



LABORATORY TRENDS



December 21, 2011

Laboratory News

Genome BC Water Grant

Earlier in 2011, PHMRL leaders Drs. Patrick Tang and Judy Isaac-Renton, along with Drs. Natalie Prystajeky and Jennifer Gardy and supported by many colleagues across BC and Canada, were awarded a Genome BC grant for the large-scale genomics study, *Applied Metagenomics of the Watershed Microbiome*.

The current model of water quality monitoring and assessment is one that is based on a reactive framework. The project will use metagenomics to identify novel microbial watershed biomarkers and develop tools to characterize source attributes of both healthy and contaminated watersheds that may have complex land use pressures. This will be a new approach to detecting changes to watershed health by enabling earlier recognition of possible causes of pollution further upstream of treatment.

Lead by Dr. N. Prystajeky, a further grant linked to the Genome Canada study, funded by the Canadian Water Network, was also awarded. This project will enable better laboratory practices for monitoring water across Canada.

Dr. William Hsiao is the newest member of the PHMRL and will assist in this project by lending his bioinformatics expertise. Dr. Hsiao also brings a wealth of genomics and computational microbiology knowledge to the various PHMRL Programs as we move towards improved molecular detection methods. Dr. Hsiao will lead in development of microbial genomics capacity including facilitating exchanges at the national level.



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Foodborne *Salmonella* Outbreak

An outbreak of *Salmonella* Enteritidis at a catered event occurred early in November. The Environmental Microbiology and Bacteriology and Mycology Programs at the PHMRL supported Vancouver Coastal Health in its investigation of the outbreak. Over 100 attendees and staff became ill at the event and tiramisu was identified as the infected food source.

All positive samples submitted to PHMRL were characterized as phage type 13a and had Pulsed Field Gel Electrophoresis pattern SENXAI.0006. Both 13a and SENXAI.0006 are commonly found in chicken and poultry products, such as the eggs, that would have been used to make the dessert.

S. Enteritidis is the most common *Salmonella* serotype in BC; since 2007, *S. Enteritidis* cases have increased each year by an average of 14-36%.

Holiday Wishes

The Public Health Microbiology & Reference Laboratory would like to wish our colleagues a wonderful holiday season. We look forward to new and continued collaborations in 2012!



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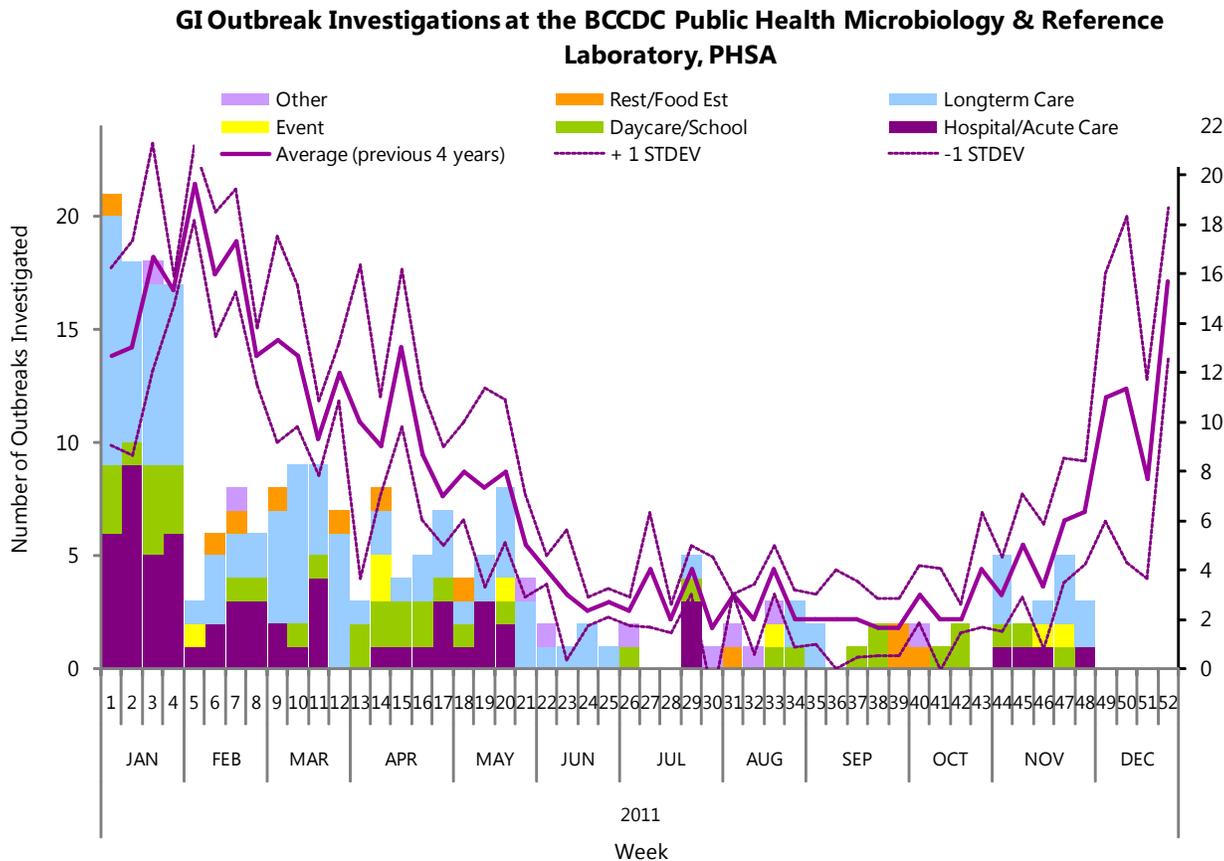


