06/07/2011 - Thursday				
Time	Туре	Abstract #	Title	Speaker
7:30 - 8:30am	Breakfast	x	Breakfast Buffet	Sponsored by NEB
8:30 - 8:45	Intro	x	Welcome Back	Chris Detter
x	Session Chair	x	Session Chairs	Chair - Patrick Chain Chair - Nadia Fedorova
8:45 - 9:30	Keynote	FF0042	Environmental Reservoirs of Human Pathogens: The Vibrio cholerae Paradigm	Dr. Rita Colwell
9:30 - 9:50	Speaker 1	FF0185	A Rapid Whole Genome Sequencing and Analysis System Supporting Genomic Epidemiology	Mike FitzGerald
9:50 – 10:10	Speaker 2	FF0173	Endosymbiont Hunting in the Metagenome of Asian Citrus Psyllid (<i>Diaphorina citri</i>)	Surya Saha
10:10 - 10:30	Speaker 3	FF0221	SPAdes: A New Genome Assembly Algorithm and its Applications to Single-Cell Sequencing	Glenn Tesler
10:30 – 10:50	Break	x	Beverages and Snacks Provided	x
10:50 – 11:10	Speaker 4	FF0263	Assembly of Large Metagenome Data Sets Using a Convey HC-1 Hybrid-Core Computer	Alex Copeland
11:10 – 11:30	Speaker 5	FF0034	Metagenomic Assembly: Challenges, Successes, and Validation	Matt Scholz
11:30 – 11:50	Speaker 6	FF0208	Metagenomics for Etiological Agent Discovery	Matthew Ross
11:50 – 12:10	Speaker 7	FF0207	Nearly Finished Genomes Produced Using Gel Microdroplet Culturing Reveals Substantial Intraspecies Diversity within the Human Microbiome	Michael Fitzsimons
12:10 - 1:30pm	Lunch	x	La Fiesta Plaza Lunch	Sponsored by Agilent
x	Session Chair	x	Session Chairs	Chair - Mike Fitzgerald Chair - Alla Lapidus
1:30 - 1:50	Speaker 8	FF0006	Rapid Phylogenetic and Functional Classification of Short Genomic Fragments with Signature Peptides	Ben McMahon
1:50 - 2:10	Speaker 9	FF0229	PanFunPro: Pan-Genome Analysis Based on the Functional Profiles	Oksana Lukjancenko
2:10 - 2:30	Speaker 10	FF0114	Preparation of Nucleic Acid Libraries for Personalized Sequencing Systems Using an Integrated Microfluidic Hub Technology	Kamlesh Patel
2:30 - 2:50	Speaker 11	FF0142	Capturing Native Long-Range Contiguity by in situ Library Construction and Optical Sequencing	Jerrod Schwartz
2:50 - 3:10	Speaker 12	FF0256	Fosmid Cre-LoxP Inverse PCR Paired-End (Fosmid CLIP-PE), A Novel Method for Generating Fosmid Pair-End Library	Ze Peng
3:10 - 3:30	Speaker 13	FF0282	Automated Sequencing Library Preparation and Suppression for Rapid Pathogen Characterization	Todd Lane
3:30 - 3:50	Speaker 14	FF0109	Evaluation of Multiplexed 16S rRNA Microbial Population Surveys Using Ilumina MiSeq Platform	Julien Tremblay
3:50 - 4:00pm	Closing Discussions	x	Closing Discussions for General Meeting - Discuss Next Year's Meeting	Chair - Chris Detter
		x	Reminder for those interested there is a special Forensic's Session Friday from 8:00am - 12:30pm	x