes in Bionumerics
- Future is whole genome sequencing

Sequencing Costs Plummet



Database of Food-Borne Pathogen Genomes Created

Bridget M. Kuehn

A NEW FREE PUBLIC DATABASE OF the genomes of 100 000 food-

nella strains to the database. Scientists from the FDA and CDC will provide expertise and guidance for the project, and these agencies, along with the US De-

A NEW FREE PUBLIC DATABASE OF the genomes of 100 000 food-borne pathogens will help speed investigations of food-borne illnesses, according to the US Food and Drug Administration (FDA). The FDA has part-

redients, finished products, and environmental samples collected during outbreaks of food-borne illness.

The FDA will contribute more than 500 whole genome sequences of *Salmo-*

countermeasure. We see this project as a way to improve quality of life for a great many people, while minimizing a major business risk for food producers and distributors." □

tion-deficit/hyperactivity disorder (ADHD), drug treatment also may prevent some children from falling behind in math.



Miodrag Gajic/Stockphoto.com

Researchers in Iceland studied 236 children born between 1994 and 1996 who began ADHD treatment, primarily with Ritalin (methylphenidate), between the fourth and seventh grades. Math scores of children who began drug treatment within 12 months of their fourth-

terchangeable with an FDA-licensed biological product.

<http://tinyurl.com/cvvpv4u>

For more on these stories and other medical news, visit <http://newsatjama.jama.com/>.

ORIGINAL ARTICLE

Rapid Whole-Genome Sequencing for Investigation of a Neonatal MRSA Outbreak

Claudio U. Köser, B.A., Matthew T.G. Holden, Ph.D., Matthew J. Ellington, D.Phil., Edward J.P. Cartwright, M.B., B.S., Nicholas M. Brown, M.D., Amanda L. Ogilvy-Stuart, F.R.C.P., Li Yang Hsu, M.R.C.P., Claire Chewapreecha, B.A., Nicholas J. Croucher, M.A., Simon R. Harris, Ph.D., Mandy Sanders, B.Sc., Mark C. Enright, Ph.D., Gordon Dougan, Ph.D., Stephen D. Bentley, Ph.D., Julian Parkhill, Ph.D., Louise J. Fraser, Ph.D., Jason R. Betley, Ph.D., Ole B. Schulz-Trieglaff, Ph.D., Geoffrey P. Smith, Ph.D., and Sharon J. Peacock, Ph.D., F.R.C.P.



A pilot study of rapid benchtop sequencing of *Staphylococcus aureus* and *Clostridium difficile* for outbreak detection and surveillance

David W Eyre,^{1,2} Tanya Golubchik,^{2,3} N Claire Gordon,^{1,2} Rory Bowden,^{2,3,4} Paolo Piazza,⁴ Elizabeth M Batty,^{2,3} Camilla L C Ip,^{2,3} Daniel J Wilson,^{1,4} Xavier Didelot,^{2,3} Lily O'Connor,^{1,5} Rochelle Lay,⁵ David Buck,⁴ Angela M Kearns,⁶ Angela Shaw,⁷ John Paul,⁸ Mark H Wilcox,⁹ Peter J Donnelly,⁴ Tim E A Peto,^{1,2,5} A Sarah Walker,^{1,2,10} Derrick W Crook^{1,2,5}



