出國報告（出國類別：國際會議）

第五屆 EPIDEMICS 國際研討會與參訪疫苗學研究專家

服務機關：衛生福利部疾病管制署
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派赴國家：美國
出國期間：民國 104 年 11 月 29 日-12 月 6 日
報告日期：民國 104 年 12 月 24 日

摘要

本出國案由疾病管制署疫情中心簡淑婉技正，於 2015 年 11 月 29 日至 12 月 6 日赴美國密西根州底特律市及佛羅里達州清水市，進行公開演講、參訪學者與參與國際學術研討會。

第五屆傳染病動態分析國際研討會(Fifth International Conference on Infectious Disease Dynamics, EPIDEMICS5)由知名出版商 Elsevier 主辦，與會人數約數百人，本屆研討會共安排多達 113 個場次口頭報告，包括 11 場大會共同演講、102 場專題演講，另包括 3 場海報論文展示，逾百篇壁報發表，相當豐富。

本報告內容除說明參訪行程內容外，摘錄會議中部分國際間關注重要傳染病議題，包括登革熱及新興傳染病相關調查與研究，提供我國未來制定登革熱及新興傳染病風險評估與綜合性防治政策參考。

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本文

目的

本案目的係參訪美國密西根州底特律市(Detroit)，偉恩州立大學藥學及健康科學學院(Eugene Applebaum College of Pharmacy and Health Science, Wayne State University) 副教授 Dr. Paul E. Kilgore，討論如何評估疫苗接種可行性。另於參訪後赴佛羅里達州清水市(Clearwater)，參加第五屆國際傳染病動態分析研討會(Fifth International Conference on Infectious Disease Dynamics, EPIDEMICS5)。藉參加國際傳染病研討會及參訪疫苗及疾病負擔評估專家，學習國際間疫苗發展現況，及防治策略評估等傳染病研究新知，並與專家交流以建立國際人脈。

過程

一、出國行程表

日期	工作日誌	地　　點	行　程　內　容
104/11/29	啟程	台北→密西根州底特律市	路程及當日抵達
104/11/30	參訪	密西根州底特律市	參訪
104/12/01	路程	密西根州底特律市→ 佛羅里達州清水市	路程
104/12/01- 104/12/04	會議	佛羅里達州清水市	研討會
104/12/05- 104/12/06	返程	佛羅里達州清水市→台北	路程

二、參訪行程

本次參訪學者 Dr. Kilgore，於 1994-1996 年完成美國疾病控制與預防中心(Centers for Disease Control and Prevention, CDC)之 EIS（Epidemic Intelligence Service）訓練，並曾任國際疫苗研究中心(International Vaccine Institute)資深研究學者達十餘年，對於亞洲地區疫苗推動及疫苗可預防性疾病之疾病負擔研究不遺餘力，合作國家包含北韓、南韓、菲律賓、中國大陸、日本、新加坡、印度、柬埔寨、蒙古、斯里蘭卡等國，亦曾赴台灣參訪及參觀疾病管制署。因家人健康因素，於 2011 年起返家鄉底特律市擔任偉恩州立大學副教授。

應 Dr. Kilgore 邀請，參訪當日首先於亨利福特醫院（Henry Ford Hospital）進行公開演講，演講內容為台灣登革熱等蟲媒類傳染病之監測及挑戰（演講公告如附錄一）。與會聽眾主要為該院醫師、亨利福克健康體系全球健康行動計畫（The Global Health Initiative, Henry Ford Health System）執行長及相關人員等。演講後問與答部份可供參考之建議，主要為基於我國具相對完善之監測體系，與有效運用雲端科技，視覺化呈現分析結果之技術，為拓展國際間區域防疫及合作網絡，如何協助鄰近高蟲媒類疾病負擔但資源相當有限之東南亞國家，建置其監測系統與評估疾病負擔，亦有助我國掌握東南亞國家疫情狀況。

會後諮詢 Dr.Kilgore 就台灣使用登革熱疫苗可行性進行討論，對方主動提出與我方就登革熱疫苗政策執行可能性，進行合作共同評估。以數理模型評估登革熱疫苗政策可行性所需參數及資料包括：1.罹病嚴重性及危險因子等臨床病例資料研究 2.Sanofi 疫苗臨床第二期老人試驗相關資料 3.近年來平均每年登革熱造成經濟損失及疫情控制成本評估 4.病媒蚊監測資料 5.臨床試驗或上市期間國際間登革熱疫苗接種不良反應事件評估 6.疫苗輸送及冷藏鏈相關設備及配送地點分佈評估 7.各年齡層民眾接種意願

調查 8.建立台灣流行地區居民單一/重複感染登革熱型別變化之世代研究（population-based cohort study），如圖一。

圖一、登革熱疫苗政策執行前成本效益分析架構圖

就現行我國登革熱監測及健保資料庫等相關資訊來源判斷，我國對於病媒蚊監測、疫苗儲備及配送、登革熱嚴重病例危險因子分析、疫苗接種後發生不良反應監測、監測資料相較完備，惟目前尚無菲律賓、墨西哥與巴西已批准適用於 9-45 歲之 Sanofi Dengvaxia 疫苗接種於老人之臨床試驗結果，因我國登革熱重症以 60 歲以上成人為主，因此該疫苗對我國登革熱控制效益仍待評估及試驗。另由於 Dengvaxia 屬四價疫苗，第二型效益較其他型別差，我國雖具登革熱型別監測，惟因登革熱不顯性感染或無症狀感染者比例可達 3/4，且已有不顯性感染者造成病毒傳播之證據(Duong et al, PNAS 2015)，目前我國尚缺乏台灣流行地區民眾代表性之單一/重複感染登革熱型別變化之世代研究，難以評估通報病例之感染型別變化與居民感染型別變化差異，此將是我國未來進行登革熱防治及疫苗政策評估重要參考資料，配合調查民眾對於疫苗之接受度與成本效益分析等重要議題，皆為未來進行登革熱疫苗接種與病媒防治並行政策執行重要參考資料。

三、會議行程

第五屆國際傳染病動態分析研討會(Fifth International Conference on Infectious Disease Dynamics, EPIDEMICS5)會議期間為104年12月1日至12月4日，地點位於美國佛羅里達州清水市，會議議題包括病媒傳染病、疫苗可預防性傳染病、統計方法、流感、HIV、新興傳染病、瘧疾、模組分析方法、族群動態演化、登革熱等，口頭報告會議議程詳如附錄二。

四、會議重點議題

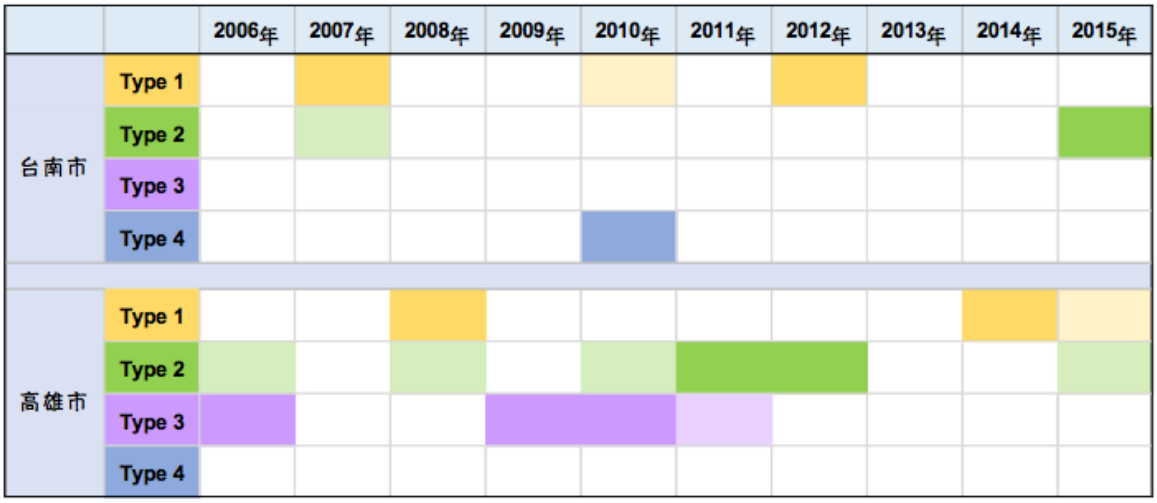
1. 登革熱

一、族群血清盛行率研究

秘魯研究：近 50 年來全球登革熱發生率及流行地區持續增加及擴大，已成為國際間重要關注公共衛生議題之一。人類感染登革熱病毒後，形成該感染血清型之終身保護力，然而登革熱具四種型別，且臨床症狀從無症狀感染至嚴重登革熱病徵皆同時存在，不顯性感染比例可達 8 成，僅透過症狀或疾病通報監測系統，無法全盤瞭解社區間登革熱流行型別變化及感染情形與疾病負擔。在人類感染某一登革熱型別後，會對其他型別產生短暫的交叉保護力（ temporary cross-immunity,下稱 TCI），TCI 與預測未來社區感染型別、感染族群比例及疾病嚴重度皆息息相關，惟若無建立族群追蹤研究，難以測量 TCI 之時間及型別間交叉保護強度之差異。美國國立衛生研究院 R.C. Reiner 研究團隊，於 1999-2010 年進行長期秘魯 Iquitos 鎮血清流行病學追蹤研究，以測量 1995 年以前出生居民登革熱感染型別，與觀察感染後 TCI 維持之時間與型別之關係。追蹤總計 14,335 人及 38,416 件血液檢體，血液採集間隔為每 6-9 個月，並以中央設限(interval-censored)法計算共 3,854 次任一型別感染。檢驗方法以溶斑減

