while the remaining genes, including attP, int, xis, Ea region, ant moron, and genes involved in regulation, immunity, serotype conversion and recombination are transcribed in the opposite direction. Complete genome analysis showed that SfX differs significantly from SfV but shares homology in several regions with Sf6 (13,14). There were also two SfII prophage genomes available from genome sequenced 2a strains 2457T and Sf301 (15,16), however most phage related genes in these two prophage genomes are absent. No homologous genes between SfII and SfX could be identified.

SfX was compared with 403 double stranded DNA phage genome sequences publicly available (www.ebi.ac.uk/genomes/phage.html) by BLASTP and was found to be most closely related to four members of phage P22 from Salmonella (10). It also shares considerable homology with five P22-like phages including HK620 and CUS-3(18,19). Based on the number of genes shared, the left side (encoding genes for virion head) is more similar to P22 while the right side (Nin region, genes for later regulation and lysis) is more similar to P22-like phages HK620 and CUS-3. Interestingly the immunity and replication regions of SfX is dissimilar to P22 and P22-like phages but shares homology

with lambda-like phages, HK97, 2851, YYZ-2008, StxI and StxII, although HK97 is unusual in that the right side is similar to P22-like phages . Therefore SfX is a mosaic phage with its genome coming from three different origins.

Genome comparison of SfX with P22 and Sf6 revealed that SfX uniquely shares nine genes with P22 . Since both phages are prevalent and are responsible for epidemics, those genes are likely to be associated with epidemic strength. The functions of these genes are all related to phage fitness, including three involved in virion assembly, two in integration and excision and two in immunity. Therefore, these genes may play an important role in the epidemic behavior of SfX and P22.

Prevalent serotypes carry serotype converting phages of higher epidemic strength

It has long been observed that certain serotypes of S.flexneri are more prevalent than others (4,6), Historically serotype 2a has been regarded as the leading serotype but recently a number of other serotypes including serotype X variant we reported previously have become frequent (11). These serotypes are often involved in epidemics and their isolation reflects how many people they infect and thus we called these

serotypes with high isolation rate as epidemic serotypes, while those with low isolation rate as nonepidemic serotypes. Based on our analysis of nine-year data in China, five serotypes, X variant, V, 2a, 1a, 2b, are epidemic serotypes.

Epidemic serotypes are not independent clones with different genetic background to give them advantage as most of the isolates studied belong to the same clone. We have shown previously that a single clone of S. flexneri defined by MLST as ST91 is predominant and frequent serotype switching occurs within the clone. This led us to conclude that the epidemic strength of certain serotypes is due to their serotype-converting phages. Converting serotype frequency to phage frequency using the known relationship allowed us to identify the three most prevalent serotype-converting phages in China: SfX, SfII and SfI, which were present in 97% of the 1608 isolates studied with the other three phages, SfIV, Sf6 and SfV, together being represented by a mere 3%. Clearly, SfX, SfII and SfI have a much higher epidemic strength than SfIV, Sf6 and SfV.

The O antigen modification genes (gtrs) are not deterministic factors to epidemic fitness

of a phage

The genetic determinants for epidemic strength of serotype-converting phages of high epidemic strength such as SfX, SfII and SfI cannot be attributed to the gtr genes that modify the O antigens. In S. flexneri, the specificity of all serotypes except Sf6 encoded by three genes (gtrABC) involved in a three-step process of the glucosylation of the O antigen (4). There is significant homology of the gtrAB genes but little homology of the gtrC gene was identified among these phages, including SfX of S. flexneri and P22 of Salmonella. Both high and low epidemic strength phages have highly homologous gtrAB genes, and there is no evidence that gtrC gene is correlated with epidemic behavior of serotypes it encoded.

Classification of serotype converting phages by epidemic strength applies across species

It was interesting to find that SfX, a phage with high epidemic strength, was only closely related with phage P22 which is also a serotype-converting phage in Salmonella. P22 is present in several common Salmonella serovars including Typhimurium which causes up to 40% of Salmonella infections(8). In a recent study P22 was found to be present in 76.9% (117 of 152) of serovar Typhimurium isolates collected from human,

animal and food sources during 2001 to 2003 in Slovakia(3). Such a high frequency of P22 in Salmonella isolates suggests that it can also be regarded as a phage with high epidemic strength similar to SfX in S. flexneri. The widespread presence of P22 within and among Salmonella serovars adds further support to the classification of serotype converting phages into high and low epidemic strength and this classification is applicable across species.