Gastrointestinal Outbreaks

In November, there were 18 gastrointestinal (GI) outbreaks investigated at the PHMRL. Outbreaks were identified from 9 longterm care facilities, 4 daycare/schools, 3 hospitals, and 2 events (Figure 1). Norovirus was confirmed for 3 of these outbreaks, *E. coli* O157:H7 in another, while the events had *Staphylococcus aureus* and *Salmonella* Enteritidis as the respective causative agents.

The data available are from outbreaks in which the PHMRL has been notified. Some acute care microbiology laboratories are also testing for norovirus in the province and these data do not include outbreaks from Vancouver Island Health Authority. Given the nature of GI outbreaks, samples are not always available for testing.

Figure 1 [Gastrointestinal outbreaks investigated since January, 2011, Environmental Microbiology, Bacteriology & Mycology, Parasitology and Virology Programs, PHMRL.](#)



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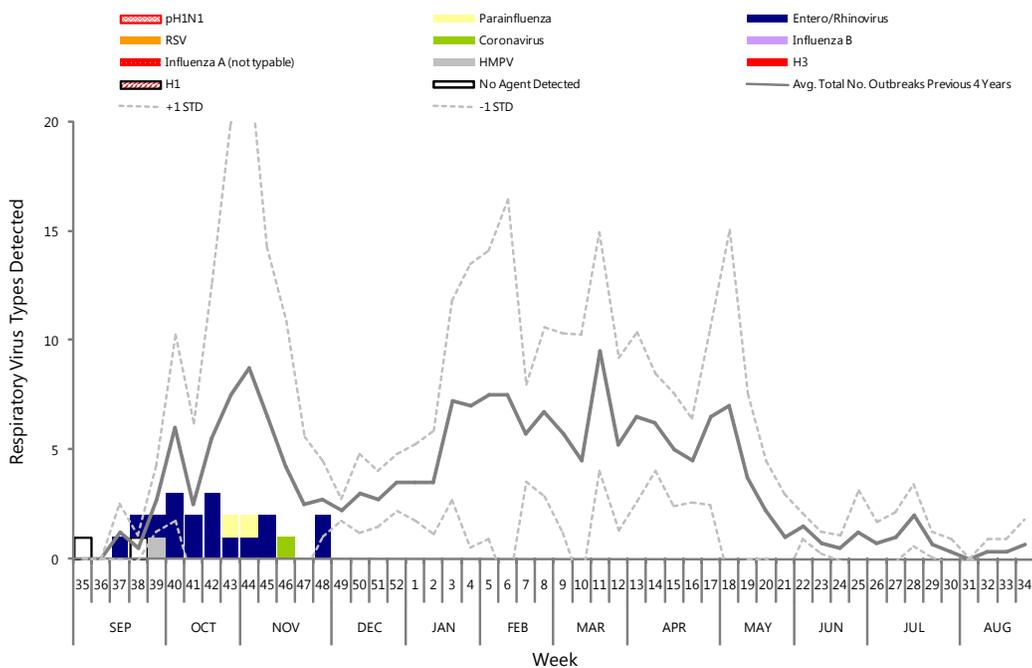