少中和抗體試驗(Dengue Plaque Reduction Neutralization Test,PRNT)第一至第四型登革熱病毒分別稀釋 1:60、1:80、1:60 及 1:40 比例，定義病毒溶斑減少 70%為血清陽轉。分析方法以 catalytic model、Adaptive Metropolis within Gibbs (AMWG) 演算法及 Markov chain Monte Carlo(MCMC)估計模型參數。研究結果發現該族群登革熱感染次數共計 422 名出現 2 次感染、39 名出現 3 次感染及 5 名出現 4 次感染，型別間感染力(平均一個具感受性的人感染病原體的感染率，Force of infection, FOI)及 TCI 出現顯著差異，TCI 期間介於 3-15 個月，感染力介於 0-0.33 之間，以第一次及第二次分別感染第一型及第二型之 TCI 最短(三個月)，感染力最強，基礎再生率（R0）估計值則介於 0.49－4.72。此結果說明族群世代研究在登革熱傳播模型分析的重要性，族群血清流行病學追蹤資料可評估流行地區民眾血清陽轉情形，及感染不同型別之感染力變化，進而推估各型別於流行季之傳播速度，及 TCI 如何影響流行型別變化與民眾感染率，進一步探討感染民眾發病百分比與臨床表徵差異等。

我國於 2004 年至 2007 年曾對 42,150 人進行大規模登革熱篩檢，發現無症狀感染人數佔 36%。2007 年後流行地區則無具族群代表性之血清世代追蹤研究，回顧 2006-2015 年我國個案傳染病通報系統（下稱法傳系統）登革熱確定病例感染型別，發現我國高屏地區登革熱各型別皆有流行紀錄（如圖一），因具臨床症狀且符合通報條件才得進行登革熱通報，且通報來源多為醫院而非診所，因此無法就法傳系統資料全盤瞭解國人登革熱感染型別比例、發病比例、通報比例等。因此考量建立我國登革熱族群世代追蹤研究，將有助於評估流行區之傳播情形與型別變化，更提供我國登革熱疫苗發展或疫苗接種政策推行前，疫苗各型別效益評估重要參考資料。



圖一、我國 2006-2015 年登革熱主要流行病毒型別，深色為主要流行型別，淺色為次要流行型別（資料來源：疾管署）。

尼加拉瓜研究：佛羅里達大學 Dr. Yang Yang 及 Dr. Ira Longini 團隊以壁報方式發表 1995-2010 年尼加拉瓜登革熱世代追蹤研究，建置登革熱傳播萌型及各型別相關危險因子，參數資料包括研究期間感染型別及次數、每次感染有無症狀、血清學資料、其他相關共變數(covariates)及歷年監測資料等。檢驗方法以 ELISA 為主，其他檢驗方法包括 PCR、RVP(reporter virus particles)及 PRNT。以 Metropolis-Hastings with Gibbs Sampler 及 MCMC 法分析，且模組包含過去感染型別、發病狀況、免疫狀態、及其他共變數，並納入往年監測資料估計歷年流行型別，以調整追蹤期間前之感染型別與症狀、實驗室診斷試劑限制、診斷資料不完整之限制等。追蹤對象之血清陽轉百分比介於 5.31-11.2，且重要研究結果如圖二，經 MCMC 法 10,000 次迭代演算後，登革熱第一型於 2004-2010 年平均感染機率介於 0.6-15.2，第二型至第四型則分別介於 1-22.7、0.5-48.4 及 0.7-4.4，另經調整共變數後，感染且產生症狀機率以第三型 0.82(90%CI:0.77-0.86)最高，此與該國往年以第一與第二型流行為主，於

08-09 年發生第三型流行型，故易感族群比例較高有關；另以第四型 0.07(0.03-0.15)最低。以第一及第二次感染後有無症狀估計感染間隔時間以第一次有症狀、第二次無症狀間隔時間 1.69(0.85-2.64)年最短；第一次無症狀、第二次有症狀間隔時間 3.87(2.50-5.14)年最長。另發現感染間隔時間有逐次遞減現象，第 1-2 次、第 2-3 次與第 3-4 次感染間隔時間分別為 2.49(2.11-2.89)、2.18(1.87-2.57)、1.92(1.50-2.67)年，且曾經感染一次者之再次感染機率為未曾感染者之 14.65 倍，兩次感染以上則為 22.5 倍；距上次感染時間達 3 年以上者，較距離 1 年者降低感染率達 71%；上次感染出現臨床症狀者，較上次感染無出現者感染率低 65%。

Table 3: Posterior means of infection ($p_v(t)$) and disease probabilities (ϕ_v) (per 1000) based on 10000 iterations after burn-in.

Parameter	Year	Serotype			
		DENV-1	DENV-2	DENV-3	DENV-4
Probability of Infection ($p_v(t)$)	04-05	10.10	8.60	2.80	2.80
	05-06	15.20	22.40	4.10	1.80
	06-07	7.10	9.30	2.80	4.40
	07-08	2.00	22.70	0.50	0.70
	08-09	0.60	1.00	6.50	1.40
	09-10	6.60	4.10	48.40	1.41
Probability of Symptom (ϕ_v)		0.46 (0.38,0.54)	0.57 (0.50,0.64)	0.82 (0.77,0.86)	0.07 (0.03,0.15)

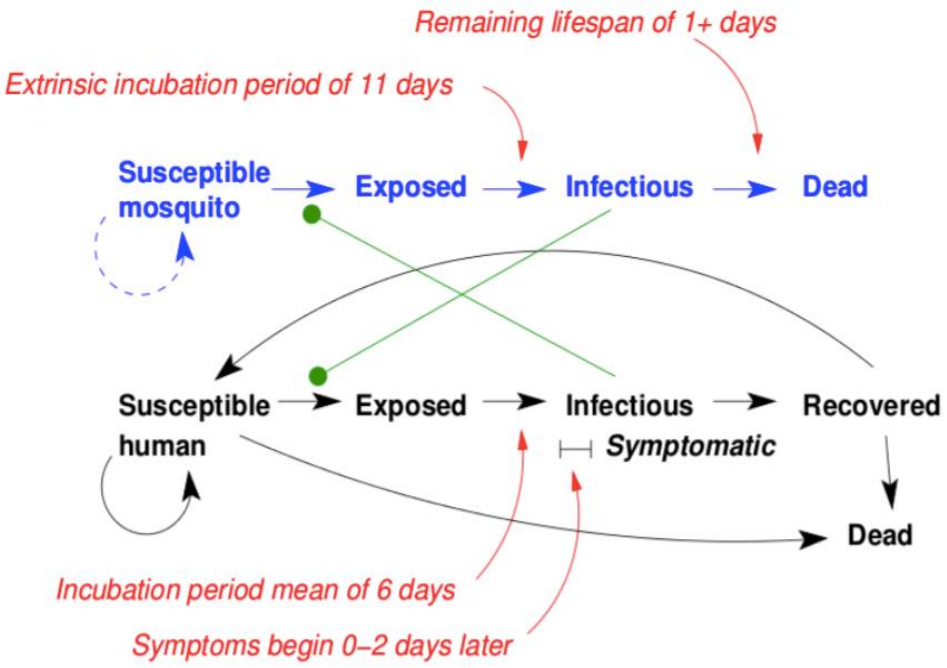
Table 4: Mean time interval between first and second infection by symptoms.

