

International Conference on

## ENVIRONMENTAL MICROBIOLOGY AND MICROBIAL ECOLOGY

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International Conference on

## ECOLOGY AND ECOSYSTEMS

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**Functional interaction of plant and its microbiome: What are these bacteria doing?****Shimaila Ali**

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Determination of functional genetics of corn microbial community can lead us to find the factors involved in higher corn productivity. Functions imparted to host plants by the microbial community include disease control by production of antibiotics, lytic enzymes, and siderophores and stimulation of host defenses. Many microorganisms can modulate plant hormonal levels by production of indoleacetic acid, ethylene, cytokinins, gibberellins, etc. We developed and standardized protocols for the quantitation of seven different functions in corn microbial community, which include nitrogen fixation (*nif*), phosphate solubilization (*pqqC*), antibiotic production (*srffA* and *fenD* mainly from *Bacillus* sp., *phlD* and *phzF* mainly from *Pseudomonas* sp.), and production of hydrogen cyanide (*hcnAB*). The functional genes were quantified in microbial community DNA extracted from roots, stem, and rhizospheric soil of corn grown in fields selected by aerial infrared photography and identified as having high or average productivity within the same fields. In almost all samples, the abundance of functional genes was directly related to high corn productivity. However, the richness in functional gene(s) in the microbial population associated with corn was not the only factor that correlated with productivity.

**Biography**

Shimaila Ali graduated with her doctorate from the University of Waterloo. Her research was based on the isolation and characterization of new plant growth-promoting bacterial endophytes. She has worked on identifying how endophytic bacteria impact plant growth and development using both physiological approaches as well as bioinformatics. Dr. Ali has developed identified a small number of proteins predicted to be key elements of endophytic colonization of plants by bacteria. She joined A & L Biologicals in 2014 as NSERC post-doctoral research scientist, where she is leading a part of a research project on functional metagenomic analysis of corn microbiome for identifying main drivers responsible for improved corn yields and other plant productivity.

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