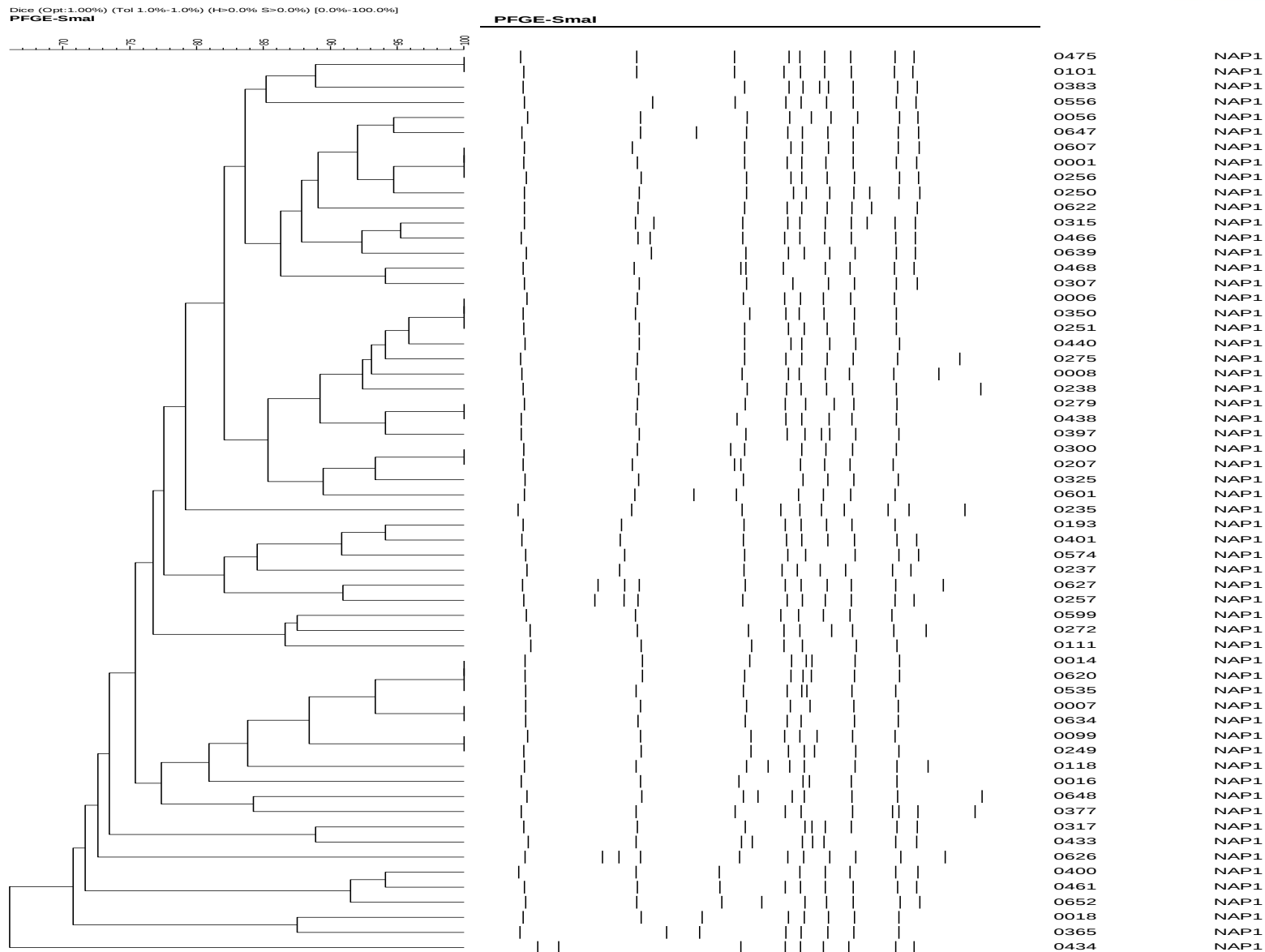
Tracking a Hospital Outbreak of Carbapenem-Resistant *Klebsiella pneumoniae* with Whole-Genome Sequencing

Evan S. Snitkin *et al.*

Sci Transl Med 4, 148ra116 (2012);

DOI: 10.1126/scitranslmed.3004129

NAP1 PFGE Subtypes (n=59)