Symptom	*time* (90% CI)
Asymptomatic-Asymptomatic	2.00 (1.71, 2.34)
Asymptomatic-Symptomatic	3.87 (2.50, 5.14)
Symptomatic-Asymptomatic	1.69 (0.85, 2.64)
Symptomatic-Symptomatic	3.90 (2.40, 5.50)

圖二、1995-2010 年尼加拉瓜登革熱世代追蹤研究，追蹤族群感染機率、發病機率及感染間隔時間表（資料來源：佛羅里達大學 Samson Ghebremariam 等人發表壁報）。

二、登革熱疫苗及病媒蚊防治併用效益評估

Dr. Longini 團隊以墨西哥 Yucatan 鎮第三期登革熱疫苗臨床試驗資料及相關參數，建立 agent-based dengue model，以描述居民及帶病毒病媒蚊之移動及傳播模式，使用之模型亦可重新參數化以套用於其他地區，模型相關參數使用資料包括衛星影像、居民戶口與經濟資料、35 年登革熱病例及型別監測資料，以估計約 180 萬居民及計 375,000 戶住家與 100,000 處工作場所及學校，另為估計資料完整度較差如當地病媒蚊數量及移動與叮咬行為等重要參數(entomological inoculation rates, vectorial capacity, force of infection)，建立貝氏參數估計法 AbcSmc (Approximate Bayesian Computation - Sequential Monte Carlo)，病媒蚊以 SEI 模型估計，病媒蚊感染後潛伏期定義為 11 天，生命週期則定義從具感染力起 1 天以上；人類則以 SEIR 模式估計，人類潛伏期定義為 6 天，發病日則為具傳染力後 0-2 天計算（如圖三）。研究結果發現，若僅使用病媒蚊防治或疫苗接種單一方法，無法有效降低登革熱發生率 6 成以上，另外病媒蚊防治若迅速停止，會導致往後疫情更加嚴重，因此，合併病媒蚊防治及疫苗接種，是降低該地區登革熱發生率最有效之方法。以接種涵蓋率而言，當 2-46 歲孩童及成年人接種率達 7 成以上時，即會出現疫情控制效果，若疫苗初期數量相較有限時，因孩童相較成人普遍為易感族群，2 歲孩童應列為每年接種對象。另外，登革熱疫苗接種計劃實施後，可能似侵襲性肺炎鏈球菌感染症疫苗，長期影響民眾感染型別變化及各型別流行情形，因此需要持續監測流行型別變化。



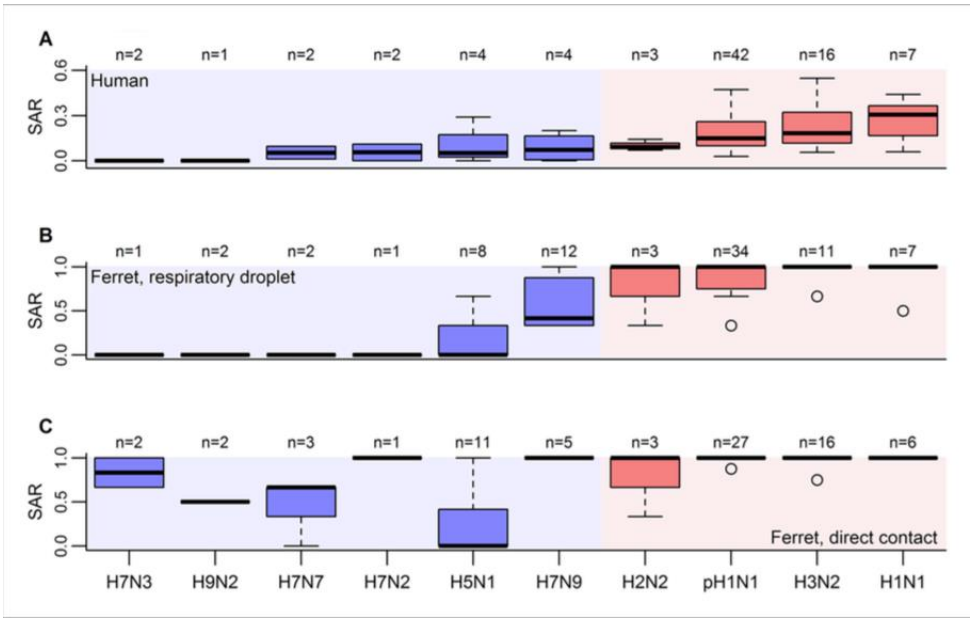
圖三、人類及病媒蚊傳播模型說明圖

2. 新興傳染病量化風險評估

一、新興傳染病風險評估

人畜共通傳染病能否演化成為新興傳染病由四個流行病學因子影響風險測量值：跨物種傳播率(cross-species spillover rates)、人傳人能力(human-to-human transmissibility)、人類族群感受性(susceptibility of human population)、人類族群間聯通性(connectivity of the human population)。一個人畜共通傳染病疫情發生時，通常現有資訊無法完整獲得此四因子之相關資料以進行量化風險評估。2003-04 年 Farrington 及 Ferguson 等人曾使用 branching process model 描述疫情規模，並以負二項回歸分佈(negative binomial offspring distribution)計算基礎再生率(R0)及離散係數(k)等因子，離散係數係以估計病例發生超級傳播(superspreading)情形，以建構疫情規模分佈。另 M.G.Bunerkempe 等人透

過雪貂實驗估計由人類病例分離出之新型流感病毒人傳人可能性，研究發現依家庭接觸者感染流感二次侵襲率排列，經由呼吸道感染隻雪貂二次侵襲率較人類傳播模式高，惟整體趨勢相似(如圖四)，且雪貂間傳播足以解釋約 66%人傳人情形之差異，因此利用實驗雪貂資料預測新型流感分離株出現大流行可能性，為量化估計人類感染風險方法之一，惟通常雪貂實驗動物總數不多，個體差異可能影響分析結果。

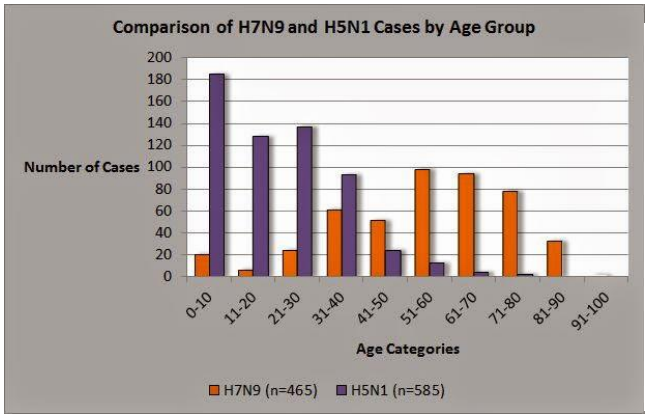


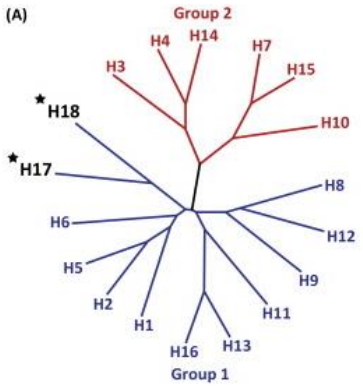
圖四、雪貂感染人類分離新型流感(藍色)與季節流感(紅色)病毒二次侵襲率(SAR)分佈盒鬚圖。

上述四流行病學因子中，人類族群感受性通常以未曾暴露該新興傳染病，即國人皆屬易感族群估計。J.O.Lioyd-Smith 教授以剛果民主共和國猴痘疫情及 H7N9 與 H5N1 流感說明，人類對於新興傳染病感受程度與個人出生年份息息相關。剛果民主共和國曾於 1980 年代，因加強監測發現較多人類感染猴痘病例，在 1990 年代僅出現散發病例，惟於 2005 年起，出現大規模疫情，因該國於 1980 年開始停止天花疫苗接種，推測疫情爆發應與出生於 1980 年後之年輕族群具感受性有關。不過在 A. Rimoin 等人進行疫

情發生率與傳播危險因子模組分析發現，需要出現跨物種傳染(spillover)或人傳人傳播能力增加 20 倍以上，才足以解釋 2005 年起之疫情規模，在考量天花疫苗交叉保護力之因子及病毒無明顯變異造成人傳人風險增加後，惟有跨物種傳染機率增加 560%(CI:310-890%)，才可解釋本次疫情規模。經查發現 1980 年代起孩童暴露齧齒類動物機率顯著增加，因大型哺乳類動物過度捕獵，導致齧齒類動物劇增，當地居民須以捕獵嚙齒類動物為食物來源，經估計孩童接觸松鼠機率增加 9 倍，其他齧齒類動物增加 3 倍，便說明觸發疫情的危險因子。此次研究驗證進行新興傳染病量化風險評估時，模組分析須綜合考量族群免疫力變化及跨物種傳播機率，才得完整估計疫情規模及相關危險因子。

Dr. Lioyd-Smith 另以 H7N9 及 H5N1 流感病例分佈，說明感染者之年齡分佈與其出生年份有關。H7N9 感染病例年齡分佈較 H5N1 高之原因(如圖五)，有不同之說法，Cowling 等人推測可能因 H5N1 為高病源性禽流感，而 H7N9 為低病原性禽流感，禽類死亡率高低差異影響人類暴露行為及頻率，影響病例年齡分佈；Kucharski 等人則認為曾於 1957 年以前感染 H1N1 流感之族群因具有 N1 抗體之交叉保護力，因此 H5N1 感染病例年齡分佈以出生於 1957 年後之族群為主；Qin 等人則認為 H5N1 及 H7N9 流行病學上呈現年齡分佈差異係因監測偏差(ascertainment bias)造成，因經分析發現 H7N9 指標病例及次波病例年齡分佈中位數分別為 59 歲及 31 歲，但 H5N1 卻無顯著差異。