Respiratory Outbreaks

In November, samples were submitted from 7 longterm care facilities for outbreak investigation at the PHMRL (Figure 2). Using PCR and Luminex methods, enterovirus/rhinovirus were detected in 4 facilities, while parainfluenza, coronavirus and adenovirus were detected in the 3 the remaining facilities, respectively. Figure 2 reflects respiratory sample results submitted for investigation to the PHMRL and is not representative of respiratory outbreaks in the entire BC community.

Figure 2 Respiratory outbreaks investigated by respiratory season, Virology Program, PHMRL.

Respiratory Outbreaks Investigations at the BCCDC Public Health Microbiology & Reference Laboratory, 2010-2011 Season



Carbapenemase Resistant Enterobacteriaceae (CRE)

The latest counts for cases of carbapenemase resistance can be found in Table 1 (updated from our October 2011 issue). 12 cases with the New Delhi Metallo-β-lactamase gene (NDM) endemic to South Asia have been detected since this work began in 2010. Two cases had the *Klebsiella pneumoniae* carbapenem (KPC) β-lactamase gene (one case with KPC as well as a Verona integron-encoded metallo-β-lactamase (VIM) gene) and 1 case with only the VIM gene. No cases with the IMP-type β-lactamase have been detected. Carbapenem resistance has been isolated in a variety of organisms including *E. coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Citrobacter freundii*, *Morganella morganii* and *Enterobacter cloacae*.

Table 1. Carbapenem Resistant Enterobacteriaceae Detected, Bacteriology & Mycology Program, PHMRL.

Type	No. of Cases	Comments
NDM	12	
KPC	2	1 case also harboured the VIM gene
VIM	1	In addition to above KPC/VIM case
IMP	none	



Influenza Surveillance

Volumes for respiratory testing have been consistently higher than this time last season for weeks 44-48 (Figure 3). Influenza A (H3N2) was the major virus type detected this period (Table 2).

National influenza trends continue at low levels of detection. More information can be found on the FluWatch website at <http://www.phac-aspc.gc.ca/fluwatch/index-eng.php>.

Overall influenza activity in the northern hemisphere and Asia was reported as being low for this period with the exception of some areas of Central America. Influenza activity was sporadic but decreasing in the southern hemisphere with circulation of A(H1N1)pdm09, A(H3N2) and B viruses as they enter their inter-seasonal period (WHO, 2 Dec 2011 Update).

Figure 3 Respiratory testing volumes and influenza percent positivity, Virology Program, PHMRL.

