Abstract:

Tomato (*Lycopersicon esculentum*) considered as one of the most important required vegetables in worldwide, with a global annual yield of over 100 million tons. Tomato production is affected by different bacterial and fungal infection with a leading bacterial infection caused by *Ralstonia solanacearum* causing a disease known as tomato wilt, in which bacteria invade and extensively colonialize in the vascular tissues blocking water conducting xylem. The main aim of the current study is to screen and to monitor the quantitative abundance of microbiome and fungal organisms in soil and plant parts collected from different tomato green houses. The central methodology of microbiome and fungal evaluation that was used in this study was based on adapting next generation sequencing (NGS) or what is called high throughput DNA sequencing method. This method is relatively new technology that allows mass sequencing and enables the production of a vast array of genomic information from many organisms in parallel and it is provides a separate quantitative counting measurement for each sequenced DNA segment type. Universal primers that amplify the 16S rRNA gene for bacterial species and the internal transcribed spacer ITS region of fungal pathogens were used and the product was sequenced by NGS technology.

The study was performed after collection of tomato plants and soil samples from 7 different greenhouses located in Jenin district over a period of four months starting from October 2017 to late December 2018. Over the collection period a total of 6 collection time points were conducted and in each visit 3 plant samples and 3 soil samples were collected from each growing green house. At the end of the samples collection period, a total of 252 of soil and plant samples were collected. For each collected sample DNA extraction was done, followed by microbiome and fungal DNA fragment amplification using specific primers adapted to be used later in Illumina

MiSeq DNA sequence analysis. The total 252 collected samples were pooled according to their samples nature, green house origin and visit time to form the 85 pooled MiSeq DNA library used in NGS analysis. A total of 170 FASTQ files were produced that consists of paired (read 1 and read 2) for each individual sample. All files were uploaded on Galaxy platform program (usegalaxy.org) and quality filtered. A workflow for sequence analysis that was based on sequence length and selection of fungi unique sequences was applied to analyzed samples after joining the relevant read1 and read2 from each specific amplicon.

The specific microbiome species that were identified in this study were considered from plant pathogenic bacteria, most important identified species are *Ralstonia, Erwina, Pseudomonas, Stenotrophomonas,* and *Achromobacter*. These species are of soil origin and causing different diseases in tomato plant, most important is *Ralstonia* bacterial species that cause tomato wilt disease. The used primers for specific fungi identification were less successful and low numbers of reads were obtained. The main plant pathogen fungi that was identified in both soil and plant leaves was *Alternaria tenuissima,* with some other plant pathogenic fungi species such as *Candida sake, Yarrowia lipolytica, Wickerhamiell apararugosa,* and others.

Different evidence were discussed that support the assumption of the soil being a source of infection since many of the identified pathogens are of soil origin and there was a type of association between microbiome finding in plant and soil samples.