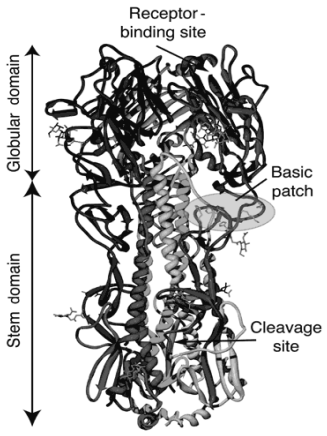




圖五、六：2014 年人類感染 H7N9 及 H5N1 病例年齡層分佈;HA 類別分佈圖(來源：Flu Trackers)。

J.O.Lioyd-Smith 利用模型分析，提出 H5N1 及 H7N9 病例年齡分佈差異的重要因素，係與人類出生時第一次接觸新型流感之 HA(hemagglutinin)型別有關，免疫系統會記憶第一次感染的新型流感型別，因此若再次感染相同 HA 類別之新型流感，則將具有部分交叉保護力，此種免疫系統記憶機制稱為 HA imprinting，而 H1 與 H5 皆屬 group1；H3 及 H7 皆屬 group2(如圖六)。1918-1957 年是 H1N1 流感大流行期，1957-1968 年是 H2N2 流感大流行期，1968 年起為 H3N2 流感大流行期，1977 年起為 H3N2 及 H1N1 流感共同流行期，因此若出生年份落於 H1N1 流感大流行期，免疫系統便可能具備 H5N1 病毒之交叉保護力，藉此推斷 HA imprinintg 為 H5N1 病例年齡分佈較年輕之重要因子。另以流行國家病例年齡分佈、病例暴露禽鳥之年齡、重症病例與年齡相關風險、neuraminidase imprinting 與出生年份、hemagglutinin imprinting 與出生年份等參數納入模型分析(multinomial models)，以估計 H7N9 及 H5N1 發生率，結果顯示發生率趨勢配適度較佳之模型皆包含 hemagglutinin imprinting 參數，就 HA 蛋白結構推斷 hemagglutinin imprinting 機制發

生於保守區(stem domain, 如圖七)，該區不如 globular domain 隨病毒亞型具差異性，亦以此原理設計廣效型流感疫苗。若此理論持續獲得實驗及其他流行病學證據支持，在量化評估新型 A 型流感大流行風險時，須審慎考量族群對於新型流感感受性之差異，非僅初步推估國人對於新興傳染病應皆屬易感族群。



圖七、血清凝集素蛋白(Hemagglutinin, HA)架構圖。(來源：scripp.edu)

心得及建議

本次參訪美國底特律市偉恩州立大學副教授 Dr.Kilgore，並於亨利福特醫院進行我國登革熱及蟲媒傳染病監測架構公開演講，及與其針對登革熱議題進行討論，對方主動提出與我方於登革熱疫苗政策及疾病負擔評估議題合作可能性，並視機會於 2016 年參訪疾病管制署，建議我方可考慮接待及邀請 Dr. Kilgore 公開演講，並於會後討論合作可能性，或供我方諮詢登革熱疫苗政策評估研究

國際傳染病動態分析研討會受邀與會者包括國際間動態模組分析知名學者，包括 Ira longini, Dirk Brockmann, Ben Cowling, Azra Ghani, Ana Maria Henao Restrepo, Burton Singer, Jamie Lloyd-Smith 等，四天與會期間密集聽取講者及壁報資訊，相當豐富，以口頭報告及壁報報告

數計算，會議中發表之亞洲學術或政府機構以香港大學公共衛生學院最多，日本學術機構如東京大學次之，澳洲及紐西蘭亦有學術機構參與。西方公共衛生機構以約翰霍普金斯大學、哈佛公衛學院、佛羅里達州立大學、美國國家衛生研究院(NIH)、英格蘭公共衛生部(PHE)、英國倫敦帝國學院(Imperial College)、荷蘭國家公共衛生及環境研究院(RIVM)、美國疾病預防及控制中心(CDC)為多。配合大數據時代，傳染病動態分析在全球新興傳染病傳播模式儼然已成顯學，明年該會議將於西班牙舉辦，建議持續派員與會。

附錄一、演講公告

附錄二、第五屆傳染病動態分析國際研討會會議議程表

(資料來源：http://www.epidemics.elsevier.com)

Oral Programme

Tuesday, 1 December 2015			
17:00-19:00	Registration		
19:00-20:30	Welcome Reception & Poster Viewing		
20:30-21:10	**[PLN01] Malaria per se and malaria suppression v. malaria modeling** B. Singer, *University of Florida, USA*		
Wednesday, 2 December 2015			
07:30-08:30	Registration		
Room			
08:30-08:40	Welcome & Opening remarks by Conference Chair		
08:40-09:10	**[PLN02] Interim results from the Guinea ring vaccination cluster-randomised trial** A.M.H. Restrepo*[1], I. Longini[2], M. Egger[3], P. Fast[4], R. Kanapathipillai[5] *[1]World Health Organization, Switzerland, [2]University of Florida, USA, [3]University of Bern, Switzerland, [4]International AIDS Vaccine Initiative, USA, [5]The New England Journal of Medicine, USA*		
09:10-09:50	**[PLN03] TBC** R. Laxminarayan, *Center for Disease Dynamics, Economics and Policy, Washington DC, USA*		
09:50-10:30	**[PLN04] Big Data in infectious disease dynamics** M.A. Suchard, *University of California, USA*		
10:30-11:10	**[PLN05] Analysis of influenza a epidemiology through community-based studies** B Cowling, *The University of Hong Kong, Hong Kong*		
11:10-11:40	**Refreshment Break**		
Rooms			
11:40-13:00	**Session 1: Influenza 1** *Session Chair:*	**Session 2: HIV** *Session Chair:*	**Session 3: Modelling Tools 1** *Session Chair:*
11:40-12:00	**[O1.1] Deep sequencing of influenza A virus from a human challenge study yields insight into the size of influenza's transmission bottleneck and the tempo of within-host viral evolution** A. Sobel*, M. McClain, C. Woods, K. Koelle *Duke University, USA*	**[O2.1] Increasing heritability of Set-Point Viral Load in the HIV epidemic in Europe** F. Blanquart*[1], C. Wymant[1], M. Cornelissen[2], A. Gall[3], C. Fraser[1] et al *[1]Imperial College London, UK, [2]University of Amsterdam, The Netherlands, [3]Wellcome Trust Genome Campus, UK*	**[O3.1] On the extinction probability in models of within-host infection: The role of latency and immunity** A.W.C. Yan*[1], P. Cao[1], J.M. McCaw[1,2] *[1]The University of Melbourne, Australia, [2]Murdoch Childrens Research Institute, Australia*
12:00-12:20	**[O1.2] High global burden and frequency of influenza H3N2 intra-subtype reassortment: attributes and implications of reassortant spread** I. Maljkovic Berry*[1], M.C. Melendrez[1], A.W. Hawksworth[2], G.T. Brice[2], P.J. Blair[2], E.S. Halsey[3], M. Williams[3], S. Fernandez[4], I.K. Yoon[4], L. Edwards[5], R. Kuschner[1], X. Lin[1], S.J. Thomas[1], R.G. Jarman[1] et al *[1]Walter Reed Army Institute of Research, USA, [2]Naval Health Research Center, USA, [3]US Naval Medical Research Unit -6, Peru, [4]Armed Forces Research Institute of Medical Sciences, Thailand, [5]US Department of State, USA*	**[O2.2] Decomposing HIV virulence: Heritability of setpoint virus load, CD4+ T cell decline and per-pathogen pathogenicity** F. Bertels[1], A. Marzel[2], G. Leventhal[1], J. Fellay[3], H. Guenthardt[2], V. Müller[4], S. Bonhoeffer[1], R. Kouyos[2], R.R. Regoes*[1] *[1]ETH Zurich, Switzerland, [2]University Hospital Zurich, Switzerland, [3]École Polytechnique Fédérale de Lausanne, Switzerland, [4]Eötvös Loránd University, Hungary*	**[O3.2] Little r: An under-rated epidemiological parameter** J. Dushoff*[1], S. Bellan[2] *[1]McMaster University, Canada, [2]University of Texas, USA*