Phage genes related to phage fitness determine the epidemic potential of a phage

From comparison of SfX and P22, both of which are serotype-converting phages with high epidemic strength, with phages of low epidemic strength, we identified nine highly homologous genes shared only by these two phages as high epidemic strength genes. Apart from the two genes of unknown function, the other seven genes are related to phage functions with three in virion assembly, two in integration and excision and two of immunity. Although it is not obvious how these genes are related to epidemic strength, these genes play a critical role in the life cycle of a phage. These genes may confer a higher fitness to the phages. This will lead to increased frequency of a serotype carrying these phages. Thus phage fitness determines the epidemic potential of a

serotype. Further studies are required to dissect the precise mechanisms.

References:

1. Allison, G. E. and N. K. Verma. 2000. Serotype-converting bacteriophages and O-antigen modification in Shigella flexneri. Trends Microbiol. 8:17-23.
2. Clemens, J. D., K. L. Kotloff, and B. Kay. 1999. Generic protocol to estimate the burden of Shigella diarrhoea and dysenteric mortality. World Health Organization .
3. Drahovska, H., E. Mikasova, T. Szemes, A. Ficek, M. Sasik, V. Majtan, and J. Turna. 2007. Variability in occurrence of multiple prophage genes in Salmonella Typhimurium strains isolated in Slovak Republic. FEMS Microbiol. Lett. 270:237-244.
4. Guan, S., D. A. Bastin, and N. K. Verma. 1999. Functional analysis of

the O antigen glucosylation gene cluster of Shigella flexneri bacteriophage SfX. Microbiology 145 (Pt 5):1263-1273.

5. Guan, S., D. A. Bastin, and N. K. Verma. 1999. Functional analysis of the O antigen glucosylation gene cluster of Shigella flexneri bacteriophage SfX. Microbiology 145 (Pt 5):1263-1273.

6. Guan, S., D. A. Bastin, and N. K. Verma. 1999. Functional analysis of the O antigen glucosylation gene cluster of Shigella flexneri bacteriophage SfX. Microbiology 145 (Pt 5):1263-1273.

7. Hans-Wolfgang Ackermann and Michael S.DuBow. 1987. Viruses of Prokaryotes. CRC Press.

8. Lan, R., P. R. Reeves, and S. Octavia. 2009. Population structure, origins and evolution of major Salmonella enterica clones. Infect. Genet. Evol. 9:996-1005.

9. Lindberg, A. A. 1997. Bacterial surface polysaccharides and phage adsorption. Academic Press .

10. Vander, B. C. and A. M. Kropinski. 2000. Sequence of the genome of Salmonella bacteriophage P22. J. Bacteriol. 182:6472-6481.

11. Ye, C., R. Lan, S. Xia, J. Zhang, Q. Sun, S. Zhang, H. Jing, L. Wang, Z. Li, Z. Zhou, A. Zhao, Z. Cui, J. Cao, D. Jin, L. Huang, Y. Wang, X. Luo, X. Bai, Y. Wang, P. Wang, Q. Xu, and J. Xu. 2010. Emergence of a new multidrug-resistant serotype X variant in an epidemic clone of Shigella flexneri. J. Clin. Microbiol. 48:419-426.

12. Ye, C., R. Lan, S. Xia, J. Zhang, Q. Sun, S. Zhang, H. Jing, L. Wang, Z. Li, Z. Zhou, A. Zhao, Z. Cui, J. Cao, D. Jin, L. Huang, Y. Wang, X. Luo, X. Bai, Y. Wang, P. Wang, Q. Xu, and J. Xu. 2010. Emergence

of a new multidrug-resistant serotype X variant in an epidemic clone of Shigella flexneri. J. Clin. Microbiol. 48:419-426.

13. Ye, C., R. Lan, S. Xia, J. Zhang, Q. Sun, S. Zhang, H. Jing, L. Wang, Z. Li, Z. Zhou, A. Zhao, Z. Cui, J. Cao, D. Jin, L. Huang, Y. Wang, X. Luo, X. Bai, Y. Wang, P. Wang, Q. Xu, and J. Xu. 2010. Emergence of a new multidrug-resistant serotype X variant in an epidemic clone of Shigella flexneri. J. Clin. Microbiol. 48:419-426.