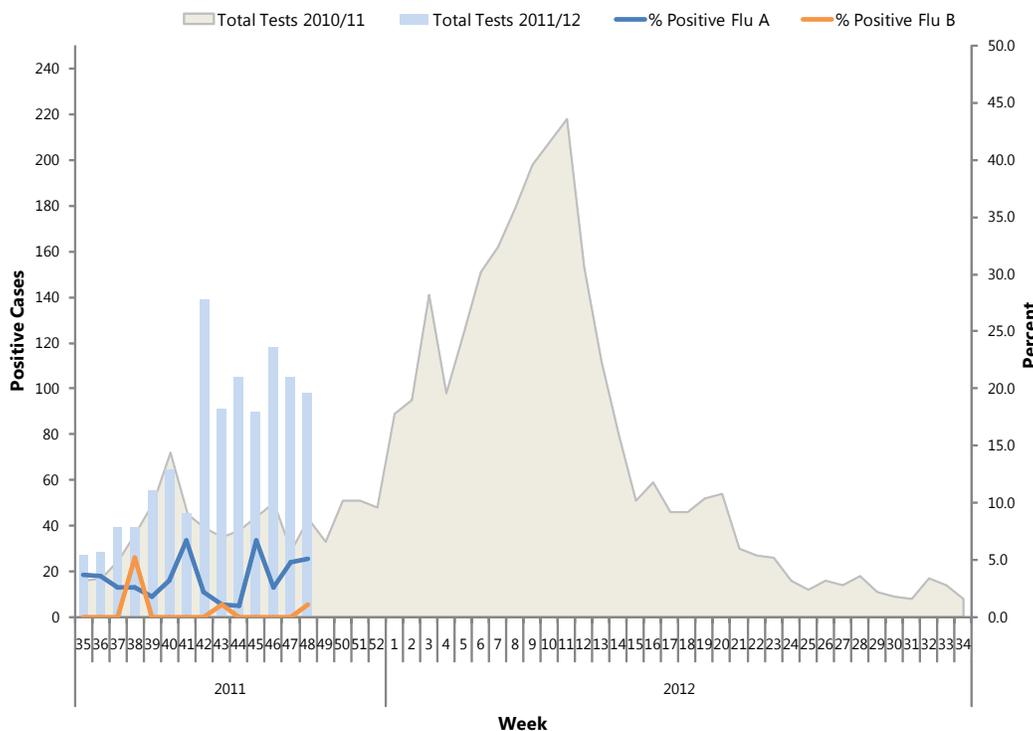


Table 2 Positive influenza A and B detections for weeks 44-48 (October 30-December 3, 2011, Virology Program, PHMRL). (H1N1)pdm09 refers to the 2009 influenza A(H1N1) pandemic virus.

	Week 44	Week 45	Week 46	Week 47	Week 48
Number of Specimens Tested	117	92	122	116	112
Number of Positive Specimens	1 (0.85%)	6 (6.52%)	3 (2.46%)	6 (5.17%)	6 (5.36%)
Influenza A	1 (0.85%)	6 (6.52%)	3 (2.46%)	6 (5.17%)	5 (4.46%)
(H1N1)pdm09					
sH3N2	1 (0.85%)	6 (6.52%)	3 (2.46%)	6 (5.17%)	5 (4.46%)
Not typeable					
Influenza B					1 (0.89%)



Norovirus Sequencing

Norovirus sequencing is one of the services provided by the Environmental Microbiology Program of PHMRL. This molecular tool has the potential to provide information for outbreak investigation including outbreak identification and source tracking as well as further knowledge on changing dynamics of the genome by offering information on the circulation of genotypes.

In previous years, the target segment of the norovirus genome sequenced at PHMRL was the polymerase gene (region B). However, starting from July 1, 2010 the target sequence was changed to the capsid gene (region C). This change was initiated in order to standardize norovirus sequence comparability with that of the rest of Canada since different target sequences (i.e. region B and C) are not comparable.

Table 3
Norovirus genotypes sequenced at PHMRL, 2008-2011.

Genotype	Region B			Region C	
	2008	2009	2010 (Jan 1 to Jun 30)	2010 (Jul 1 to Dec 31)	2011 (Jan 1 to Aug 31)
GI.1	0	0	0	0	2
GI.14	0	0	0	0	2
GI.2	0	1	2	0	0
GI.3B	10	0	0	0	0
GI.4	0	2	2	1	0
GI.6	0	0	0	1	0
GII.1	0	6	5	1	0
GII.10	1	0	0	0	0
GII.12	8	2	0	2	0
GII.14	0	0	0	1	0
GII.16	0	0	1	0	0
GII.2	1	0	0	1	0
GII.3	0	0	0	1	2
GII.4G	6	13	43	0	0
GII.4G/J/K	0	0	0	0	1
GII.4H	8	2	0	0	0
GII.4I	135	71	44	6	3
GII.4J/K	0	0	0	0	9
GII.4K	0	0	0	54	95
GII.6	1	5	0	1	2
GII.7	2	6	0	0	1
GII.8	0	1	1	0	0
GII.9	1	0	0	0	0

Norovirus genotypes detected from 2008 through 2011 are listed in Table 3. GII.4 are the predominate genotypes for norovirus outbreaks reported in BC. Genogroup I norovirus, which is highly associated with foodborne or waterborne transmission, only occurs sporadically in BC. In 2008 there was only one genogroup I strain (GI.3B) present in BC; unfortunately it is unknown why GI.3B dominated in 2008.

ViroNet Canada is a national BioNumerics database for norovirus genomic sequence information. This Canadian Public Health Laboratory Network initiative not only provides a repository of sequence data but supports a communication platform between partner members across Canada.

Staff in all Programs of the PHMRL were recently introduced to some of the new laboratory genomic analytic tools. A Super-Users team, lead by Dr. William Hsiao, will work on following up to further develop our public health microbiology genomics pipeline.

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