12:20-12:40	**[O1.3] The Possible impact of vaccination for seasonal influenza on emergence of pandemic Influenza via reassortment** X-S. Zhang*[1,2], R. Pebody[1], D. De Angelis[1,3], P.J. White[1,2], A. Charlett[1], J.W. McCauley[4] *[1]Public Health England, UK, [2]Imperial College, UK, [3]MRC Biostatistics Unit, Cambridge, UK, [4]MRC National Institute for Medical Research, Mill Hill, UK*	**[O2.3] Effect of the latent reservoir on the evolution of HIV at the within- and between-host levels** H.M. Doekes[1], C. Fraser[2], K.A. Lythgoe*[2,3] *[1]Utrecht University, The Netherlands, [2]Imperial College London, UK, [3]University of Oxford, UK*	**[O3.3] Estimating finite-population reproductive numbers in heterogeneous populations** L.T. Keegan*, J. Dushoff *McMaster University, Canada*
12:40-13:00	**[O1.4] The roles of innate and adaptive immunity in controlling influenza infection** J.M. McCaw*[1], P. Cao[1], A.W.C. Yan[1], K. Laurie[2] *[1]University of Melbourne, Australia, [2]WHO Collaborating Centre for Reference and Research on Influenza at the Peter Doherty Centre, Australia*	**[O2.4] Genetic diversity of HIV reveals the epidemiological role of high risk groups in Nigeria** E.M. Volz*[1], R. Nowak[2], N. Ndembi[3], G. Kijak[4], S. Baral[5], W. Blattner[2], M. Charurat[2] *[1]Imperial College London, UK, [2]University of Maryland School of Medicine, USA, [3]Institute of Human Virology Nigeria, Nigeria, [4]U.S. Military HIV Research Program and Henry M. Jackson Foundation, USA, [5]Johns Hopkins University Bloomberg School of Public Health, USA*	**[O3.4] Estimating the effective reproductive number for a novel viral pathogen using a stochastic compartmental model** C. Zimmer*[1], R. Yaesoubi[2], T. Cohen[2] *[1]Brigham and Women's Hospital, USA, [2]Yale School of Public Health, USA*
13:00-14:00	**Lunch**		
Rooms			
14:00-15:40	**Session 4: Influenza 2** *Session Chair:*	**Session 5: Malaria** *Session Chair:*	**Session 6: Modelling Tools 2** *Session Chair:*
14:00-14:20	**[O4.1] Inference of seasonal and pandemic influenza transmission dynamics** W. Yang*[1], M. Lipsitch[2], J. Shaman[1] *[1]Columbia University, USA, [2]Harvard School of Public Health, USA*	**[O5.1] Variation in relapse frequency and the transmission potential of *Plasmodium vivax* malaria** M. White*[1], G. Shirreff[1], S. Karl[2,3], A. Ghani[1], I. Mueller[2,3] *[1]Imperial College London, UK, [2]Walter and Eliza Hall Institute, Australia, [3]University of Melbourne, Australia*	**[O6.1] Beyond endemicity: Taxonimizing the epidemic dynamics of cholera and measles** J. Lessler*, S.M. Moore, M. Graham, A.S. Azman, H.S. McKay *Johns Hopkins Bloomberg School of Public Health, USA*
14:20-14:40	**[O4.2] Influenza spatial diffusion varies with age patterns of infection and antigenic novelty** V. Charu[1,2], S. Zeger[2], J. Gog[3,1], O. Bjornstad[4,1], S. Kissler[3], F. Khan[5], L. Simonsen[6,1], B. Grenfell[7,1], C. Viboud*[1] *[1]Fogarty International Center, NIH, USA, [2]Johns Hopkins University, USA, [3]University of Cambridge, UK, [4]Pennsylvania State University, USA, [5]IMS Health, USA, [6]George Washington University, USA, [7]Princeton University, USA*	**[O5.2] Understanding the historical spread of antimalarial resistance in Africa** L.C. Okell*[1], J.T. Griffin[1], H. Slater[1], A.C. Ghani[1], C. Roper[2] *[1]Imperial College London, UK, [2]London School of Hygiene & Tropical Medicine, UK*	**[O6.2] The influence of seasonal drivers on the predictability of measles dynamics** Q. Caudron*[1], J.C.E. Metcalf[1], M. Gottfredsson[2], B.T. Grenfell[1] *[1]Princeton University, USA, [2]University of Iceland, Iceland*

14:40-15:00	**[O4.3] Spatiotemporal patterns in age structure in the 2009 influenza pandemic in the US** S.M. Kissler*[1], J.R. Gog[1,3], C. Viboud[3], V. Charu[3,4], O. Bjornstad[5], L. Simonsen[3,6], B.T. Grenfell[2,3] *[1]University of Cambridge, UK, [2]Princeton University, USA, [3]National Institutes of Health, USA, [4]Johns Hopkins Bloomberg School of Public Health, USA, [5]Pennsylvania State University, USA, [6]George Washington University, USA*	**[O5.3] Synergistic and antagonistic interactions between bed-nets and vaccines in the control of malaria** Y. Artzy-Radrup*[1,2], A. Dobson[3,4], M. Pascual[1,4] *[1]University of Michigan, USA, [2]University of Amsterdam, The Netherlands, [3]Princeton University, USA, [4]Santa Fe Institute, USA, [5]University of Chicago, USA*	**[O6.3] Assessing the promise of tolerance-based therapy** N. Hoze*, S. Bonhoeffer, R.R. Regoes *ETH Zurich, Switzerland*
15:00-15:20	**[O4.4] Heterogeneous shedding of influenza by human subjects and its implications for control** L. Canini*[1], M.E.J. Woolhouse[1], T.R. Maines[2], F. Carrat[3,4] *[1]University of Edinburgh, UK, [2]Centers for Disease Control and Prevention, USA, [3]INSERM, France, [4]UPMC University Paris 06, France*	**[O5.4] Modeling the dynamics of immunological memory to malaria** L.M. Childs*, C.O. Buckee *Harvard T. H. Chan School of Public Health, USA*	**[O6.4] Employing simple mathematical models of within-host viral dynamics to improve the design of clinical trials of novel immunotherapies against influenza A** C. Hadjichrysanthou*, E. Cauet, C. Vegvari, E. Lawrence, F. de Wolf, R.M. Anderson *Imperial College London, UK*
15:20-15:40	**[O4.5] Mitigating pandemic influenza: An assessment of England's National Pandemic Flu Service phone- & internet-based patient assessment and antiviral distribution system in the 2009 influenza A/H1N1 pandemic** P.J. White*[1,2], P. Pelosse[1,2], A. Charlett[1], T. Nichols[1], R. Pebody[1], N.M. Ferguson[2] *[1]Public Health England, UK, [2]Imperial College London, UK*	**[O5.5] On the mechanisms of artemisinin action in plasmodium falciparum clearance** P. Cao*[1], S. Zaloumis[1], J.A. Simpson[1], J.M. McCaw[1,2] *[1]University of Melbourne, Australia, [2]Murdoch Childrens Research Institute, Australia*	**[O6.5] The impact of dose-dependence on disease spread** J.C. Miller*[1], Y. Grad[2], M. Lipsitch[2] *[1]Monash University, Australia, [2]Harvard School of Public Health, USA*
15:40-16:10	**Refreshment Break**		
Rooms			
16:10-17:50	**Session 7: Phylodynamics 2** *Session Chair:*	**Session 8: Dengue** *Session Chair:*	**Session 9: Vaccination 1** *Session Chair:*
16:10-16:30	**[O7.1] Real-time evolutionary forecasting for influenza vaccine strain selection** T. Bedford*[1], R.A. Neher[1] *[1]Fred Hutchinson Cancer Research Center, USA, [2]Max Planck Institute for Developmental Biology, Germany*	**[O8.1] Assessing the dynamics of within-host interactions between dengue serotypes using individual-level longitudinal serological data** R.C. Reiner*[1,2], S.T. Stoodard[1,3], B.M. Forshey[4], C. Guevara[5], R. Hontz[5], E.S. Halsey[5], A. Morrison[3], T.J. Kochel[5], T.W. Scott[1,3] *[1]Fogarty International Center, USA, [2]Indiana University School of Public Health, USA, [3]University of California, USA, [4]US Department of Defense, USA, [5]US Naval Medical Research Unit No. 6, Peru*	**[O9.1] Can measles elimination be maintained? Inferring impact of measles vaccination campaigns with realistic demographic and epidemiological settings** J. Prada*[1], C.J.E. Metcalf[1], S. Takahashi[1], J. Lessler[3], A. Tatem[4], M. Ferrari[2] *[1]Princeton University, USA, [2]Pennsylvania State University, USA, [3]Johns Hopkins, USA, [4]University of Southampton, UK*

