Under FSMA the tree fruit industry is required to validate on-site sanitizing wash water systems, but food safety issues limit using actual pathogens for testing. Therefore, we hypothesize that the native microbiome present on tree fruits can be utilized as surrogates to validate sanitization. Currently, the tree fruit microbiome is limited particularly throughout a growing season, thus we are first establishing the microbiome of three types of tree fruits, apples (pome), peaches (stone), and navel oranges (citrus) with the goal of establishing an on-site validation bacterial index. Fruits were harvested during the early, middle, and late part of the growing season and rinsed with a solution (0.15 M NaCl, 0.1% Tween 20) to remove bacteria. To differentiate between viable and total community composition, we treated half the rinsate with propidium monoazide, which removed ‘relic’ DNA from non-viable cells. The other half was untreated and represented the total community. DNA was extracted from both rinsate samples and 16S rRNA gene sequencing was performed using two different sets of barcoded primers, 799F – 1115R (chloroplast excluding) and 515F – 926R. Barcoded amplicons were sequenced on an Illumina MiSeq, and the UPARSE pipeline used for operational taxonomic units (OTUs) and QIIME calculated alpha and beta diversity metrics. Taxonomy was assigned using the RDP classifier against the GreenGenes database. Analysis of total DNA (viable cells and relic DNA) demonstrated that peaches have the highest amount of bacterial diversity followed by oranges, then apples. We observed significant shifts in overall bacterial community composition during the growing season regardless of fruit type. Additionally, the overall bacterial community composition for each tree fruit type was unique. However, among the viable community, Planococcaceae, Sphingomonas sp., and Bacillus flexus, among others, were consistently present on all fruits, and these taxa represent potential surrogates for on-site validating tree fruit sanitizing systems.
**Introduction:** Under FSMA the tree fruit industry is required to validate on-site sanitizing wash water systems, but food safety issues limit using actual foodborne pathogens for testing. Therefore, we hypothesize that the native microbiome present on tree fruits can be utilized as surrogates to validate sanitization.

**Purpose:** Currently, tree fruit microbiome data is limited, particularly throughout a growing season, thus we are establishing the microbiome of three tree fruit types, apples (pome), peaches (stone), and navel oranges (citrus) with the goal of establishing an on-site validation bacterial index.

**Methods:** Fruits were harvested during the early, middle, and late parts of the growing season and rinsed with a solution (0.15 M NaCl, 0.1% Tween 20) to remove bacteria. Viable and total community composition were differentiated by treating half the rinsate with propidium monoazide, which removed ‘relic’ DNA from non-viable cells, and the untreated other half represented the total community. DNA was extracted from both rinsate samples, and 16S rRNA gene sequencing was performed using two sets of barcoded primers, 799F – 1115R (chloroplast excluding) and 515F – 926R. Barcoded amplicons were sequenced on an Illumina MiSeq, and the UPARSE pipeline used for operational taxonomic units (OTUs), QIIME calculated alpha and beta diversity metrics, and taxonomy assigned using the RDP classifier against the GreenGenes database.

**Results:** Total DNA (viable cells and relic DNA) analysis demonstrated that peaches have the highest amount of bacterial diversity followed by oranges, then apples. We observed significant shifts in overall bacterial community composition during the growing season regardless of fruit type. Additionally, the overall bacterial community composition for each tree fruit type was unique.

**Significance:** Among the viable communities, *Planococcaceae*, *Sphingomonas* sp., *Bacillus flexus*, and several other types of bacteria, were consistently present on all fruits, and these taxa represent potential surrogates for on-site validating tree fruit sanitizing systems.