

**Type: Poster Presentation**

Final Abstract Number: 52.031

Session: *Epidemiology and Public Health II*

Date: Friday, April 4, 2014

Time: 12:45–14:15

Room: Ballroom

**Analysis of a *Salmonella* Saintpaul outbreak using whole genome mapping**B. Pot<sup>1,\*</sup>, R. Burggrave<sup>2</sup>, P. Scheldeman<sup>1</sup>, T. Walker<sup>3</sup>, V. Sapiro<sup>3</sup>, K. Vranckx<sup>1</sup><sup>1</sup> Applied Maths NV, Sint-Martens-Latem, Belgium<sup>2</sup> Piext BV, Rosmalen, Netherlands<sup>3</sup> OpGen Inc., Gaithersburg, MD, USA

**Background:** During a foodborne outbreak of salmonellosis, it is critical to rapidly determine the serotype and discriminate outbreak- from non-associated strains. PFGE is widely used as the 'gold standard' for epidemiological analyses of *Salmonella*. Recently, it was shown that Whole Genome Mapping (WGM), a technique generating ordered restriction maps across entire microbial genomes, produced results equivalent to PFGE data for *Salmonella* (1). Here we investigated the capability of the OpGen<sup>®</sup> WGM technology in combination with the BioNumerics<sup>®</sup> Seven software to discriminate outbreak from non-outbreak related strains.

**Methods & Materials:** For a total of 37 *Salmonella* Saintpaul strains from a well-defined outbreak in alfalfa sprouts (2), WGMs were generated using the Argus<sup>™</sup> Whole Genome Mapping System (OpGen<sup>®</sup>), with the NcoI restriction enzyme. Overlapping single-molecule maps were assembled with a minimum of 30X coverage over any part of the genome, yielding highly accurate consensus WGMs. These maps were compared using the BioNumerics<sup>®</sup> Seven software (Applied Maths NV).

**Results:** Cluster analysis of the WGMs accurately identified outbreak isolates from a background of closely related isolates. Moreover, using the BioNumerics<sup>®</sup> automated search function, two WGM fragments of resp. 29,7 Kb and 2,6 Kb were identified as putatively unique to the group of outbreak isolates.

WGM has a significant value as epidemiological analysis tool for the real-time investigations of foodborne *Salmonella* outbreaks. WGM often provides a higher level of discrimination and resolution than PFGE, SPA typing, or ribotyping, can detect novel genomic changes, is highly reproducible, and data can be correlated directly with the DNA sequence. The rapid analysis time is less than 24 hrs. The identification of outbreak related fragments could speed up the development of specific PCR tests used in a large scale screening of possible outbreak substrates.

**Conclusion:** Together, OpGen<sup>®</sup> WGM technology and the new analysis tools of the BioNumerics<sup>®</sup> Seven software allow the construction of large reference databases that can be used for the comparison of new isolates to historical strains and allow to perform directed data mining on aligned fragments.

<http://dx.doi.org/10.1016/j.ijid.2014.03.948>**Type: Poster Presentation**

Final Abstract Number: 52.032

Session: *Epidemiology and Public Health II*

Date: Friday, April 4, 2014

Time: 12:45–14:15

Room: Ballroom

**Spatial analysis of cholera outbreak in Egbeda local government area of Oyo State, Nigeria, June, 2013**A.O. Gbolahan<sup>1,\*</sup>, W.A. Abass<sup>1</sup>, P. Adewuyi<sup>2</sup>, O.B. Olawoyin<sup>1</sup><sup>1</sup> Oyo State Ministry of Health, Ibadan, Nigeria<sup>2</sup> Nigerian Field Epidemiology Training Program, Ibadan, Nigeria

**Background:** The spatial distribution of cases for infectious diseases that are environmentally driven, such as those of water-borne and vector-borne transmission, reflect the combined effect of an environmental heterogeneity and disease dynamics. As such, spatial patterns can be used to examine hypotheses on route of transmission of diseases. GIS was employed to determine the relationship that exists in the spatial pattern of cholera outbreak in Egbeda LGA, Oyo state and also the spatial pattern of the predisposing factors in the area.

**Methods & Materials:** Descriptive cross sectional survey was conducted and spatial data was collected using Global Positioning System (GPS). The spatial location of cases was also confronted against the spatial location of water sources. Stool and water samples were collected to confirm the outbreak. Data on predisposing factors like their sources of drinking water, toilet facilities, dump site and the only available Primary Health Care facility in the study area were also collected.

**Results:** Spatial clustering of cholera cases were detected at different temporal and spatial scales. Cases relative to water sources also exhibit spatial clustering. Stool samples and water samples were positive for *Vibrio cholerae*. 97 (80 percent) out of 122 houses surveyed had no toilet facilities. Most of the houses constructed shallow and uncovered wells.

**Conclusion:** The clustering of cases support an important role of secondary transmission in the dynamics of cholera epidemics in Egbeda LGA of Oyo state. The spatial clustering of cases relative to water sources suggests an effective role of water reservoirs during the onset of cholera outbreak. The contaminated well was sealed off, other wells were chlorinated, needs for standard toilet facilities was emphasized and health education was done on improved personal hygiene for the community members.

<http://dx.doi.org/10.1016/j.ijid.2014.03.949>