16:30-16:50	**[O7.2] Phylogenetic modelling of temporal heterogeneity in the circulation of human influenza lineages** N. Sequeira Trovão*[1], G. Baele[1], F. Bielejec[1], M.A. Suchard[2], P. Lemey[1] *[1]KU Leuven, Belgium, [2]University of California, USA*	**[O8.2] Statistical fits to within-host dengue models provide insight into processes driving variation in viral load patterns** R. Ben-Shachar*, K. Koelle *Duke University, USA*	**[O9.2] Did large-scale vaccination drive changes in the circulating rotavirus population in Belgium?** V.E. Pitzer*[1,2], J. Bilcke[3], E. Heylen[4], F.W. Crawford[1], M. Callens[5], F. De Smet[4,5], M. Van Ranst[4], M. Zeller[4], J. Matthijnssens[4] *[1]Yale School of Public Health, USA, [2]Fogarty International Center, National Institutes of Health, USA, [3]University of Antwerp, Belgium, [4]KU Leuven - University of Leuven, Belgium, [5]National Alliance of Christian Sickness Funds, Belgium*
16:50-17:10	**[O7.3] Ecological factors shaping the phylogeography of influenza** F. Wen*[1], T. Bedford[2], S. Cobey[1] *[1]University of Chicago, USA, [2]Fred Hutchinson Cancer Research Center, USA*	**[O8.3] Forecasting for decision-making: The Dengue Forecasting Project experience** M.A. Johansson*[1,2], J.P. Chretien[3], D.B. George[4] *[1]Centers for Disease Control and Prevention, USA, [2]Harvard TH Chan School of Public Health, USA, [3]Armed Forces Health Surveillance Center, USA, [4]White House Office of Science and Technology Policy, USA*	**[O9.3] The impact of vaccination programmes on mortality burden among children and young adults in the Netherlands over the 20th century** M. van Wijhe*[1,2], S. McDonald[1], H. de Melker[1], M.J. Postma[2], J. Wallinga[1] *[1]National Institute for Public Health and the Environment, The Netherlands, [2]University of Groningen, The Netherlands*
17:10-17:30	**[O7.4] Algorithms linking phylogenetic and transmission trees for molecular infectious disease epidemiology** E. Kenah*[1], T. Britton[2], M.E. Halloran[3,4], I.M. Longini[1] *[1]University of Florida, USA, [2]Stockholm University, Sweden, [3]Fred Hutchinson Cancer Research Center, USA, [4]University of Washington, USA*	**[O8.4] Dengue dynamics in rural Cambodia: Comparing hypothesis through epidemiologic mechanistic model selection** C. Champagne[1], D.G. Salthouse[1], S. Ly[2], V. Duong[2], P. Buchy[2], A. Tarantola[2], B. Cazelles*[1,3] *[1]IBENS, France, [2]Institut Pasteur du Cambodge, Cambodia, [3]UMMISCO, France*	**[O9.4] Accounting for response timing in the deployment of reactive oral cholera vaccines** C.M. Peak*[1], A. Hill[2], L. Ganda[3], D. Legros[2], C.O. Buckee[1] *[1]Harvard T.H. Chan School of Public Health, USA, [2]World Health Organization, Switzerland, [3]World Health Organization, Sierra Leone*
17:30-17:50	**[O7.5] Quantifying the effect of public health interventions on the spread of ebola virus disease using phylodynamic methods** L. du Plessis*, T. Stadler *ETH Zürich, Switzerland*	**[O8.5] Evidence for transmission enhancement in incidence patterns of dengue in Thailand** H.E. Clapham*[1], N. Reich[2], K. Sakrejda[2], I. Yoon[3], L. Macareo[3], A. Nisalak[3], J. Lessler[1], D.A.T. Cummings[1] *[1]Johns Hopkins School of Public Health, USA, [2]University of Massachusetts, USA, [3]AFRIMS, Thailand*	**[O9.5] Stopping silent polio circulation before stopping oral polio vaccine use** J.S. Koopman*, M.C. Eisenberg, C.J. Henry, J.H. Park, D.W. Hutton, J.N. Eisenberg, E.L. Ionides *University of Michigan, USA*
17:50-19:30	**Poster Session 1**		

Thursday, 3 December 2015			
Room			
08:30-09:10	**[PLN06] Evaluating interventions to reduce malaria transmission: the role of mathematical modelling to guide policy** A. Ghani, *Imperial College, UK*		
09:10-09:50	**[PLN07] Achieving the 2020 goals for neglected tropical diseases** D. Hollingsworth, *University of Warwick, UK*		
09:50-10:30	**[PLN08] What multi-level selection (and microcosm man) might tell us about the evolution of pathogens** P.B. Rainey[1], *[1]New Zealand Institute for Advanced Study, Massey University, New Zealand, [2]Max Planck Institute for Evolutionary Biology, Germany*		
10:30-11:00	**Refreshment Break**		
Rooms			
11:40-12:40	**Session 10: Ebola 1** *Session Chair:*	**Session 11: Phylodynamics 2** *Session Chair:*	**Session 12: Transm. Dynamics** *Session Chair:*
11:00-11:20	**[O10.1] Inferring the yellow fever force of infection from the observed age distribution of confirmed cases** T. Garske*[1], K. Jean[1], M.D. Van Kerkhove[1,2], S. Yactayo[3], W. Perea[3], J. Biey[4], A. Sall[5], C.A. Donnelly[1], N.M. Ferguson[1] *[1]Imperial College London, UK, [2]Institute Pasteur, France, [3]World Health Organization, Switzerland, [4]WHO-AFRO, Burkina Faso, [5]Institute Pasteur, Senegal*	**[O11.1] Phylodynamic inference of sexual contact network structure** D.A. Rasmussen*, T. Stadler *ETH Zurich, Switzerland*	**[O12.1] Evaluating spatial interaction models to regional mobility for directly transmitted and vector-borne disease dynamics** A. Wesolowski*[1], W. Prudhomme O'Meara[2], N. Eagle[1], A.J. Tatem[3], C.O. Buckee[1] *[1]Harvard School of Public Health, USA, [2]Duke University, USA, [3]University of Southampton, UK*
11:20-11:40	**[O10.2] The role of rapid diagnostics in managing Ebola epidemics** P. Nouvellet*[1], T. Garske[1], H. Mills[1], G. Nedjati-Gilani[1], W. Hinsley[1], I.M. Blake[1], M.D. Van Kerkhove[1,2], A. Cori[1], I. Dorigatti[1], T. Jombart[1] et al *[1]Imperial College London, UK, [2]Institute Pasteur, France*	**[O11.2] Identifying the effect of patient sharing on between-hospital genetic differentiation of methicillin-resistant *Staphylococcus aureus*** H-H. Chang*[1], J. Dordel[2,3], T. Donker[4], C. Worby[1], W.P. Hanage[1], S.D. Bentley[2], S.S. Huang[5], M. Lipsitch[1] *[1]Harvard T.H. Chan School of Public Health, USA, [2]The Wellcome Trust Sanger Institute, UK, [3]Drexel University, USA, [4]University of Groningen, The Netherlands, [5]University of California Irvine School of Medicine, USA*	**[O12.2] Chance and transmission in vector-borne diseases** S.P.C. Brand*, K.S. Rock, M.J. Keeling *University of Warwick, UK*
11:40-12:00	**[O10.3] Contact patterns driving Ebola transmission in West Africa** I.M. Blake[1], A. Cori*[1], H.L. Mills[1], W.H.O. Ebola response team[2] *[1]Imperial College London, UK, [2]World Health Organization, Switzerland*	**[O11.3] Testing degree distributions in HIV phylogenetic clusters** B.L. Dearlove*, F. Xiang, S.D.W. Frost *University of Cambridge, UK*	**[O12.3] Estimating the number of dengue transmission chains circulating in Bangkok using spatial and genetic data** H. Salje*[1,2], R. Jarman[4], J. Lessler[1], M. Melendrez[4], I. Maljkovic[4], A. Nisalak[3], L. Macareo[3], I-K. Yoon[3], D.A.T. Cummings[5] *[1]Johns Hopkins University, USA, [2]Institut Pasteur, France, [3]AFRIMS, Thailand, [4]Walter Read Army Institute of Research, USA, [5]University of Florida, USA*

12:00-12:20	**[O10.4] Characterizing epidemic growth patterns during the Ebola epidemic in West Africa** G. Chowell*[1,2], C. Viboud[2], J.M. Hyman[3], L. Simonsen[4] *[1]Georgia State University, USA, [2]National Institutes of Health, USA, [3]Tulane University, USA, [4]George Washington University, USA*	**[O11.4] Statistical inference of *Plasmodium falciparum* malaria transmission networks based jointly on epidemiological and genetic data** A. Perkins*[1], R. Nielsen[2], D. Smith[3,4], B. Greenhouse[5] *[1]University of Notre Dame, USA, [2]University of California, Berkeley, USA, [3]University of Oxford, UK, [4]Sanaria Institute for Global Health and Tropical Medicine, USA, [5]University of California, San Francisco, USA*	**[O12.4] The role of demography in shaping inter-country differences in epidemiological patterns of measles** F. Trentini*[1], P. Poletti[1,2], A. Melegaro[1] *[1]Bocconi University, Italy, [2]Bruno Kessler Foundation, Italy*
12:20-12:40	**[O10.5] Impact of spatial dispersion, evolution, and selection on Ebola Zaire Virus epidemic waves** T. Azarian[1], A. Lo Presti[2], M. Giovanetti[2], E. Cella[1,2], B. Rife[1], A. Lai[3], G. Zehender[3], M. Ciccozzi[2,4], M. Salemi*[1] *[1]University of Florida, Gainesville, USA, [2]Istituto Superiore di Sanità, Rome, Italy, [3]University of Milan, Milan, Italy, [4]University Hospital Campus Bio-Medico, Italy*	**[O11.5] Livestock disease transmission pattern inference using integrated phylodynamics** S. Lycett*[1], G. Russell[2], R. Zadoks[2,3], R. Kao[3] *[1]University of Edinburgh, UK, [2]Moredun Research Institute, UK, [3]University of Glasgow, UK*	**[O12.5] Opportunities for managing risks in the polio eradication endgame** K.M. Thompson*, R.J. Duintjer Tebbens *Kid Risk, Inc., USA*
12:40-14:00	**Lunch**		
Rooms			
14:00-16:00	**Session 13: Ebola 2** *Session Chair:*	**Session 14: Social structure** *Session Chair:*	**Session 15: Zoonoses & Vet.** *Session Chair:*
14:00-14:20	**[O13.1] Analysis of an Ebola vaccine trial using a ring vaccination design in Guinea, West Africa** N.E. Dean*, I.M. Longini *University of Florida, USA*	**[O14.1] Accurate epidemic predictions: how much social structure do we need?** L. Pellis*[1], S. Cauchemez[2], N.M. Ferguson[3], C. Fraser[3] *[1]University of Warwick, UK, [2]Institute Pasteur, France, [3]Imperial College London, UK*	**[O15.1] Pigs and pandemics: the evolutionary dynamics of influenza A viruses in swine** M.I. Nelson*[1], C. Viboud[1], P. Lemey[2], A.L. Vincent[3] *[1]National Institutes of Health, USA, [2]KU-Leuven University, Belgium, [3]United States Department of Health, USA*
14:20-14:40	**[O13.2] Measuring the impact of Ebola control measures in Sierra Leone** A.J. Kucharski*, A. Camacho, S. Flasche, R. Glover, W.J. Edmunds, S. Funk *London School of Hygiene & Tropical Medicine, UK*	**[O14.2] Forecasting seasonal influenza with dynamic models assimilating digital social data** Q. Zhang*[1], N. Perra[1], A. Vespignani[1,2] *[1]Northeastern University, USA, [2]ISI Foundation, Italy*	**[O15.2] A comparative and computational study of population structure and pathogen richness in bats** T.C.D. Lucas*, H.M. Wilkinson-Herbots, K.E. Jones *University College London, UK*