14. Ye, C., R. Lan, S. Xia, J. Zhang, Q. Sun, S. Zhang, H. Jing, L. Wang, Z. Li, Z. Zhou, A. Zhao, Z. Cui, J. Cao, D. Jin, L. Huang, Y. Wang, X. Luo, X. Bai, Y. Wang, P. Wang, Q. Xu, and J. Xu. 2010. Emergence of a new multidrug-resistant serotype X variant in an epidemic clone of Shigella flexneri. J. Clin. Microbiol. 48:419-426.

STUDY TITLE: Organization of PFGE Workshop for Training and Technology transfer for Asia Pacific countries/ areas in February 2011

STUDY FACILITY: (Name and address of institute)

Public Health Laboratory Centre, 7/F,

382 Nam Cheong Street, Shek Kip Mei,
Kowloon, Hong Kong.

STUDY DIRECTOR:

(name of the research director) Signature, date

Dr. Kai Man KAM, M.D.

Project leader:

Haruo Watanabe, M.D. Ph.D.
Deputy Director-General
National Institute of Infectious Diseases
Toyama 1-23-1, Shinjuku-ku
Tokyo 162-8640, Japan

:

Issue Date: February 28, 2011.

1) **OBJECTIVE:**

(1) To organize a Workshop to enhance the laboratory capacity of countries/ areas in Asia and Pan Pacific region in performing PFGE in February 2011;

(2) To train up key laboratory personnel so they acquire the ability to build up the laboratory capacities in their own country/ area;

(3) To build up a network of trainer and trainees that have shared experiences in PFGE laboratory work, and which can work together in partnership during outbreak investigations.

2) **STUDY DESIGN:**

(1) Organization of Workshop in the Public Health Laboratory Centre in Hong Kong for training of laboratory personnel in the Asia Pacific Region in February 22- 25, 2011.

(2) Co-organizers were: NIID, Japan; CDC, USA.

(3) The Public Health Laboratory Centre in Hong Kong was responsible for the use of fund monies of 2,000,000 yen in the overall organization of the Workshop.

(4) The Workshop took place in the Public Health Laboratory Centre in Hong Kong.

(5) The Workshop lasted 4 days and covered the setting up of PFGE laboratory data analysis software, requisite computer technique, commonly encountered problems, quality control/ quality assurance issues, and network requirements.

3) **RESULTS:**

(1) Participants of the Workshop had hands-on experience in performing PFGE' data analysis and management. (listed Appendix I)

(2) PFGE Data input and analysis in relation to outbreak investigations were also covered in the Workshop. (Schedule in Appendix II)

(3) Key trainers from advanced institutions (including NIID, Japan and CDC, USA) were invited to participate in the Workshop.

(4) Evaluation of the Laboratory Workshop by participants were done to gather experiences for development of future work in the Asia Pacific Region. (Appendix III)

(5) A report was generated after the Workshop.

Appendix I

Participants List for PulseNet Asia Pacific PFGE Workshop 2011 (22 -25 FEB 2011)

		Name	Sex	Email	Institution	Arrival Date	Departure Date
1	**Trainer**	Mr. Steven Stroika	M	fru3@cdc.gov	Division of Foodborne, waterborne and Environmental Diseases National Center for emerging and zoonotic infectious diseases Centers for Disease Control and Prevention, USA	19 Feb	26 Feb
2	**Trainer**	Ms Kristy Kubota	F	kristy.kubota@aphl.org	Association of Public Health Laboratories, USA	20 Feb	25 Feb
3	**Trainer**	Dr. Jun Terajima	M	terajima@nih.go.jp	Department of Bacteriology National Institute of Infectious Diseases, Japan	21 Feb	26 Feb
4	**Trainer**	Dr. M. Kuroda	M	makokuro@nih.go.jp	Pathogen Genomics Center National Institute of Infectious Diseases, Japan	23 Feb	25 Feb
5	Trainee	Ms Anne Lee	F	Anne_LEE@ava.gov.sg	Veterinary Public Health Laboratory Division Agri-Food and Veterinary Authority, Singapore	21 Feb	27 Feb
6	Trainee	Ms Ngoi Soo Tein	F	ngoisootein@hotmail.com	Microbiology Division, Institute of Biological Science Faculty of Science, University of Malaya, Malaysia	20 Feb	26 Feb
7	Trainee	[c]Shah Manzur Rashed	M	rashed_mb@yahoo.com	Laboratory Sciences Division, ICDDR,B Bangladesh	21 Feb	26 Feb
8	Trainee	Mohammed Badrul Amin	M	bmbamin@icddrb.org	Laboratory Sciences Division, ICDDR,B Bangladesh	21 Feb	26 Feb
9	Trainee	Jinghua Cui	F	cuijinghua@icdc.cn	National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, PR China	21 Feb	26 Feb
10	Trainee	Xiaoli Du		Duxiaoli@icdc.cn	National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, PR China	21 Feb	26 Feb
11	Trainee	Chen Hongyou 陈洪友	M	hychen@scdc.sh.cn	Shanghai Municipal Center for Disease Control and Prevention, PR China	21 Feb	26 Feb
12	Trainee	Mei Qu	F	meiqu@126.com	Beijing Center for Disease Control and Prevention, PR China	21 Feb	26 Feb

