## Comparison of two gene targets for the prevalence of *Cyclospora cayetanensis* in Irrigation Waters from US Southwest Fresh Produce Growing Regions

Hannah Martinez<sup>1</sup>, Khai Truong<sup>1</sup>, Dominic Rodriguez, Cesily Cirerol<sup>1</sup>, Miely A. Suarez<sup>1</sup>, Ximena German<sup>1</sup>, Avril Perez<sup>1</sup>, Chloe Wilcox<sup>1</sup>, Alyssa M. Gregory<sup>1</sup>, Leila C. Yazzie<sup>2</sup>, Scarlett Leon<sup>1</sup>, Jessica Cruz<sup>1</sup>, Celina Arredondo<sup>1</sup>, and Gerardo U. Lopez<sup>1</sup>, Ph.D.\*

University of Arizona, College of Agriculture, Life, and Environmental Sciences, <sup>1</sup>School of Animal & Comparative Biomedical Sciences; <sup>2</sup>School of Plant Sciences Tucson, AZ

Cyclospora cayetanensis is a parasitic, human-specific foodborne illness that causes diarrhea, vomiting, nausea, and fatigue. Steadily, domestic cases of cyclosporiasis are on the rise in the United States. C. cayetanensis infection occurs by indirect fecal-oral transmission, where unsporulated oocysts are shed into the environment, then subsequently the sporulated oocysts contaminate fresh produce. The present study is determining the prevalence of C. cayetanensis oocysts in water and fomites. Water samples from endemic regions were processed using the FDA's BAM 19c protocol, where ten liters of irrigation waters were collected via Dead-End Ultrafiltration (Hollow fiber ultrafilter Rexeed-25S; Asahi Kasei Medical Co.). Subsequently, samples were sieved (100 um, 70 um, and 40 um) and concentrated prior to DNA isolation and quantitative polymerase chain reaction (qPCR). Two different gene targets were used when determining the prevalence of C. cavetanensis oocysts as the Mit1C was recently developed to replace the 18S rRNA due to concerns with cross-reactivity with Eimeria. Preliminary data indicates 166/279 samples processed, with positive results from the 18S rRNA target coming from water (14/20) and fomites (6/20). Currently, 10 of the 20 18S rRNA positive samples were negative with the Mit1C. Further analysis will proceed to downstream sequencing with the Oxford Nanopore MinION to determine the sensitivity and specificity of both gene targets in a water matrix. This would provide an insight on the validity of Mit1C in irrigation waters in comparison to the 18S rRNA. Furthermore, identification of C. cayetanensis oocysts in agricultural waters could aid in epidemiological investigations of cyclosporiasis outbreaks as possible environmental reservoirs could be determined. In addition, knowing the source of contamination in fresh produce growing regions could lead to future preventative measures.