14:40-15:00	**[O13.3] Spatiotemporal spread of the 2014 Ebola epidemic in Liberia and the effectiveness of non-pharmaceutical interventions** S. Merler[1], M. Ajelli*[1], L. Fumanelli[1], M.F.C. Gomes[2], A. Pastore y Piontti[2], L. Rossi[3], D.L. Chao[4], I.M. Longini[5], M.E. Halloran[4,6], A. Vespignani[2,7] *[1]Bruno Kessler Foundation, Italy, [2]Northeastern University, USA, [3]Scientific Interchange Foundation, Italy, [4]Fred Hutchinson Cancer Research Center, USA, [5]University of Florida, USA, [6]University of Washington, USA, [7]Harvard University, USA*	**[O14.3] Estimating the contribution of asymptomatic infection using social contact data** E. Santermans*[1], K. Van Kerckhove[1], A. Azmon[2], K.T.D. Eames[3], P. Beutels[4], W.J. Edmunds[3], N. Hens[1,4] *[1]Hasselt University, Belgium, [2]Novartis Pharma AG, Switzerland, [3]London School of Hygiene & Tropical Medicine, UK, [4]University of Antwerp, Belgium*	**[O15.3] The multi-strain dynamics of avian influenza in live bird markets** A. Pinsent*[1], K.M. Pepin[2], M.T. White[1], H. Zhu[3,4], Y. Guan[3,4], S. Riley[1] *[1]Imperial College London, UK, [2]National Wildlife Research Center, USA, [3]Shantou University Medical College, China, [4]The University of Hong Kong, Hong Kong*
15:00-15:20	**[O13.4] Spatial analysis of Ebola virus outbreak in West Africa: transmission patterns within and between countries** J.A. Backer*, J. Wallinga *RIVM, The Netherlands*	**[O14.4] Estimating seasonal influenza dynamics with 2.7 billion geo-tagged tweets** T.J. Bodnar[1], M. Salathe*[1,2] *[1]Penn State University, USA, [2]EPFL, Switzerland*	**[O15.4] Host phylogenetic distance and viral host breadth predict zoonotic viral spillover from mammals** K.J. Olival*, P.R. Hosseini, T.L. Bogich et al *EcoHealth Alliance, USA*
15:20-15:40	**[O13.5] Evaluating classic epidemiological methods, mathematical modeling and phylodynamic analyses to infer the transmission dynamics of Ebola virus disease** C.L. Althaus*[1], R.R. Regoes[2], T. Stadler[2] *[1]University of Bern, Switzerland, [2]ETH Zurich, Switzerland*	**[O14.5] Tracking social contact networks with online respondent-driven detection** M.L. Stein*[1,2], P.G.M. van der Heijden[3,4], V. Buskens[3], J.E. van Steenbergen[2,5], L. Bengtsson[6,7], C.E. Koppeschaar[8], A. Thorson[6], M.E.E. Kretzschmar[1,2] *[1]University Medical Center Utrecht, The Netherlands, [2]National Institute for Public Health and the Environment, The Netherlands, [3]University Utrecht, The Netherlands, [4]University of Southampton, UK, [5]Leiden University Medical Centre, The Netherlands, [6]Karolinska Institutet, Sweden, [7]Flowminder Foundation, Sweden, [8]Science in Action BV, The Netherlands*	**[O15.5] Spread and control of enzootic cattle diseases: A data-driven multiscale modelling framework to prioritize complex regional strategies** P. Ezanno*[1], G. Beaunée[1,2], B.L. Dutta[1,2], P. Pandit[1], T. Hoch[1], F. Beaudeau[1], E. Vergu[2] *[1]LUNAM Université, France, [2]INRA, France*
15:40-16:00	**[O13.6] Detecting changes in community transmission of Ebola in Lofa County, Liberia** S. Funk*[1], B. Reeder[2], A. Camacho[1], R.M. Eggo[1], A.J. Kucharski[1], W.J. Edmunds[1] *[1]London School of Hygiene & Tropical Medicine, UK, [2]University of Saskatchewan, Canada*	**[O14.6] Socio-spatial human behaviour and the transmission of respiratory infections** J.M. Read*[1,2], H.L. Mills[3], J. Lessler[1], L.J. Tan[5], K.O. Kwok[6], Y. Guan[6,7], C.Q. Jiang[5], S. Riley[3] *[1]University of Liverpool, UK, [2]University of Lancaster, UK, [3]Imperial College, UK, [4]Johns Hopkins Bloomberg School of Public Health, USA, [5]Guangzhou Hospital Number 12, China, [6]Hong Kong University, Hong Kong, [7]Shantou University, China*	**[O15.6] Supershedders not so super? Linking supershedding to transmission for Escherichia coli O157:H7 in feedlot cattle** S.E.F. Spencer*[1], T.E. Besser[2], R. Cobbold[3], N.P. French[4] *[1]University of Warwick, UK, [2]Washington State University, USA, [3]University of Queensland, Australia, [4]Massey University, New Zealand*
16:00-16:20	**Refreshment Break**		

Rooms			
16:20-17:40	**Session 16: Ebola 3** *Session Chair:*	**Session 17: Statistical Methods 1** *Session Chair:*	**Session 18: Vaccination 2** *Session Chair:*
16:20-16:40	**[O16.1] The 2014 EVD outbreak in Pujehun, Sierra Leone: Insights for epidemic containment at the source** S. Parlamento[1], M. Ajelli*[1], D. Bome[2], A. Kebbi[2], E. Pisani[3], C. Frasson[3], G. Putoto[3], D. Carraro[3], S. Merler[1] *[1]Bruno Kessler Fundation, Italy, [2]Pujehun Hospital, Sierra Leone, [3]Doctors with Africa - CUAMM, Italy*	**[O17.1] A systematic Bayesian integration of epidemiological and genetic data** M.S.Y. Lau*[1], G.J. Gibson[2], G. Marion[3], G. Streftaris[2] *[1]Princeton University, USA, [2]Heriot-Watt University, UK, [3]BioSS, UK*	**[O18.1] Ethical tradeoffs between alternative vaccine trial designs during acute emerging epidemics: A quantitative simulation-based framework** S.E. Bellan*[1], J.R.C. Pulliam[2], R. van der Graaf[3], J. Dushoff[4], L.A. Meyers[1,5] *[1]The University of Texas at Austin, USA, [2]University of Florida, Gainesville, USA, [3]University Medical Center, Utrecht, The Netherlands, [4]McMaster University, Canada, [5]The Santa Fe Institute, USA*
16:40-17:00	**[O16.2] Estimating, evaluating, and visualizing uncertainty in the cost-effectiveness of quarantine policies for Ebola** N.G. Reich*[1], S. Cauchemez[2], J. Lessler[3] *[1]University of Massachusetts Amherst, USA, [2]Institut Pasteur, France, [3]Johns Hopkins Bloomberg School of Public Health, USA*	**[O17.2] Causal inference in infectious disease ecology** S. Cobey*, E. Baskerville *University of Chicago, USA*	**[O18.2] The public health impact and cost-effectiveness of malaria vaccine candidate RTS,S/AS01: A systematic comparison of predictions from four mathematical models** M.A. Penny[1,2], R. Verity*[3], C. Bever[4], C. Sauboin[5], K. Galactionova[1,2], S. Flasche[6], M.T. White[3], E.A. Wenger[4], N. Van de Velde[5], P. Pemberton-Ross[1,2] et al *[1]Swiss Tropical and Public Health Institute, Switzerland, [2]University of Basel, Switzerland, [3]Imperial College London, UK, [4]Institute for Disease Modelling, USA, [5]GSK Vaccines, Belgium, [6]London School of Hygiene and Tropical Medicine, UK, [7]PATH, USA, [8]Public Health England, UK, [9]WHO, Switzerland*
17:00-17:20	**[O16.3] Can we predict without explaining? Real-time modelling and forecasting of the Ebola outbreak in West Africa** A. Camacho*, A.J. Kucharski, R.M. Eggo, S. Funk, W.J. Edmunds *London School of Hygiene & Tropical Medicine, UK*	**[O17.2] Bayesian model selection for evaluation of epidemiological hypotheses: The epidemiology of *Escherichia coli* O157:H7 in feedlot cattle** P. Touloupou*, S.E.F. Spencer, B. Finkenstädt *University of Warwick, UK*	**[O18.2] Yellow fever vaccine impact in Africa: accounting for human herd immunity in the face of zoonotic transmission** K. Jean*[1], N.M. Ferguson[1], M.D. Van Kerkhove[2], S. Yactayo[3], W. Perea[3], J. Biey[4], M.E. Shibeshi[5], T. Garske[1] *[1]Imperial College London, UK, [2]Institut Pasteur, France, [3]WHO, Switzerland, [4]AFRO West Africa Inter-country Support Team, Burkina Faso, [5]AFRO Eastern and Southern Africa Inter-country Support Team, Zimbabwe*