Appendix II

Agenda for PulseNet Asia Pacific PFGE Workshop Hong Kong 2011

Date: February 22- 25, 2011

Venue: Conference Room at Public Health Laboratory Centre (PHLC), Hong Kong

February 22, 2011 (Tuesday)

Chairperson of the day: Jun Terajima

Time	Activities	Speakers/Modulators
8:30 am	Shuttle from Hotel to PHLC	
9:00 am	Arrive at PHLC	
9:05 – 9:15 am	Registration	
9:15 – 9:30 am	Welcome remarks, expectations of the Workshop	KM Kam, PHLC, HK Kristy Kubota, APHL, USA Steven G. Stroika, CDC, USA Jun Terajima, NIID, Japan
9:30 – 9:45 am	Overview of Workshop	Danny Cheung, PHLC, HK
9:45 – 10:20 am	Installation and Overview of BioNumerics/ PulseNet MasterScripts	Steven Stroika, CDC, USA
10:20 – 10:30 am	Group Photo	
10:30 – 11:00 am	Coffee Break	
11:00 – 11:40 am	Analysis of PFGE Gel Images, Linking Gel Lanes, and Entering Data	Cindy Luey, PHLC, HK
11:40 – 1:00 pm	Exercise 1: Analyze a PFGE Gel Image and Link Entries to a Database	Cindy Luey, PHLC, HK
1:00 – 2:00 pm	Lunch	
2:00 – 2:30 pm	PulseNet USA: Overview of Molecular Subtyping Network for Foodborne Diseases Surveillance	Kristy Kubota, APHL, USA
2:30 – 2:45 pm	Creation and File Location of PulseNet Bundle Files	Kristy Kubota, APHL, USA
2:45 – 3:45 pm	Exercise 2: Prepare and Create a PulseNet Bundle File for Distribution	Kristy Kubota, APHL, USA
3:45 – 4:00 pm	Coffee Break	
4:00 – 4:15 pm	Laboratory Experience Sharing- Singapore	Participant presentation
4:15 – 4:30 pm	Laboratory Experience Sharing - Malaysia	Participant presentation
4:30 – 5:00 pm	Q and A	
5:00 pm	End of Day 1 – Shuttle back to Hotel	

February 23, 2011 (Wednesday)

Chairperson of the day: Jun Terajima

Time	Activities	Speakers/Modulators
8:30 am	Shuttle from Hotel to PHLC	
9:00 am	Arrive at PHLC	
9:05 – 9:20 am	Data Importing into and Exporting from BioNumerics	Alf Chu, PHLC, HK
9:20 – 10:30 am	Exercise 3: Analyze a PFGE Gel Image; Data Import into and from BioNumerics	Alf Chu, PHLC, HK
10:30 – 11:00 am	Coffee Break	
11:00 – 11:45 am	Querying and Performing Comparisons in BioNumerics	Steven Stroika, CDC, USA
11:45 – 1:00 pm	Exercise 4: Query the Database and Perform Comparisons	Steven Stroika, CDC, USA
1:00 – 2:00 pm	Lunch	
2:00 – 2:20 pm	Advanced Queries of Local Databases	Cindy Luey, PHLC, HK
2:20 – 3:00 pm	Exercise 5: Query the Database Using the Advanced Query Tools	Cindy Luey, PHLC, HK
3:00 – 3:30 pm	QA/QC and Factors that Influence Data Analysis	Kristy Kubota, APHL, USA
3:30 – 3:45 pm	Coffee Break	
3:45 – 4:15 pm	Identify the Problems	Steven Stroika, CDC, USA
4:15 – 4:30 pm	Laboratory Experience Sharing – China (Chinese CDC)	Participant presentation
4:30 – 4:45 pm	Laboratory Experience Sharing – China (Beijing CDC)	Participant presentation
4:45 – 5:00 pm	Q and A	
5:00 pm	End of Day 2 – Shuttle back to Hotel	

