EVAN LAU, MARCUS KINKER, ZACHARY DILLARD, DANIEL LUKICH, KATYLN YAUCH, NICOLE MIHALIK, and EDWARD NOLAN, Department of Natural Sciences and Mathematics, West Liberty University, West Liberty, WV, 26074**. Survey of microbial community in the gut of three healthy and one celiac individuals**.

The human microbiome is composed of the symbiotic, commensalistic, and pathogenic bacteria that live on and in different sites of the human body. Recent studies on the human microbiome has provided insights into its implications for human health and physiology. Several recent studies have examined the relationship between human behavior (such has diet) on the microbiome. Other studies have tried to discern the association between human genome and microbiome on human health, focusing on conditions such as Irritable Bowel Disease and Celiac Disease, diet and gut microbiome. In this study, DNA samples were extracted from fecal samples of three healthy individuals and one with Celiac Disease. Microbial diversity and abundance was analyzed using multiplex sequencing targeting the V4-V5 region of the 16S rDNA gene. Bioinformatics analysis of the gut microbial community of the three individuals were determined to genus level taxonomic distinction. Further phylogenetic and statistical analyses of selected show similarities and differences between the microbiota of Celiac and non-Celiac subjects.