17:20-17:40	**[O16.4] International spreading risk associated with the 2014 West African Ebola outbreak** M.F.C. Gomes[1], A. Pastore y Piontti[1], L. Rossi[2], D.L. Chao[3], M.E. Halloran[3], I.M. Longini[4], A. Vespignani*[1] *[1]Northeastern University, USA, [2]Institute for Scientific Interchange, Italy, [3]Fred Hutchinson Cancer Research Center, USA, [4]University of Florida, USA*	**[O17.4] Integrating multi-scale data into spatial and spatiotemporal models of disease incidence and risk** S.M. Moore*, A.S. Azman, J. Lessler *Johns Hopkins Bloomberg School of Public Health, USA*	**[O18.4] Estimating dengue vaccine efficacy in the presence of missing data in both outcome and covariates** Y. Meng*[1,2], Y. Yang[1,2], I. Longini[1,2] *[1]University of Florida, USA, [2]CSQUID, USA*
17:40-19:20	**Poster Session 2**		
19:30-22:00	**Conference Dinner – Ticket holders only**		
Friday, 4 December 2015			
Room			
08:30-09:10	**[PLN09] Niche partitioning in epidemiology: extensions of strain theory and empirical evidence** M. Pascual[1,2], *[1]University of Chicago, USA, [2]The Santa Fe Institute, USA*		
09:10-09:50	**[PLN10] TBC** Dirk Brockmann, *Robert Koch-Institute, Berlin, Germany*		
09:50-10:20	**Refreshment Break** | *Room:*		
Rooms			
10:20-12:00	**Session 19: Statistical Methods 2** *Session Chair:*	**Session 20: Vector Borne** *Session Chair:*	**Session 21: Emerging Infections** *Session Chair:*
10:20-10:40	**[O19.1] Estimating the severe outcome burden associated with influenza and the respiratory syncytial virus** E. Goldstein*[1], C. Viboud[2], W.P. Hanage[1], M. Lipsitch[1] *[1]Harvard TH Chan School of Public Health, USA, [2]National Institutes of Health, USA,*	**[O20.1] Effective control of dengue in Mexico by combining vaccines with vector reduction** T.J. Hladish*[1], C.A.B. Pearson[1], D.L. Chao[2], D.P. Rojas[1], G.L. Recchia[3], H. Gomez Dantes[4], M.E. Halloran[2], J.R.C. Pulliam[1], I.M. Longini[1,2] *[1]University of Florida, USA, [2]University of Washington, USA, [3]University of Cambridge, UK, [4]National Institute of Public Health, Mexico*	**[O21.1] Unravelling the key drivers of MERS-CoV transmission** S. Cauchemez*[1], P. Nouvellet[2], A. Cori[2], T. Jombart[2], T. Garske[2], H. Clapham[3], S. Moore[3], H. Mills[2], H. Salje[1,3], C. Collins[2] et al *[1]Institut Pasteur, France, [2]Imperial College, UK, [3]Johns Hopkins, USA, [4]Ministry of Health, Saudi Arabia*
10:40-11:00	**[O19.2] Transmission patterns of human cytomegalovirus uncovered by analysis of cross-sectional serological data** M. van Boven*, M.J. Korndewal, H.E. de Melker, J. van de Kassteele *National Institute for Public Health, The Netherlands*	**[O20.2] How hot is malaria? - open challenges in evaluating the impact of climate on the transmission of vector-borne disease** L.R. Johnson*[1], T. Ben-Horin[2], K.D. Lafferty[3,4], A. McNally[4], E. Mordecai[5], K.P. Paaijmans[6], S. Pawar[7], S.J. Ryan[8] *[1]University of South Florida, USA, [2]Rutgers University, USA, [3]U.S. Geological Survey, USA, [4]Univeristy of California Santa Barbara, USA, [5]Stanford University, USA, [6]Universitat de Barcelona, Spain, [7]Imperial College London, UK, [8]University of Florida, USA*	**[O21.2] Transmission characteristics of MERS and SARS in the healthcare setting: a comparative study** G. Chowell*[1,2], F. Abdirizak[1], S. Lee[3], J. Lee[4], E. Jung[4], H. Nishiura[5,6], C. Viboud[2] *[1]Georgia State University, USA, [2]National Institutes of Health, USA, [3]Kyung Hee University, Republic of Korea, [4]Konkuk University, Republic of Korea, [5]The University of Tokyo, Japan, [6]Japan Science and Technology Agency, Japan*

11:00-11:20	**[O19.3] Characterizing pandemic severity and transmissibility from FF100 data** A.J. Black[1], N. Geard[2], J.M. McCaw[2], J. McVernon[2], J.V. Ross*[1] *[1]The University of Adelaide, Australia, [2]The University of Melbourne, Australia*	**[O20.3] The performance of Wolbachia in Aedes aegypti in reducing human dengue cases: A two serotype model** M.Z. Ndii[1], D. Allingham[1], R.I. Hickson*[2], K. Glass[3] *[1]University of Newcastle, Australia, [2]IBM Research--Australia, Australia, [3]Australian National University, Australia*	**[O21.3] Quantifying spatiotemporal heterogeneity of MERS-CoV transmission in the Middle East region: a combined modeling approach** C. Poletto*[1], V. Colizza[1,2], P.Y. Boëlle[1] *[1]INSERM & UPMC, France, [2]ISI Foundation, Italy*
11:20-11:40	**[O19.4] Inference of reporting rate and variance of the offspring distribution from epidemiological and genetic data** L.M. Li*, N.C. Grassly, C. Fraser *Imperial College London, UK*	**[O20.4] Density-dependent population dynamics in *Aedes aegypti* mosquitoes alter the invasion dynamics of *Wolbachia* bacteria: implications for *Wolbachia* release strategies for dengue control** P.A. Hancock*[1], V.L. White[2], A.G. Callahan[2], H.C.J. Godfray[1], A.A. Hoffmann[2], S.A. Ritchie[3] *[1]University of Oxford, UK, [2]University of Melbourne, Australia, [3]James Cook University, Australia*	**[O21.4] A multi-pathogen hierarchical Bayesian spatio-temporal model for transmission of hand, foot, and mouth disease in China** X. Tang*, Y. Yang, N. Bliznyuk, I. Longini *University of Florida, USA*
11:40-12:00	**[O19.5] Assessing the role of different age groups, and of vaccination, during disease outbreaks using case reporting data** C.J. Worby*[1], C. Kenyon[2], R. Lynfield[2], S.S. Chaves[3], L. Finelli[3], J. Wallinga[4], M. Lipsitch[1], E. Goldstein[1] *[1]Harvard TH Chan School of Public Health, USA, [2]Minnesota Department of Health, USA, [3]Centers for Disease Control and Prevention, USA, [4]National Institute of Public Health and the Environment, The Netherlands*	**[O20.5] Modelling the role of host heterogeneity in Gambian human African trypanosomiasis** K.S. Rock*[1], S.J. Torr[2], M.J. Keeling[1] *[1]Warwick University, UK, [2]Liverpool School of Tropical Medicine, UK*	**[O21.5] Early-warning signals for emerging and re-emerging disease outbreaks** T.S. Brett*[1,2], P. Rohani[1] *[1]University of Michigan, USA, [2]University of Georgia, USA*
12:00:12:20	**Refreshment Break**		
Room			
12:20-13:00	**[PLN11] Epidemiology, ecology and rational risk assessment for pathogen emergence** J.O. Lloyd-Smith[1], *[1]UCLA, USA, [2]Fogarty International Center, National Institutes of Health, USA*		
13:00-13:20	**Close of Conference, Poster prize**		