February 24, 2011 (Thursday)

Chairperson of the day: Jun Terajima

Time	Activities	Speakers/Modulators
8:30 am	Shuttle from Hotel to PHLC	
9:00 am	Arrive at PHLC	
9:00 – 9:20 am	Database Management Tools	Cindy Luey, PHLC, HK
9:20 –9:40 am	Exercise 6: Database Settings and Layouts, Pick List and Printing Reports	Cindy Luey, PHLC, HK
9:40 – 10:25 am	Use of Groups and the Chart and Statistics Tool	Steven Stroika, CDC, USA
10:25 – 11:10 am	Exercise 7: Create Charts and Graphs to Create Reports	Steven Stroika, CDC, USA
11:10 – 11:40 am	Coffee Break	
11:40 – 12:10 pm	Extended Forum (Open to all PHLC colleagues)	APHL, USA
12:10 – 12:40 pm	Extended Forum (Open to all PHLC colleagues)	NIID, Japan
12:40– 1:10 pm	Extended Forum (Open to all PHLC colleagues) **Genome analysis of multi-drug resistance Salmonella Typhimurium strain**	Dr. Makoto Kuroda, NIID, Japan
1:10 – 2:10 pm	Lunch	
2:10 – 2:30 pm	PulseNet Communication	Kristy Kubota, APHL, USA
2:30 – 3:00 pm	Composite Data Sets	Alf Chu, PHLC, HK
3:00 – 3:30 pm	Exercise 9: Cluster analysis using a composite data set for *Salmonella*	Alf Chu, PHLC, HK
3:30 – 3:45 pm	Coffee Break	
3:45 – 4:05 pm	Life of a Cluster in PulseNet USA	Steven Stroika, CDC, USA
4:05 – 4:20 pm	Laboratory Experience Sharing – China (Shanghai Municipal CDC)	Participant presentation
4:20 – 4:35 pm	Laboratory Experience Sharing – Bangladesh (ICDDR, B)	Participant presentation
4:35 – 5:00 pm	Q and A	
5:00 pm	End of Day 3 – Shuttle back to Hotel	

February 25, 2011 (Friday)

Chairperson of the day: Jun Terajima

Time	Activities	Speakers/Modulators
8:30 am	Shuttle from Hotel to PHLC	
9:00 am	Arrive at PHLC	
9:00 – 9:30 am	PIC WG Update	Dr. Edman Lam, PHLC, HK
9:30 – 9:50 am	Naming Patterns and Creating Local Unique Pattern Lists	Kristy Kubota, APHL, USA
9:50– 10:45 am	Exercise 10: Identifying and Naming Unique Patterns in the database	Kristy Kubota, APHL, USA
10:45– 11:00 am	Coffee Break	
11:00 – 1:00 pm	<*Split group session*> Demo on PFGE protocols (Group A) Practical Session on BioNumerics with vibrios (Group B)	Demo by APHL, USA and PHLC, HK BioNumerics practices by CDC, USA
1:00 – 2:00 pm	Lunch	
2:00 – 4:00 pm	<*Split group session*> Demo on PFGE protocols (Group B) Practical Session on BioNumerics with vibrios (Group A)	Demo by APHL, USA and PHLC, HK BioNumerics practices by CDC, USA
4:00 – 4:15 pm	Coffee Break	
4:15 – 5:00 pm	Discussion Summary Certificate presentation	All participants KM Kam, PHLC, HK Kristy Kubota, APHL, USA Steven G. Stroika, CDC, USA Jun Terajima, NIID, Japan
5:00 pm	End of Workshop – Shuttle back to Hotel	

WORKSHOP EVALUATION

Course name: The Eighth PulseNet Asia Pacific PFGE Workshop

Location: Public Health Laboratory Centre (PHLC), 382 Nam Cheong Street
Shek Kip Mei, Kowloon, Hong Kong

Dates: February 22-25, 2011

Offered by:
- Public Health Laboratories Centre (PHLC), Department of Health, Hong Kong
- Association of Public Health Laboratories (APHL)
- National Institute of Infectious Diseases (NIID), Department of Bacteriology, Japan
- PulseNet Program, Enteric Diseases Laboratory Branch (EDLB), Centers for Disease Control and Prevention (CDC), USA

Please complete this evaluation so that we can improve this workshop when it is given again.

