Breakout Group Questions:

~Workgroup #1: Water Sampling Methods for Enteric Pathogens

In this WG we would like to address two major questions regarding the collection of the water sample to be analyzed for enteric pathogens:

Q1: Where do we stand at as a community in water sampling?

- What are the available collection methods?
- What are the advantages and disadvantages of each methods?
- What is needed to validate the methods? Is Validation needed?
- What is available for method sharing?
- Are there any modifications needed for the existing water sampling methods to make them specific for Whole Genome Sequencing?

Q2: What is a universal sampling design for a water sampling study?

- Sampling strategies (statistical support);
- Minimum set of metadata collection for cross comparison;
- What other parameters need to be recorded during water collection (physical/chemical properties of the water)?

Q3: What else should we be discussing, what have we overlooked?

~Workgroup #2: Laboratory Methods Improvements, and Genomics

In this WG we would like to address three major questions regarding the methods used to isolate the enteric pathogens and subsequently sequence their genomes:

Where do we stand at a valid/universal workflow for multiple enteric pathogen detection?

- What are the available water sampling method?
- What are the methods used by collection method and by enteric pathogen?
- What are the available universal enrichment broth to capture diverse set of enterica pathogens?
- Do you use rapid methods after enrichments? What are the methods available?
- What about whole genome sequencing? In-house or out sourcing? Any bioinformatics support? Limitations?
- What other rapid methods are on the horizon?

How to enhance the sensitivity/specificity/inclusivity of our method

- Any observation on enrichment bias? How do you overcome enrichment bias?
- Were there any methods that you tried to enhance the sensitivity/specificity/inclusivity that did not work or ones worked very well? Cross-comparison?
- CRISPR-SeroSeq?
- Metagenomics vs. Quasi-metagenomics?

Hurdles, difficulties, and barriers

- Bioinformatics difficulties: collection of bioinformatic tools
- Toward method validation; prohibitive cost
- Sharing of the laboratory methods
- Training on the bioinformatics tools

What else should be discussed, and what would you like to see at the future meeting to keep this working group together?

~Workgroup #3: Global Opportunities and Challenges Surrounding Water Sampling

In this WG we would like to discuss the geo-political barriers, possible solutions and funding opportunities for water sampling with food safety endpoints.

- (1) What are some of the barriers or challenges that environmental microbiologists around the world face when conducting studies involving water sampling and pathogen surveillance? Can these barriers be prioritized?
- (2) Which challenges/barriers are common across geopolitical boundaries?
- (3) Which challenges/barriers are unique to specific countries and what are some examples from different countries?
- (4) How can these specific challenges be mitigated from a global perspective?
- (5) What opportunities exist to support specific scientific efforts in various countries?
- (6) What partnerships can be formed to support mutual efforts in this area of microbiology?
- (7) What scientific boundaries are predominant to the environmental microbiologist in different countries? (ie) (1) access to samples; (2) access to microbiology tools such as genome sequencing instrumentation; (3) bioinformatics support; (4) wet lab support.