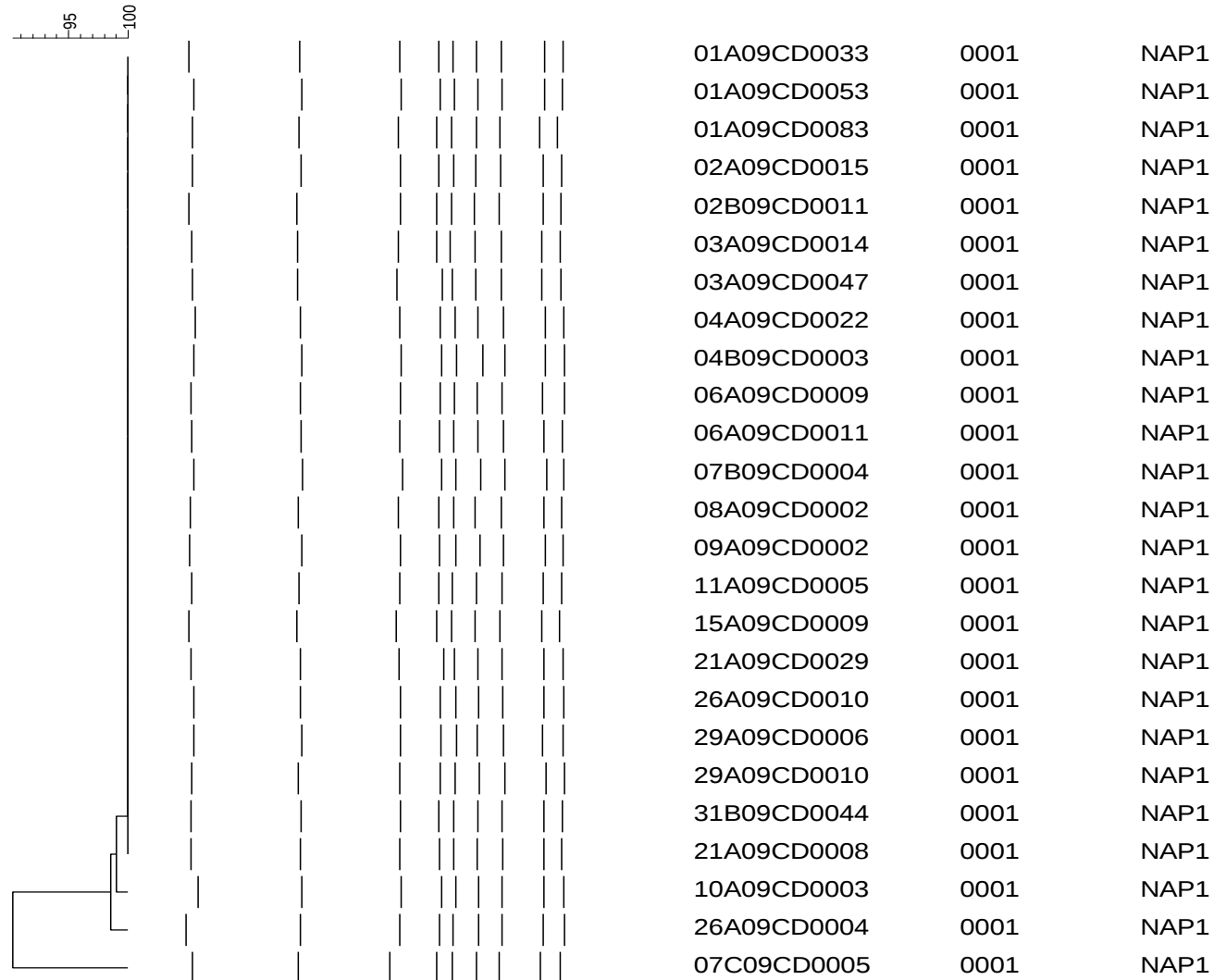


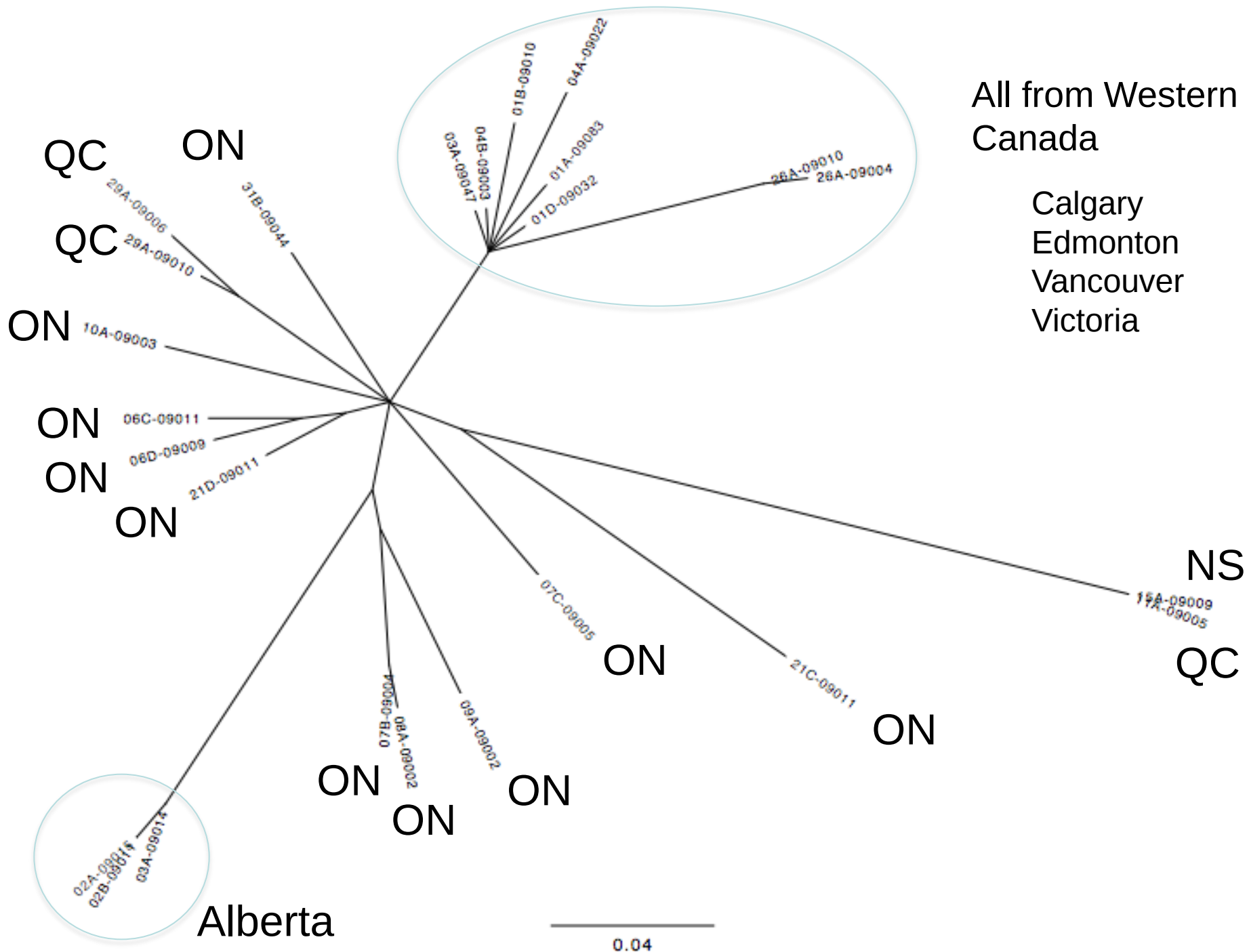
NAP1/027 Genomes Sequenced from 2009

Dice (Opt:1.00%) (Tol 1.0%-1.0%) (H>0.0% S>0.0%) [0.0%-100.0%]