1. What is your overall evaluation of this course?

Excellent_____ Good_____ Satisfactory_____ Unsatisfactory_____

2. Were the objectives of the course clearly defined? Yes____ No____

3. Were the objectives of the course met? Yes____ No____

4a. Please rate the quality and usefulness of handouts.

Excellent_____ Good_____ Satisfactory_____ Unsatisfactory_____

4b. Please rate the quality and usefulness of the practices.

Excellent_____ Good_____ Satisfactory_____ Unsatisfactory_____

5. Please rate how this course will influence your ability to perform and interpret molecular subtyping of *Salmonella* serotypes,
E. coli, Shigella, Listeria, Campylobacter, Vibrio and other organisms in the future.

Very positively_____ Positively_____ Not much_____ Not at all_____

6. Would you recommend this course to others in public health laboratories? Yes_____ No_____
Please explain:

7. Please rate each of the following lectures:

"Subject Matter": 1 = material was not at all pertinent; 5 = it was very pertinent
"Presentation": 1 = material was not at all clear; 5 = it was very clear
"Time Allotted": TS = lecture was too short; S = short; R = right amount of time; L = long; TL = lecture was too long

Date of sessions: Feb 22, 2011

	Subject Matter					Presentation					Time Allotted				
A. Installation and Overview of BioNumerics/ MasterScripts	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
B. Analyzing of PFGE Gel Images, Linking Gel Lanes, and Entering Data			1	2	3	4	5	1	2	3	4	5	TS	S	R
			L	TL											
C. Exercise 1: Analyzing a PFGE Gel Image and Link Entries to Database			1	2	3	4	5	1	2	3	4	5	TS	S	R
			L	TL											
D. PulseNet USA: Overview of Molecular Subtyping Network for Foodborne Diseases Surveillance	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
E. Creation and File Location of PulseNet Bundle Files	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
F. Exercise 2: Prepare and Create a PulseNet Bundle file for Distribution			1	2	3	4	5	1	2	3	4	5	TS	S	R
			L	TL											

Date of sessions: Feb 23, 2011

	Subject Matter					Presentation					Time Allotted				
A. Data Importing into and Exporting from BioNumerics	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
B. Exercise 3: Analyze a PFGE Gel Image; Import Data from Excel			1	2	3	4	5	1	2	3	4	5	TS	S	R
L TL															
C. Querying and Performing Comparisons in BioNumerics	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
D. Exercise 4: Query the Database and Perform Comparisons			1	2	3	4	5	1	2	3	4	5	TS	S	R
L TL															
E. Advanced Queries and Plugin Tools	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
F. Exercise 5: Query the Database Using the Advanced Query Tools			1	2	3	4	5	1	2	3	4	5	TS	S	R
L TL															
G. QA/QC and Factors that Influence Data Analysis	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
H. Identify the Problems	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL

Date of sessions: Feb 24, 2011

	Subject Matter					Presentation					Time Allotted				
A. Database Management Tools	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
B. Exercise 6: Database Settings and Layout, Pick List Printing Reports	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
C. Use of Groups and the Chart and Statistics Tool	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
D. Exercise 7: Create Charts and Graphs to Create Reports	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
E. PulseNet Communication	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
F. Composite Data Sets	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
G. Exercise 8: Cluster analysis using a Composite Data Set For *Salmonella*	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
H. Life of a cluster in PulseNet USA	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL

Date of sessions: Feb 25, 2011

	Subject Matter					Presentation					Time Allotted				
A. PIC WG Update	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
B. Naming Patterns and Creating Local Unique Pattern Lists	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
C. Exercise 9: Identifying and Naming Unique Patterns in the databasae	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
D. Demo on PFGE protocols	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL
E. Practical Session on BioNumerics with *Vibrios*	1	2	3	4	5	1	2	3	4	5	TS	S	R	L	TL

8. Do you have suggestions for any topics that were not included in this course that should be included in future courses?

9a. What activities did you find most helpful in the computer laboratory?

9b. What activities did you find least helpful in the computer laboratory?

10. Was the time allotted for each topic or practice session appropriate? Yes_____ No_____

a. For which activities should more time be allowed?

b. For which activities should less time be allowed?

11. In your opinion, should we have this course again for other PulseNet participating Laboratories?
Yes_____ No_____ _____

12. Other comments about course:

Name (Optional):_____ Date: _____