

SMBE Satellite Workshop

on Genome Evolution in Pathogen Transmission and Disease

22-25 February 2016

PROGRAM

MONDAY 22nd

16:00	17:30		Welcome reception and poster session 1 Opening talks
17:30	18:05	Tetsuya Hayashi	Nation-wide high-resolution phylogenomic analysis of <i>Rickettsia japonica</i> in Japan
18:05	18:40	Susan Holmes	Using all the data for analyses of the Human Microbiome
19:00			DINNER

TUESDAY 23rd

8:30	9:05	Nigel French	Incursion, evolution and transmission of zoonotic pathogens in an isolated ecosystem: three tales from New Zealand
9:05	9:40	Stephen Beres	Population pathogenomics of a current ongoing <i>Streptococcus pyogenes</i> invasive disease epidemic
9:40	10:15	Hattie Chung	Selection and migration timescales that shape the spatial diversity of a pathogen in the human lung
10:15	10:45		BREAK
10:45	11:20	Denise Kühnert	Phylogenetic analysis of (rapidly) evolving pathogens
11:20	11:55	Jennifer Gardy	Genomics in the public health TB lab: what have we done, where are we going, and why does evolution keep screwing everything up?
			AFTERNOON BREAK
17:00	17:35	Ashlee Earl	Rewinding the clock on drug resistant tuberculosis
17:35	18:10	Christophe Fraser	Transmission and genetic paraphyly
18:10	18:45	Alan McNally	Pan-genome analysis provides an unprecedented resolution view of an emerging bacterial pathogen
18:45	19:15		BREAK
19:15	19:50	Yonatan Grad	Using within-host RSV and population-level influenza viral diversity to explore the impact of host selective pressure on viral evolutionary dynamics
19:50	20:25	Edward Feil	How much should we care about the variation in intergenetic sites?
20:30			DINNER

WEDNESDAY 24th

8:30	9:05	Nobuto Takeuchi	Gene-specific selective sweeps in bacteria and archaea caused by negative frequency-dependent selection
9:05	9:40	Jukka Corander	Whole-genome linkage analysis reveals co-evolutionary mechanisms of antibiotic resistance in the pneumococcus
9:40	10:15	Vegard Eldholm	Out of Africa? A phylodynamic analysis of TB transmission within a large immigrant group in Norway
10:15	10:45		BREAK
10:45	11:20	Caitlin Pepperell	Adaptation of the Type VII secretion system
11:20	11:55	Bill Hanage	Evolution in the short term - the potential and the limits for studying transmission
			AFTERNOON BREAK
16:00	16:35	Tami Lieberman	Inpatient pathogen diversity reveals past selective pressures and patterns of within-host dissemination
16:35	17:10	Paul Rainey	Untangling the origins of a plant disease outbreak
17:10	17:45	Caroline Colijn	Two flavours of tree comparisons with applications
17:45	18:15		BREAK
18:15	18:50	Steve Baker	A novel ciprofloxacin-resistant subclone of H58 <i>Salmonella</i> Typhi is associated with fluoroquinolone treatment failure
18:50	19:25	Stephen Bentley	Increased incidence and increased virulence of <i>listeria monocytogenes</i> sequence type 6 meningitis explained through pathogen population genomics
19:30	21:00		DINNER
21:00	22:00		Poster session 2

THURSDAY 25th

8:30	9:05	Kelly Wyres	Exploring Klebsiella capsule diversity through analysis of whole-genome sequences
9:05	9:40	Lucy Weinert	Replicated transitions from carriage to disease is associated with genome reduction in a zoonotic pathogen
9:40	10:15	Nick Croucher	'Intragenomic conflict' and the evolution of bacterial transformation
10:15	10:45		BREAK
10:45	11:20	Danny Wilson	Within-host evolution of Staphylococcus aureus during asymptomatic carriage and invasive disease
11:20	11:55	Ben Cooper	Reconstructing transmission trees for multiply antibiotic-resistant bacteria using densely sampled genomic data
			AFTERNOON BREAK
17:00	17:35	Koji Yohara	Methods for studying recombination hot regions and population structure in bacteria
17:35	18:10	Nadia El-Mabrouk	Detection of codon reassignment and tRNA shift of function -Application to Bacillus genomes
18:10	18:45	Kathryn Holt	Genomic insights into the evolution and transmission of drug resistant <i>Acinetobacter baumannii</i>
18:45	19:15		BREAK
19:15	19:50	Craig Winstanley	Use of genomics to study the evolution of Pseudomonas aeruginosa populations
19:50	20:25	Alison Mather	Investigating long-term and short-term transmission using genomics
20:30			DINNER

FRIDAY 26th**Departures****Poster session 1** Monday 22nd 16:00 – 17:30

Siouxie Wiles	Evolution in Action: in vivo experimental evolution of the pathogenic bacterium <i>Citrobacter rodentium</i>
Michael Gutmann	Fast Likelihood-Free Inference via Bayesian Optimization
Tadasuke Ooka	Genomic diversity and evolutionary insights of <i>Escherichia albertii</i> , an emerging enteropathogen closely related to <i>Escherichia coli</i>
Claire Gorrie	Asymptomatic carriage of <i>K. pneumoniae</i> and its role in hospital acquired infection
Yoshitoshi Ogura	Identification of high Stx2-producing <i>Escherichia coli</i> O157 clades by WGS-based phylogenetic analysis
Yasuhiro Gotoh	Explosive amplification of MITEs and a possible genome evolution pathway of <i>Treponema phagedenis</i>
Minna Vehkala	Sequence element enrichment analysis to determine the genetic basis of bacterial phenotypes

Poster session 2 Wednesday 24th 21:00 - 22:00

Rene Niehus	Migration and horizontal gene transfer divide microbial genomes into multiple niches
Ken-ichi Lee	Diffuse outbreak investigation in enterohemorrhagic <i>Escherichia coli</i> O121 by whole genome sequencing
Takayuki Wada	Estimation of transmission routes of <i>Mycobacterium tuberculosis</i> based on genotypic and genomic analysis of a local prefectural surveillance in Japan
Sayaka Mino	Genetic structure and spatial distribution pattern of chemolithoautotrophic Epsilonproteobacteria from deep-sea hydrothermal vents
Takahiko Shiba	Dissimilarities of functional keystone species in co-occurrence network enable discrimination of intractable polymicrobial infectious diseases
Fumito Maruyama	A hot-region promoting intraspecific divergence by shift of genetic elements related to defense systems against invading DNA
Iwamoto Tomotada	Dynamic changes in genomic architecture of <i>Mycobacterium avium</i> in accordance with its phylogenetic diversification