PFGE-Smal

PFGE-Smal



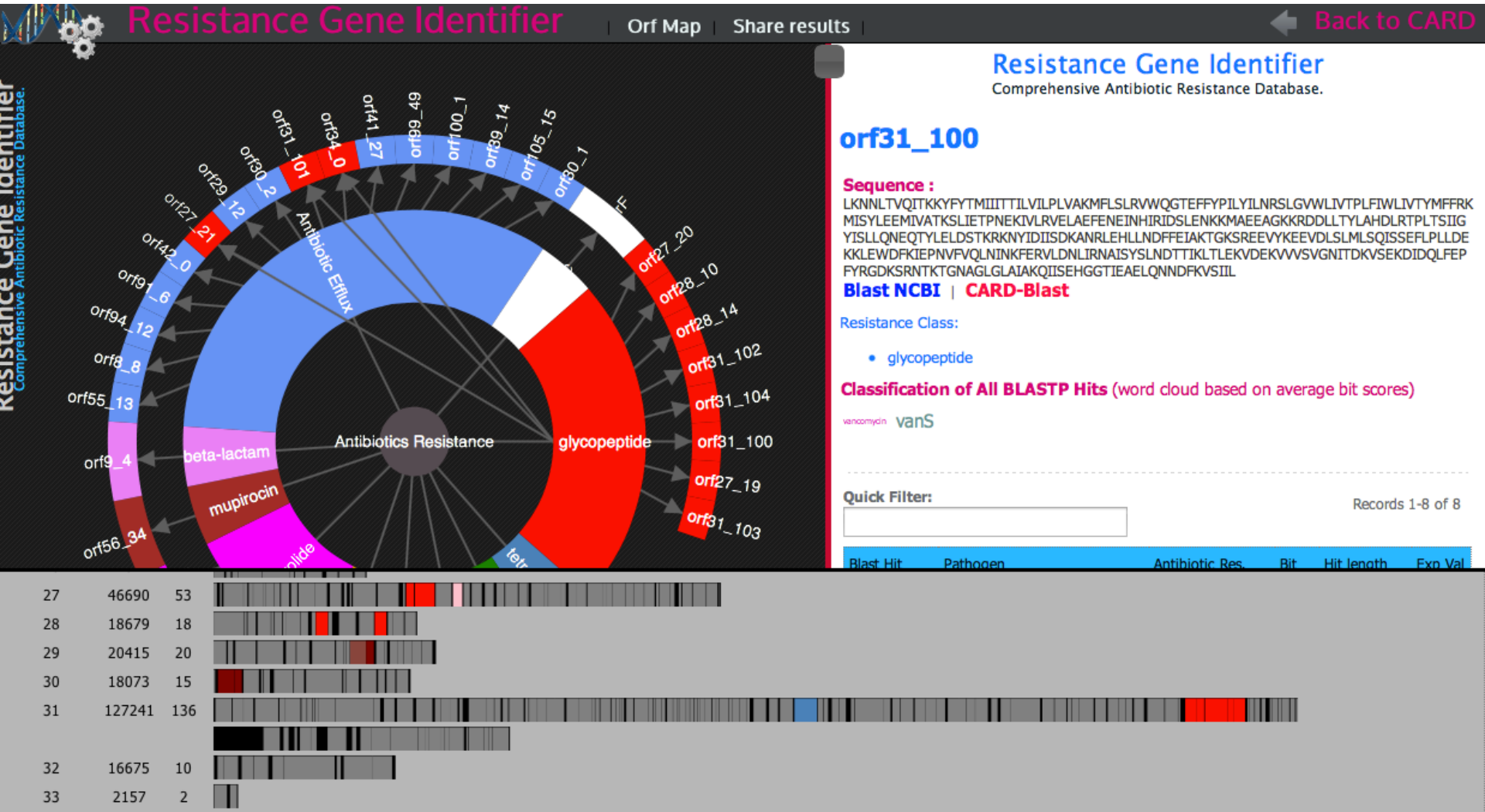


Need Standards

- Bioinformatics tools
- Warehousing of the data
- Need more studies with epidemiologic data to determine how to interpret the data during outbreaks
- Need to develop standards for data analysis
 - Core genome only?
 - Rules for filtering out low confidence SNVs
- Data sharing agreements/data ownership
- User friendly software package that can quickly do the types of analysis and data sharing we need – ie. BioNumerics

The Comprehensive Antibiotic Resistance Database

<http://arpcard.mcmaster.ca>



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